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# 2014 SACNAS

## NATIONAL CONFERENCE

### RESEARCH PRESENTATION ABSTRACTS

*Creativity, Vision & Drive: Towards Full Representation in STEM*

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# Abstract Review Process

The SACNAS Student Presentations Committee organizes activities related to the student scientific sessions. These sessions advance the organization's strategic efforts to support students' preparation for their professional science careers and, more specifically, the demanding rigors of discipline-focused professional conferences. Our goal is to provide a fair, positive, and nourishing experience to students through the abstract review, presentation mentoring and judging, and awards-selection processes. Accordingly, our abstract selection and scientific presentation evaluation processes are focused on constructive, student-professional engagement and mentoring. We feel this dialogue between students and scientists is invaluable in providing experience, insight, and professional growth for emerging scientists, mathematicians, and engineers.

Students and mentors alike respond positively to our efforts. This year, more than 1,400 abstracts were submitted for the 2014 SACNAS National Conference. Professionals recruited from our membership generously and enthusiastically volunteer their time and energy to reviewer abstracts. Reviewers provide a fair and unbiased appraisal of the abstract's quality in the overall score, and also give each student constructive feedback and suggested improvements. Each abstract is reviewed by at least two experts in this manner, similar to evaluations in traditional scientific societies. Student abstracts are evaluated according to the following criteria, and given a numerical score:

- Clarity—the research topic and motive are easily identified
- Communication—language and style are appropriate for a general scientific audience
- Scientific Essentials—the purpose or goal of the study, project methods and analyses, results (or predictions), and impact/value are present and easily identified

As the size of the Student Presentations effort has grown considerably, we are limited in the number of presentations we are able accommodate at the National Conference. We are unable to accept abstracts scoring less than 60% in the review process. However, as a testament to the quality of the submissions from students, this year our acceptance rate is nearly 89%.

At the conference, all student presentations are offered with no scheduling conflict to promote attendance and interaction with our presenters. We coordinate the efforts of our volunteer judges who preside over oral presentations, visit numerous posters, and provide a mentoring experience through their critical, yet constructive, interaction with the students. The Student Presentations Committee is indebted to the hundreds of professionals who graciously and tirelessly volunteer as judges on site—without their sharing of our vision, our efforts at the conference could never be as successful as they are.

Sincerely,  
2014 SACNAS Student Presentations Committee



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SACNAS appreciates the many dedicated individuals who work to mentor and develop the next generation of SACNAS talent.

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# Undergraduate Poster Abstracts

## BIO/AGR/ENV LIFE SCIENCES ANIMAL SCIENCES

### SAT-726

#### IMPROVEMENT OF BONE HISTOTECHNOLOGY FOR LARGE ANIMAL MODEL SYSTEMS

Diamond Stevens, Matthew Wheeler.

*University of Illinois at Urbana-Champaign, Urbana, IL.*

Developing tissue engineering implants for use in addressing severe bone injuries requires studies to be completed in large-animal model systems, such as swine, before testing in human clinical trials can be considered. Use of large animals for bone tissue studies is complicated by the need to use harsh chemical agents to decalcify the bone. The goal of this work is to determine which decalcifying agent treatment gives the best combination of sectioning, histochemical staining, and immunostaining competence in swine radius bone specimens. The three decalcifying agents chosen were 5% trifluoroacetic acid (TFA), 5% nitric acid (HNO<sub>3</sub>), and CalciClear Rapid. This study will help us develop better experiments using swine as a model for tissue engineering studies.

### FRI-716

#### URINALYSIS OF FERAL AND DOMESTIC FELINES IN SOLANO COUNTY

Marissa Bass, Jose Ballesteros.

*Solano Community College, Fairfield, CA.*

For this study, students of Solano Community College, MESA Student Society (MSS), evaluated the urine of feral and domestic felines. All urine samples were donated by the Solano County SPCA and were marked as feral or domestic in origin. The feral and domestic urine samples were evaluated using Solid Gold pH testing, pHHydriion, and Siemens multistix urinalysis sticks. We hypothesize the test results will reflect differences between feral and domestic feline urine due to differences in nutrition. Because feral felines consume more protein in their diet such as mice, birds, and bugs, we believe their test results will differ from domestic felines who would be fed wet/dry feline food. This diet leads to greater levels of protein in the urine in the case of feral felines. Another difference is pH. Domestic feline urine pH ranges from 6.5 to 7.5, whereas the pH of feral felines can be significantly higher. We are currently testing new samples and hope to correlate our findings with our hypothesis.

**FRI-725****POPULATION VARIATION IN OVIDUCT RETENTION AND ESTROGEN SENSITIVITY IN MALE AFRICAN CLAWED FROGS (*XENOPUS LAEVIS*)**

Flor Gowans, Tyrone Hayes, Faye Pon, Alejandra Cabrera, Cara He, Rupali Sood, Xuan (Susan) Luong.

*University of California, Berkeley, Berkeley, CA.*

The herbicide atrazine is an endocrine disruptor that reduces androgen production and increases estrogen production. In *Xenopus laevis*, estrogens are important for the induction and maintenance of oviducts. The purpose of the current study is to understand how different populations vary in estrogen sensitivity. In the current study (n = 900), we investigated estrogen sensitivity in developing males and females between two populations of *Xenopus laevis*. In one group (population1), male frogs retain their oviducts, whereas males in the other group (population 2) do not. We examined the role of estrogen in developing oviduct tissues by exposing frogs to exogenous estrogen (estradiol), atrazine (which increases estrogen production), an inhibitor of estrogen synthesis (miconazole), or an estrogen receptor antagonist (tamoxifen). Estradiol and atrazine were expected to cause retention and hypertrophy of the oviducts. Miconazole and tamoxifen were expected to block estrogen action thus inhibiting oviduct retention. For both populations, we analyzed animals at three time points: metamorphosis, six months post metamorphosis, and nine months post metamorphosis. At time point 1, estradiol feminized males based on the presence of ovaries: 93% females in population 1 and 86% females in population 2. Atrazine resulted in 61% females in population 2, but 50% in population 1. Miconazole appeared to result in masculinization with only 37% females in population 1, but with a female bias, 62%, in population 2. Tamoxifen appeared to masculinize animals: 41% and 36% females in populations 1 and 2 respectively. Ongoing genotype analysis will reveal whether exposed animals were truly sex reversed in these studies.

**FRI-726****USING NUCLEAR AND MITOCHONDRIAL DNA TO IDENTIFY CAPTIVE *CROCODYLUS RHOMBIFER* INDIVIDUALS IN ZOOLOGICAL INSTITUTIONS**

Mia Perkins<sup>1</sup>, Lou Densmore<sup>2</sup>.

<sup>1</sup>*South Plains College, Levelland, TX,* <sup>2</sup>*Texas Tech University, Lubbock, TX.*

*Crocodylus rhombifer* (Cuban Crocodile) is considered to be endangered due to anthropogenic effects such as habitat loss and alteration, hunting, and competition with introduced species. Their survival depends on being able to differentiate between purebred *C. rhombifer* and hybrids. Institutions interested in the management and conservation of this particular species rely on genetic screenings that weed out genetically compromised crocodiles through the examination of nuclear DNA (nDNA) and mitochondrial DNA (mtDNA). Nuclear DNA coincides with classical Mendelian inheritance in that there is information from both the male and female parents, unlike mtDNA which adheres to matrilineality. Separately, both pieces of genetic information only partially illuminate a specimen's genetic lineage, especially when hybridized individuals are being considered. Using both mtDNA and nDNA can provide a much more accurate view of an individual's genetic background. The accuracy of this information is crucial

when screening or considering candidates for breeding and eventually reintroduction programs; only purebred individuals should be used to ensure the success of such programs. Our main objective is to use this information to facilitate the identification of purebred *C. rhombifer* for breeding programs and hopefully the eventual reintroduction of populations in areas where the species has been locally extirpated.

#### **SAT-725**

##### **PHYSIOLOGICAL CORRELATES OF REPRODUCTIVE STATE AND AGGRESSION ACROSS SEASONS IN FEMALE SIBERIAN HAMSTERS (*PHODOPUS SUNGORUS*)**

Andrea Amez, Gregory Demas, Nikki Rendon.

*Indiana University, Bloomington, IN.*

Seasonally breeding animals undergo marked physiological and behavioral responses to changing photoperiods, including changes in reproduction and aggression. Aggression is an adaptive behavior important for dictating which animals gain access to limited resources and which do not. Photoperiod is a cue used to predict change in seasons well in advance. Siberian hamsters use photoperiod as their primary cue, becoming reproductively inactive and displaying increased aggression during short winter-like days (SD) and remaining reproductively active and displaying significantly decreased aggression during long summer-like days (LD). Aggression expressed during a period of reproductive inactivity when reproductive physiology is collapsed suggests that aggression is inversely related to reproductive function. However, after prolonged exposure to SDs, animals become insensitive to SDs and gonadally recrudescence, re-growing their gonads and becoming reproductively active despite persistence in SDs. The goal of this study was to use gonadal changes to separate the effects of photoperiod and reproductive state on aggression, estradiol levels, and brain estrogen receptors. Our data show that LD and gonadally recrudescenced females were indistinguishable in both levels of aggression and estradiol compared with gonadally regressed females, suggesting that reproductive state predicts changes in aggression. Work is under way to measure estrogen receptor alpha cell counts in behaviorally relevant brain regions and will be coupled with behavioral and hormonal measures to further examine the interactions of photoperiod and reproductive state with respect to aggression. This study expands our understanding of the physiological mechanisms underlying aggression and animal response to environmental changes across the seasons.

#### **BIOCHEMISTRY/BIOPHYSICS**

#### **SAT-310**

##### **SPLIT - GFP AS A TOOL FOR MEMBRANE PROTEIN EXPRESSION**

Anthony Jones<sup>1</sup>, William Clemons<sup>2</sup>.

<sup>1</sup>*California State University Dominguez Hills, Carson, CA*, <sup>2</sup>*California Institute of Technology, Pasadena, CA.*

Green fluorescent protein (GFP) has been a powerful and versatile tool in biochemistry. It has been used to study membrane proteins, allowing researchers to quantify expression and determine topology. While the use of GFP has facilitated higher throughput membrane protein

expression tests, it has several key limitations. We have observed that expression studies of TatC membrane proteins that use a whole GFP reporter result in large amounts of soluble GFP observable by western blot assays. Because fluorescence from TatC-GFP fusion proteins and soluble GFP cannot be distinguished, the usefulness of GFP as a reporter in measuring TatC expression is limited. Our ongoing research seeks to determine if a split GFP reporter will provide greater utility for testing membrane protein expression. The split GFP reporter involves fusing the final beta strand from GFP to a membrane protein and separately expressing a full-length GFP molecule truncated to the final beta strand. The two components of the GFP can interact to yield a functional GFP molecule. Fluorescence is expected to increase with membrane protein expression because more of the final GFP beta strand will be present to interact with the truncated GFP. Split GFP, however, has only been used in membrane protein topology studies for the purpose of mapping the N- or C-terminus of a particular protein. The aim of our studies is to develop a method in which split GFP can be used for the quantification of membrane protein expressed by a cell without the production of background GFP.

### **SAT-301**

#### **THE ROLE OF TRANSALDOLASE IN GLUCOSE METABOLISM IN *ACIDOBACTERIUM CAPSULATUM*: CLONING PUTATIVE TRANSALDOLASE GENES AND DETERMINATION OF TRANSALDOLASE ACTIVITY IN CELL LYSATES**

Hollie Wall, Pariss Trujillo, Amanda Broad, Leslie Sommerville.  
*Fort Lewis College, Durango, CO.*

*Acidobacterium capsulatum*, a mildly acidophilic and chemotrophic aerobe with the ability to grow on glucose, is found in diverse soil and aquatic conditions worldwide, suggesting a significant role in carbon and nutrient cycling in the environment. *A. capsulatum* has been successfully cultured and its genome completed, allowing for genome-directed studies of the organism's glucose metabolizing capabilities. Based on the genomic information, this organism may lack the enzyme aldolase, thereby blocking the traditional glycolytic pathway for glucose metabolism. However, there are two putative transaldolase genes annotated in the genome, suggesting these enzymes may play a critical role in regulating the flux of glucose between biomass formation and energy production. To test this hypothesis, enzyme assays on whole cell lysates and cloning of the putative transaldolase genes are being done to characterize transaldolase enzyme activity from *A. capsulatum*. Cell lysis is accomplished by lysozyme digestion, freeze-thawing, and bead beating. Preliminary cell lysate results show that we can obtain active enzymes, but we are currently in the process of establishing an appropriate transaldolase assay. One of two putative transaldolase genes has been amplified, cloned into a pET151 directional TOPO expression vector, and transformed into *E. coli*. Experiments to determine whether the transaldolase gene can be expressed are in progress. Further experiments will establish transaldolase activity in cell lysates and characterize the cloned and purified enzyme. The evidence from these studies will allow a better understanding of the role of transaldolase as a mediator between energy production and biomass formation in *A. capsulatum*.

**SAT-329****BIOPHYSICAL CHARACTERIZATION OF H3 AND H4 FROM *C. ELEGANS***

Andrea Coleman, Raymond Esquerra.

*San Francisco State University, San Francisco, CA.*

Chromatin, a key component of the chromosome structure, contains an entire coil of DNA that is constructively packaged around a histone octamer, organizing the various nucleosome structures that sequence repetitively to compose the nucleosome core particle. Four major classes of histones are responsible for this octameric formation: H2A, H2B, H3, and H4. The composition of the nucleoprotein structure determines the overall gene expression and replication of a cell. Differences in nucleosome structure play fundamental roles in cell differentiation and in the progression of a variety of diseases. We are interested in understanding how the overall structure of histones influences gene expression. The goal of this project interrogates the stability of H3 and H4 histones in their monomeric and tetrameric states. We hypothesize that the H3-H4 tetrameric structure will be more stable chemically and thermodynamically than the isolated H3 and H4 histones in their monomeric states. These histones are expressed in bacteria and purified through chromatography. We will monitor the chemical and thermodynamic stability of each protein using far-UV circular dichroism spectroscopy. This work will help to uncouple the energetics and overall stability associated with the incorporation of H3 and H4 in the H3/H4 tetramer.

**FRI-327****EXPLORING THE FOLDING PATHWAYS OF SMALL HELICAL POLYPEPTIDES USING MULTISCALE STRING METHOD**

Patrick Morgan<sup>1</sup>, Jeremy Tempkin<sup>2</sup>, Aaron Dinner<sup>2</sup>, Edward Dean<sup>2</sup>.

<sup>1</sup>*DePaul University, Chicago, IL*, <sup>2</sup>*University of Chicago, Chicago, IL*.

Biochemists and biophysicists have extensively investigated protein folding for years because the misfolding of proteins causes diseases such as Parkinson's, Alzheimer's, and Huntington's. Proteins must fold into their native three dimensional confirmation in order to function properly. Studying the folding of small helical polypeptides allows us to study the formation of secondary structures computationally. The goal of this study is to explore the minimum energy pathway (MEP) transitions between important metastable states in the folding of small alpha-helical polypeptides. Calculations of these intermediate energetic barriers yield information on the kinetics of small polypeptide folding. An algorithm known as the multiscale string method was used to calculate the MEP. The multiscale string method is a formalism for accelerating the convergence of the string method by preconditioning a relatively expensive calculation with a relatively cheaper model. To accelerate the string calculations, an all atom protein model was preconditioned with a simplified plastic network model (PNM). We observed that the multiscale string method allowed us to explore the MEP transitions between important metastable states.

**SAT-326****MOLECULAR INTERACTION OF STYRENE MONOOXYGENASE WITH ARYLALLENES AS SUBSTRATES**

Gabriel Cabrera Dorantes, George Gassner.

*San Francisco State University, San Francisco, CA.*

Organisms such as *Pseudomonas putida* have evolved to metabolize styrene from their environment through the enzyme styrene monooxygenase. The enzymatic degradation of styrene-like compounds by styrene monooxygenases could have important biosynthetic applications as antitumor antibiotic compounds. In this study, we observed the interactions among Buta-2,3-dien-2-ylbenzene, propa-1,2-propa-1-ylbenzene, terminally histidine tagged styrene monooxygenase (NSMOA), and four variants having increased and decreased hydrophobic active site volume. The allenes were used as substrates in SMOA and reduced coenzyme FAD. Stop flow experiments were done using the allenes and the reaction rates of reduction and oxidation were evaluated; enzymatic products were collected and evaluated via NMR and mass spectrometry. The target molecules in this study are similar to naturally occurring sesquiterpenes Illudin M and S, which have been shown to have potential antitumor properties.

**SAT-323****EXPRESSION AND PURIFICATION OF PROPERLY FOLDED *PSEUDO-NITZSCHIA* PRENYLTRANSFERASES: A PRECURSOR TO DOMOIC ACID**

Michael Flores, Thomas Savage.

*California State University Sacramento, Sacramento, CA.*

Domoic acid (DA) is a neurotoxin synthesized by the marine diatom *Pseudo-nitzschia australis*, which accumulates in fish, causing harm to humans and high mortality rates in other vertebrates. DA accumulates in high concentration during algal blooms, which may be influenced by anthropogenic factors. It is undetermined what and how environmental signals stimulate DA biosynthesis. Geranyl diphosphate has been identified as a precursor to DA. It is determined that DA biosynthetic enzymes that catalyze the formation of geranyl diphosphate are homologous to enzymes (e.g., prenyltransferases) catalyzing similar reactions. Here, we are trying to identify conditions that allow for proper folding and functional testing of *E. coli*-expressed prenyltransferases. Transformed *E. coli* were cultured, inoculated, then induced using IPTG (isopropyl- $\beta$ -D-thiogalactopyranoside). Cells were then isolated and lysed using lysozyme and sonication. Proteins were obtained by centrifugation. Ni-agarose affinity chromatography was used to isolate the expressed protein. SDS-PAGE analysis was used to confirm the isolation of the properly folded protein. Functional testing of the prenyltransferase can help determine geranyl diphosphate production during the biosynthesis of DA. Determining the biosynthetic pathway of DA production will help us to understand what environmental factors influence the production of DA.

### SAT-312

#### DOMAIN STRUCTURE OF BACTERIAL RED LIGHT PHOTORECEPTORS AS REVEALED BY ATOMIC FORCE MICROSCOPY

Rima Rebiai, Zain Malik, Marie Kroeger, Emina A. Stojkovic, Stefan Tsonchev, Kenneth Nicholson.

*Northeastern Illinois University, Chicago, IL.*

Bacteriophytochromes (BphPs) are red light photoreceptors found in photosynthetic and non-photosynthetic bacteria. These photoreceptors are responsible for perceiving light and initiating an important physiological response to optimize growth and development of bacteria. Structural characterization of these proteins may also play an essential role in the engineering of infrared fluorescent tissue markers. The goal of this research is to determine the structure of intact BphPs from non-photosynthetic *Stigmatella aurantiaca* (SaBphP2) and photosynthetic *Rhodospseudomonas palustris* (RpBphP3). Both P2 and P3 are composed of a light sensing module linked to a histidine kinase signaling effector domain. A biliverdin chromophore is covalently bound to the light-sensing module. Upon absorption of a photon, both photoreceptors photoconvert and undergo global conformational changes initiated at a covalently bound biliverdin chromophore. Intact BphPs are very challenging to crystallize, especially in the light-adapted state for X-ray crystallography and are too large for analysis by nuclear magnetic resonance. Therefore, atomic force microscopy (AFM) has been employed to characterize the structure of these BphPs in a biologically relevant media. Using peakforce quantitative nanomechanical mapping (PF-QNM), multiple orientations of P2 and P3 have been observed on mica and compared to models of intact BphPs generated using existing X-ray crystallography of similar truncated photoreceptors in the dark-adapted state using PyMOL software. The cross-sectional analysis and total volume measurements of the dimers are in close agreement with the models. AFM experiments are currently underway to analyze the dark-adapted state of BphPs in order to observe the anticipated structural changes.

### SAT-304

#### DOES V-ATPASE RECRUIT THE EGO COMPLEX TO THE VACUOLAR MEMBRANE

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Vacuolar Proton ATPase (V-ATPase) is a membrane protein complex, present in all eukaryotic cells, that hydrolyzes ATP to pump protons into organelles against a concentration gradient. Our long-term goal is to understand how V-ATPase affects pH physiology and diverse signaling pathways. V-ATPase activity is necessary for activation of the target of rapamycin complex 1 (TORC1), which is a major regulator of cell growth. However, the mechanism by which V-ATPase activates TORC1 is unknown. We use budding yeast as a model system to study the V-ATPase-TORC1 axis. The Ego complex, which includes Ego1 and Ego3, is part of a super complex present on the vacuolar membrane that includes V-ATPase, TORC1, and other possible proteins. We have shown that in a V-ATPase mutant (*vma3D*), Ego3 expression is reduced at the vacuolar membrane. We hypothesize that V-ATPase controls TORC1 activity through Ego3 by recruiting



Ego3 to the vacuolar membrane and stabilizing the Ego complex. To test this idea, we asked whether Ego3 is present in vacuolar membranes from wild-type cells and several V-ATPase mutant strains that cannot assemble the V-ATPase complex or assemble inactive V-ATPases because they lack a structural V-ATPase gene. We have added antigenic tags to Ego3 in wild type and V-ATPase mutant strains that will allow us to detect Ego3. Immunoprecipitations will be used to determine if there is binding between the V-ATPase and Ego3.

#### **SAT-320**

##### **FUNCTIONAL ANALYSIS OF INDUCED LOCUS-SPECIFIC MUTATIONS OF LIN9 PROTEIN IN MUVB COMPLEX**

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The LIN9 protein is one of the components of the multi-vulval class B (MuvB) complex which is responsible for repression of most if not all cell cycle gene expression during quiescence. Despite fruitful biochemical analyses of the MuvB complex, the LIN9 protein remains largely uncharacterized. One aspect of LIN9 that has been annotated is its central tudor domain, which is a plausible starting point to characterize LIN9. Tudor domains are generally responsible for protein-protein interactions, leading to the hypothesis that the LIN9 tudor domain mediates protein interactions within the MuvB complex and is necessary for complex formation. LIN9's tudor domain's direct involvement in protein interactions in MuvB complex can be checked through observing the overall ability of the mutant LIN9 proteins to bind with the four other main proteins (LIN37, LIN52, LIN54, and RBBP48) of the MuvB complex through immunoprecipitation assays. This can be achieved by inducing six locus-specific mutations (L230A, L237A, L272A, F238A, F256A, and R229E/R231E) within the tudor domain of the LIN9 protein, via PCR (Polymerase Chain Reaction) with specifically-designed primers, cloning these mutant constructs into mammalian cell vector, and transfecting these vectors into T98G mammalian cells. Further understanding of the roles played by LIN9's tudor domain and these specific LIN9 mutants in their interaction with the rest of the MuvB complex and how they affect the MuvB complex's ability to repress cell cycle gene expression can help advance both cancer research and development of tumor suppression treatments.

#### **FRI-320**

##### **LONGER LOOPS OF PSEUDOKNOTS WITH APPROPRIATE SEQUENCE FORM LOCAL TRIPLEX SEGMENTS THAT STABILIZE DNA MOLECULES**

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Pseudoknots have been found to play significant roles in RNA function such as ribosomal frameshifting. The presence of local triplex segments on their terminal stems may enhance its stability and the efficiency of ribosomal frameshifting. Previous research has shown a loop-length dependence on pseudoknot stability and triplex formation. Our laboratory investigated the

unfolding of a pair of pseudoknots with sequence: d(TCTCTT<sub>n</sub>-AAAAAAGAGAT<sub>5</sub>TTTTTTT), where T<sub>n</sub> (n= 5 or 9) and T<sub>5</sub> are thymine loops. It was demonstrated that the pseudoknot with the longer T<sub>9</sub> loop was more stable due to the formation of three T<sup>\*</sup>A·T triplets. In this work, we used a combination of UV spectroscopy and differential scanning calorimetry to determine standard thermodynamic profiles for the unfolding of two sets of pseudoknots with sequences: d(TCTCTLoop5AAAGAGAAGAGAT<sub>5</sub>TCTCTTT), d(TCTCTLoop5AAAAAGAAGAGAT<sub>5</sub>TCTTTTT), d(TCTCTLoop9AAAGAGAAGAGAT<sub>5</sub>TCTCTTT), and d(TCTCTLoop9AAAAAGAAGAGAT<sub>5</sub>TCTTTTT); where Loop5 corresponds to a TCTCT or TCTTT loop, and Loop9 is a TCTCTTTTT or TCTTTTTTT loop; T<sub>5</sub> is the second loop of 5 thymines. The sequences under investigation will give more insight into whether or not more stable triplexes are actually forming due to the replacement of 1 and 2 T<sup>\*</sup>A·T->C<sup>+</sup>\*G·C base-triplet substitutions in the pseudoknots with the longer loops. Furthermore, the cytosine needs to be protonated in the formation of a stable C<sup>+</sup>\*G·C triplet. Therefore, we expect the formation of more stable triplexes at lower pHs. The overall thermodynamic results will be discussed in terms of the specific contributions of these base-triplets. (Supported by National Science Foundation grant MCB-1122029 and U.S. Department of Education GAANN grant P200A120231 (C.R.).)

#### **FRI-326**

#### **IDENTIFICATION OF MORGANA PROTEIN INTERACTORS IMPORTANT IN CELL DIVISION**

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Cancer is a disease caused by abnormal cells with the capacity to undergo many cycles of cell division. Understanding cell division, and more specifically how different proteins coordinate the formation of the mitotic spindle, is necessary because inhibition of spindle function may be a potential way to stop the proliferation of cancer cells. The protein morgana is involved in the assembly of the mitotic spindle and has been linked to centrosome amplification. Centrosome amplification increases errors in chromosome segregation and can potentially give rise to malignant cells. Morgana has been shown to have protein-protein interactions with Hsp90, ROCK1 and ROCK2, yet very little is known about their role during mitosis. This study aims to further characterize morgana's role in cell division by identifying the proteins that interact with it during mitosis. To identify Morgana interactors, a stable cell line expressing LAP-tagged (localization and affinity purification tagged) morgana was generated. The LAP-tagged protein complexes were purified by tandem-affinity purification and new morgana interactors were identified by mass spectrometry, including BUB3 and MAP 1B. To verify these interactions, we are immunoprecipitating morgana from cell extracts and using Morgana antibodies and immunoblotting for BUB3 and MAP 1B. Since these new interactors are involved in mitotic spindle assembly, it suggests that morgana has an important role in promoting proper cell division. In the future, we will probe the significance of these interactions to further understand cancer proliferation.

**FRI-307****ANALYSIS OF THE ROLE OF A RABGAP IN CYTOKINESIS**

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Vesicular membrane trafficking is important for many critical cellular processes such as protein biosynthesis and secretion, nutrient uptake via endocytosis, and cell expansion. In plants, cytokinesis is primarily accomplished by the targeted delivery of membrane and cell wall materials necessary for the assembly of the cell plate, an organelle that forms the new cell wall and plasma membrane separating daughter cells. Membrane trafficking during cytokinesis and cell expansion is a highly regulated process partially controlled by the Rab protein family. Rabs are small GTPases required for many trafficking roles such as targeting and vesicle fusion through interactions with a myriad of Rab effector proteins. Rab GTPases are themselves regulated by Rab guanine nucleotide exchange factors (GEFs) and Rab guanine nucleotide activating proteins (GAPs), which promote the conversion of Rabs to their active (GTP-bound) and inactive (GDP-bound) forms, respectively. A mutant screen for defects in stomatal guard cell cytokinesis identified two genes, *Stomatal Cytokinesis Defective 1 & 2 (SCD1/SCD2)*, that encode subunits of a RabGEF complex that regulates RabE1-dependent vesicular trafficking pathway(s) required for cell plate formation and cell expansion. A subsequent screen for suppressors of the *scd1-1* mutant phenotype identified a gene (*At2g30710*) encoding a putative RabGAP. Here, we investigate the role of this RabGAP in membrane trafficking via biochemical and genetic techniques, including elucidation of RabGAP-cognate Rabs via binding assays and phenotypic characterization of RabGAP knock-out mutants, respectively. These data will help identify pathways involving RabGAP function and any relation to *SCD1/SCD2* mediation of vesicular trafficking.

**SAT-324****INVESTIGATION OF PLK1 FUNCTION BY MASS SPECTROMETRY-BASED PROTEOMICS**

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Mitosis is a crucial step of the cell, in which a cell divides into two identical daughter cells. Faithful mitosis is essential for cellular survival and errors in this process lead to birth defects and cancer. Mitosis is tightly regulated through the interplay of many proteins, including protein kinases. Protein kinases are enzymes that modify other proteins by adding a phosphate group to serine, threonine, or tyrosine residues, a process called protein phosphorylation. Polo-like kinase 1 (Plk1) is a protein kinase that regulates many steps of mitosis from entry to exit and is often amplified in cancer. Besides its kinase domain, Plk1 contains a substrate recognition domain, the polo-box domain (PBD) that binds to phosphorylated residues on Plk1 substrates. Upon binding, Plk1 phosphorylates its substrates at specific sites. Mutation of essential residues within the PBD abolishes Plk1 subcellular localization and substrate recognition in cells. Using purified Plk1 and naturally-derived peptide libraries, we have determined Plk1 activity and substrate preferences in the absence of phosphorylation-

dependent substrate priming by mass spectrometry-based proteomics. We hypothesize that substrate priming is essential for Plk1 phosphorylation in cells, but not *in vitro*. To test this, we will purify wild-type, PBD mutant, and kinase-dead Plk1 and will compare their activity and substrate preferences *in vitro* by mass spectrometry-based proteomics. We predict that wild-type and PBD-mutant Plk1 have comparable kinase activities and substrate preferences, while kinase-dead Plk1 has reduced or no kinase activity. These experiments will provide insight into Plk1 substrate recognition, mechanisms, and function.

#### **FRI-315**

##### **EFFECTS OF POLYGLUTAMINE EXPANSION IN MYOGLOBIN: A COMPUTATIONAL STUDY TO ELUCIDATE POLYQ DISEASE MECHANISMS**

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Polyglutamine diseases are a group of at least nine genetic diseases produced by a tri-nucleotide expansion leading to longer poly glutatimine (polyQ) expansions in the expressed proteins. Their common phenotype shows progressive neurodegeneration and loss of coordinative and cognitive abilities. The molecular pathogenic mechanisms leading to their symptoms are unclear, but existing evidence indicates that the polyQ expansion destabilizes proteins and causes a pathological function. There are very few experimental studies on these proteins, and it is our hypothesis that modern computational studies can provide important insights. This study seeks to assess and quantify the effects of location and length of polyQ expansion on the structure of a protein, not associated with these diseases but for which experimental data exists, to provide independent validation of our studies in other proteins for which no experimental data exists. We used these computational tools: I-TASSER for 3D structure prediction, University of California, San Francisco chimera for 3D structure comparison, DSSP (dissecting sequence similarity scores) for secondary structure prediction, and University of California, Berkeley weblogo for secondary structure comparison. The preliminary results show that there are noticeable structural changes in the mutated proteins that can be correlated to the experimental findings.

#### **FRI-329**

##### **DETERMINING HOW THE DISTAL POCKET ENVIRONMENT MODULATES THE CHEMISTRY BETWEEN HEME PROTEINS AND HYDROGEN SULFIDE**

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Hydrogen sulfide, once known only as a toxic gas, is a recently discovered gasotransmitter that is involved in many processes in the mammalian body including the vascular system. Hydrogen sulfide binds to a variety of heme proteins and can trigger a variety of reactions. These reactions include 1) forming a stable heme-H<sub>2</sub>S moiety, 2) reducing the iron in the heme complex, and 3) facilitating the oxidation of the pyrrole ring of the heme resulting in a sulfheme complex. The reaction of heme and H<sub>2</sub>S depends on environmental factors including

concentration of H<sub>2</sub>S, pH, and exposure to oxygen. Although different heme proteins have different propensities for these reactions, how the distal environment modulates these chemistries is poorly understood. The goal of this project is to determine how the distal pocket environment controls these reactions with the hypothesis that polar environments and large pockets promote the reduction and the formation of sulfheme. Wild-type and distal mutant myoglobins were exposed to hydrogen sulfide under a range of conditions and then analyzed using time-resolved spectroscopy. These data were used to determine how the distal pocket environment impacted the reactions of hydrogen sulfide with the heme. This work will promote understanding of the molecular factors that modulate the differential chemistries of hydrogen sulfide with heme proteins.

#### **SAT-307**

##### **LIPID NANOTECHNOLOGY FOR STRUCTURAL STUDY OF THE TENASE COMPLEX**

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Coagulation proteins factor VIII (FVIII) and factor IX (FIX) play crucial roles in the blood coagulation pathway as they are the key components of the membrane-bound tenase complex, responsible for normal blood coagulation. Deficiencies or defects of FVIII or FIX lead to severe bleeding disorders known as hemophilia A or B, respectively. On another hand, elevated activity of these proteins increases the risk of developing thrombosis. The lack of structural information on tenase complex assembly during blood coagulation hampers the discovery of new effective drugs against blood disorders such as hemophilia and thrombosis. Nanodiscs (NDs) are stable lipid bilayer nanoparticles which can mimic successfully the activated platelet surface required for the tenase complex assembly and function. In this study, we investigate the structural organization of the tenase complex *in vitro* as assembled on NDs. The ND-tenase complex assembly's monodispersity and size have been optimized and monitored by transmission electron microscopy (TEM) followed by single-particle analysis and 3D reconstruction of tenase complex on the ND's surface. We have optimized a procedure that yielded the assembly of a homogenous population of NDs with 12 ± 1 nm diameter. The ND-tenase complexes were visualized by TEM, and the acquired images are suitable for further SPA and 3D reconstruction of the ND-tenase complex. Knowing the 3D organization of the membrane-bound tenase complex is essential to advance the discovery of important functional sites on the FVIII and FIX molecules which can be targeted for improving existing and designing novel therapeutic interventions against both hemophilia and thrombosis.

**FRI-323****SYNTHESIS AND PURIFICATION OF BAFF-R TO UNDERSTAND SPECIFIC INTERACTIONS WITH ITS RNA APTAMER**

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B cell activating factor (BAFF) is a cell survival and maturation factor for B cells. BAFF-R was found to be the predominant BAFF receptor expressed on peripheral B cells in both humans and mice. Elevated levels of BAFF and BAFF-R have been tied to the occurrence of non-Hodgkin's lymphoma. An RNA aptamer, which binds specifically to BAFF-R, has been identified and shown to be capable of delivering therapeutic siRNA. In this study, we addressed the problem of finding an optimized procedure for expression and purification of the BAFF-R protein in *Escherichia coli*. SDS PAGE was then done in order to detect BAFF-R protein. Once this procedure is optimized, we plan to study the binding between the aptamer and BAFF-R using structure probing and gel shift assays. Understanding the specific interactions between BAFF-R and its aptamer allows us to increase specificity, making this a more plausible therapeutic approach to treating non-Hodgkin's lymphoma.

**FRI-302****CLINICAL MUTATION PROLINE-21 AS A STRUCTURE-FUNCTION PROBE OF SRY, THE MALE DETERMINING TRANSCRIPTION FACTOR**

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The mammalian Y chromosome encodes male-determining factor SRY (sex-determining region on the Y chromosome), the transcription factor that initiates male development. SRY contains a high mobility group (HMG) box domain, required for specific DNA binding and bending. The structure of the HMG box domain contains three  $\alpha$ -helices separated by loops, a structurally conserved domain among an entire family of transcription factors. Clinical mutations in SRY are associated with sex-reversal, which can be genetically sub-grouped. Characterization of these mutations elucidates the molecular functions governing this developmental pathway. We exploit a proline mutation in an  $\alpha$ -helix, clinically identified as probe of the structure-function relationship in the HMG box. The amino acid proline typically attenuates helices, hence its designation as an  $\alpha$ -helical "breaker". However, this mutation, an Arg (R) to Pro (P) in the first helix of the HMG box of SRY, is tolerated. Furthermore, initial DNA binding studies suggest that this mutation does not detrimentally affect DNA binding. Therefore, we sought to further characterize this mutation, focusing on various facets of HMG box structure and function. To do this, our primary methods are spectroscopic related and include intrinsic tryptophan fluorescence, circular dichroism, and fluorescence energy resonance transfer (FRET). Similar to previously characterized inherited mutations, the R21P mutant displays a variety of moderate defects in a broad range of HMG box functions such as conformation, secondary structure, and DNA binding and bending.

**FRI-318****INVESTIGATION OF HALM2 ACTIVATION BY THE ALLOSTERIC EFFECTOR, LANA LEADER PEPTIDE**

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Lanthipeptides are ribosomally produced and postrationally modified peptides characterized by thioether cross-linkages. An understanding of the enzyme-catalyzed biosynthesis of lanthipeptides could allow for the production of more potent drugs. The biosynthesis of haloduracin, a two-component lantibiotic, was studied to elucidate the molecular recognition of the precursor peptides HalA1 and HalA2 by their respective lanthipeptide synthetases HalM1 and HalM2. HalM2 and HalA2 were over-expressed and purified with affinity and gel filtration chromatography. Matrix-assisted laser desorption ionization (MALDI) and SDS PAGE were used to confirm over-expression and purity. HalM2 and peptides containing a fluorescein derivative were subjected to fluorescence polarization assays to obtain the binding-dissociation constants. The dissociation constants were obtained for HalA2 (1.5  $\mu$ M), HalA2 leader sequence (3.7  $\mu$ M), and HalA2 core sequence (85  $\mu$ M). Understanding the molecular interactions that occur between the lanthipeptide biosynthetic machinery and its substrates will allow for the development of new antimicrobial agents.

**SAT-308****LYSINE-SPECIFIC CROSS-LINKING LEADS TO IMPAIRMENT OF LIPID BINDING OF RAT APOLIPOPROTEIN E**

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Apolipoprotein E (apoE) is a plasma protein that transports cholesterol and other lipids between various cells and serves as a ligand for the low density lipoprotein receptors (LDLr) family of proteins. It is considered an anti-atherogenic protein that plays a key role in cardiovascular disease. ApoE is 299 amino acids long with an N-terminal domain that houses the LDLr-binding site and a C-terminal domain that bears high lipid binding affinity and is also responsible for apoE tetramerization. We hypothesize that cross-linking of apoE will alter its ability to dissociate and bind lipids. Specifically, we investigated the mechanism of binding by following the effect of dimethyl suberimidate (DMS) dihydrochloride, a lysine-specific cross-linker, on the ability of rat apoE to bind lipids. Rat apoE was over-expressed in *Escherichia coli* and purified by affinity chromatography. ApoE was cross-linked at different molar excess ratios with DMS followed by SDS-PAGE analysis which revealed formation of dimers, trimers, and tetramers. Subsequently, the ability of apoE to bind lipids was followed in a turbidimetric assay which involves conversion of multi lamellar phospholipid vesicles (~200 nm diameter) to discoidal complexes composed of a bilayer of phospholipids and apoE (~20 nm diameter). In the presence of 100-fold molar excess of DMS, the rate of binding of apoE to phospholipid vesicles decreased by ~34%, suggesting that cross-linking impairs its ability to bind lipids. The significance of this data is that lipid binding of apoE likely involves dissociation of a tetramer to either a monomer or dimer which is inhibited by cross-linking.

**FRI-306****INVESTIGATION OF MEMBRANE PROTEIN STRUCTURE FROM NMR DATA USING ARIA**

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Determining the structure of membrane proteins has long been difficult, despite their high degree of biological significance. While new techniques in nuclear magnetic resonance (NMR) have made it possible to determine the structure of these proteins in their native environments, structures published using these methods have presented unusual architectures. This is highlighted by published structures of two different homo-oligomeric membrane proteins: diacyl glycerol kinase (DAGK) of *E. coli* and the p7 ion channel of the hepatitis C virus, both determined using NMR in a lipid micelle environment. These structures from NMR in micelles differ from other published structures of these proteins and do not resemble structures of similar proteins deposited in the Protein Data Bank (PDB). The goal of this project was to determine whether the unusual architectures seen in these proteins are truly a result of the micelle environment and collected NMR data or artifacts from calculation methods used. This was done by utilizing a novel method for determining the structure of oligomeric proteins from NMR data developed in the lab and using the program ARIA. This calculation method, known as the strict-symmetry method, has been shown to work successfully with other homo-oligomeric proteins. By using this method, it will be possible to determine the reliability of solution NMR in micelles as a method to determine membrane protein structure and to assess the validity of the DAGK and p7 published structures.

**FRI-312****LOSS OF AGR QUORUM SENSING AND VIRULENCE FUNCTION LEADS TO EARLY GROWTH ADVANTAGE IN *STAPHYLOCOCCUS AUREUS* INFECTION**

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*Staphylococcus aureus* infections present frequently to the emergency department and regularly cause significant tissue damage and systemic bacteremia. Between resistance to most available antibiotics and the failure of all anti-virulence vaccine trials to date, novel therapies are crucial to successfully combat this infection. Previous studies show that accessory gene regulation (*agr*) quorum sensing is an important virulence regulation pathway that mediates hundreds of genes enhancing infectivity and exacerbating disease. However, natural *agr*-deletion mutants ( $\Delta$ *agr*) have been isolated from hospitalized patients, suggesting that the loss of *agr* may have a selection advantage in some situations. We hypothesize that *agr* mutants will have a competitive growth advantage in immunocompromised patients compared to *agr*-competent strains. We have measured competitive growth of each strain following neutrophil exposure by comparing survival of  $\Delta$ *agr* versus wild-type strains in normal or antimicrobial-defense inhibited neutrophils. In addition, the effect of pharmacological inhibition (via Savirin)



of the agr system on strain viability has been analyzed. We have confirmed the defect in neutrophil lysis by  $\Delta$ agr strains and show that there is a small decrease in bacterial killing within the first 30 minutes. After this, the kinetics of bacterial viability are similar. Using Savirin in abscess fluids taken from patients infected with *S. aureus*, we have identified an initial increase in bacterial viability followed by a decrease in surviving bacteria. This suggests that the regulation of bacterial virulence by agr quorum sensing has a more complex effect on bacterial survival of host immune system defenses than previously thought.

#### **FRI-321**

##### **THE USE OF A HUMAN BRAIN CDNA LIBRARY TO IDENTIFY PROTEINS THAT INHIBIT A $\beta$ 42 AMYLOID PLAQUE FORMATION**

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Amyloid Beta 42 (A $\beta$ 42) is an amyloidogenic protein that is naturally expressed in the human brain. Similar to other amyloid proteins, A $\beta$ 42 possesses the ability to misfold into insoluble fibrillar aggregates, leading to the formation of amyloid plaque which is found in the brains of the majority of those afflicted with Alzheimer's disease. This amyloid plaque is believed to be responsible for neuronal cell death, resulting in the neurodegenerative symptoms associated with the disease. Increasing evidence suggests that inhibiting the aggregation of A $\beta$ 42 could provide an effective treatment in the slowing of or preventing altogether the onset of this disease. Utilizing an *in vivo* screen based on the enzyme enhanced green fluorescent protein (EGFP), a cDNA library containing all of the genes present in a healthy human brain were scanned to identify proteins capable of naturally interacting with and potentially preventing A $\beta$ 42 aggregation. From this initial screen, several candidate genes were selected and sent for DNA sequencing to determine the identity of the protein. Further experimental methods will be employed to characterize and analyze the ability of these proteins to prevent the toxic aggregation of amyloidogenic A $\beta$ 42.

#### **SAT-317**

##### **CHARACTERIZATION OF THE CALCIUM-BINDING PROPERTIES OF ARRHYTHMOGENIC CALMODULIN MUTANTS AND THEIR INTERACTION WITH THE CARDIAC RYANODINE RECEPTOR PEPTIDE**

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Calmodulin (CaM) is a vital Ca<sup>2+</sup> sensor within the eukaryotic cell. It plays a key role in the modulation of the many calcium-regulated cellular processes by interacting with effector and regulator proteins. CaM is encoded by 3 non-allelic genes in the human genome, *CALM1-3*, and is greatly conserved among vertebrates. Recently, a number of mutations have been identified in the *CALM* genes to cause severe cardiac arrhythmias. Two missense mutations (N53I and N97S) in *CALM1* have been shown to cause symptoms similar to catecholaminergic polymorphic ventricular tachycardia, or CPVT, which is characterized by sudden cardiac arrest and/or

syncope upon physical exertion or acute emotion. An additional 3 mutations, also missense and arrhythmogenic (*F141L-CALM1*, *D129G-CALM1*, and *D95V-CALM2*), have been associated with long-QT syndrome (LQTS), which causes a prolonged QT interval. In this study, we will characterize the calcium-binding properties of the CPVT and LQTS disease mutations using both steady-state and kinetic analyses with intrinsic and extrinsic fluorescent probes. In addition, we will determine the effect of target peptide binding on the  $\text{Ca}^{2+}$  affinity of the disease mutants using the CaM-binding domain of the cardiac ryanodine receptor (RyR2), a calcium release channel modulated by CaM. Wild-type CaM inhibits RyR2 release of calcium from the sarcoplasmic reticulum, the main calcium-storage site within the cardiomyocyte, which is crucial for normal rhythmic heart contraction. Being able to understand the behavior of these CaMs and their interaction with RyR2 may lead to development of targeted therapies for patients suffering from these heart conditions.

#### **SAT-306**

##### **TRYPTOPHAN FLOURESCENCE MEASURING PROTEIN DYNAMIC ACTIVATIONS OF THE LOV DOMAIN EL222**

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Light-oxygen-voltage (LOV) domains are signaling modules found in photosensory proteins across Eukarya, Archea, and Bacteria. The engineered LOV domain EL222 presents itself as a possible genetic tool for controlled gene transcription with rapid activation (<10 s) and deactivation (<50 s) protein kinetics, making it suitable for optogenetic control. Upon photoillumination (~450 nm) EL222 forms a cysteine-flavin covalent adduct, a mechanical response within the protein leading to a dissociation of LOV domain's  $\beta$ -sheet surface interacting with the  $\alpha$  helix of the helix-turn-helix (HTH) domain. Prior molecular dynamic simulations lead us to believe that these interactions between the N-terminal cap and C-terminal  $\alpha$  linker can be significantly altered by mutating the glutamine 138 in the  $\beta$ -sheet of the core EL222. These structural changes were monitored by expressing EL222 in *E. coli*, purified using affinity chromatography, and tryptophan as an endogenous fluorescent marker for Foster resonance energy transfer (FRET). Our data demonstrate that tryptophan is capable of measuring timing differences in the protein's photocycle and unfolding kinetics, further showing that EL222's ability to undergo DNA binding is delayed (<1 s). We present a possible addition to EL222's optogenetic utility, thus broadening its application as a powerful light-gated gene encryption tool.

#### **FRI-309**

##### **QUANTIFYING BUTANOL PRODUCTION OF A GENETICALLY ENGINEERED HALOPHILE**

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The University of California, Santa Cruz iGEM (international genetically engineered machines) team is engineering *Haloferax volcanii* to produce butanol from cellulose. Butanol is a four-carbon chain alcohol that is more energy dense than ethanol, a commonly used biofuel.

Modern methods for processing cellulose from agricultural waste yield high amounts of glucose that can be used for biofuel production. The resulting solution has high salinity, making it uninhabitable for most organisms. *H. volcanii* is a salt-tolerant archaea that is well suited for thriving in these processing environments. Our subgroup is focused on quantifying the butanol produced by both the genetically engineered cultures and the wild type. This will be achieved using gas chromatography (GC). We chose to use GC as opposed to mass spectroscopy or HPLC (high-performance liquid chromatography), because of its capability to distinguish between small organic molecules based on boiling point differences. We will use a polar column instead of a non-polar column because butanol and butyric acid, the metabolic precursor to butanol, have different levels of polarity. We will optimize measurements by using internal standards and calculating partition coefficient values to infer total butanol production.

### **SAT-309**

#### **CATALYTIC REDUCTION OF OXYGEN TO WATER USING G65Y-Fe<sub>B</sub>MB, A MYOGLOBIN BASED MIMIC OF NITRIC OXIDE REDUCTASE**

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The enzymatic reduction of oxygen to water is the driving force of cellular ATP production in all aerobic life. Despite significant structural differences, the heme containing metalloenzymes cytochrome c oxidase (CcO) and nitric oxide reductase (NOR) have both demonstrated the ability to catalyze this reaction with minimal production of cytotoxic reactive oxygen species (ROS). However, CcO and NOR's are large, complex, membrane-bound proteins with several metal binding sites, which makes the systematic study of their catalytic centers difficult. To better understand oxygen metabolism, we have designed a functional myoglobin mutant that retains structural features from the active sites of both CcO and NOR. This mutant (named G65Y-Fe<sub>B</sub>Mb) has been successfully purified from *E. coli*, and has allowed for a series of experiments that would be difficult to perform in the native complexes. We have used UV-Vis spectroscopy to show that G65Y-Fe<sub>B</sub>Mb is capable of incorporating both Fe(II) and Cu(I) in the non-heme-site. Enzymatic turnovers, as measured with a Clark type O<sub>2</sub> electrode, show a significant increase in activity as compared to wild-type myoglobin. Furthermore, the high yield of the model complex has also allowed for crystallization experiments which have demonstrated successful optimization from thin needles to well-formed crystals. In future work, we aim to characterize and capture reaction intermediates formed by using stopped-flow absorption spectroscopy and free-quench electron paramagnetic resonance spectroscopy (EPR).

**FRI-317****EXPLORING TRANSULFURATION PATHWAY IN HUMAN CYSTATHIONINE  $\beta$ -SYNTHASE**

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Human cystathionine  $\beta$ -synthase (CBS) is a pyridoxal phosphate-dependent (PLP) enzyme that contains heme and catalyzes the  $\beta$ -replacement reactions of either serine or cysteine by homocysteine to give cystathionine. Mutation in this key mammalian enzyme can result in hyperhomocysteinemia. Aggressive arterial diseases are a clinical phenotype of these patients. Although the role of PLP is similar to other PLP dependent enzymes that catalyze the exchange of the hydroxyl group of the substrate, serine or cysteine, to thiolate in homocysteine; little is known about the role heme plays in regulating the catalytic process. The goal of this work is to use time-resolved absorption and circular dichroism spectroscopy to integrate how small ligand binding to the heme induces conformational changes at the PLP active site in CBS. After cloning, expressing and purifying wild-type CBS and a truncated CBS lacking 143 amino acids in the C-terminus, we compare conformational dynamics associated with the ligation of variety of gasotransmitters (CO, NO, and H<sub>2</sub>S) to the heme regulatory site. The outcome of the proposed work will unravel the mechanism associated with heme-active site interactions and provide evidence for a ligand specific regulation mechanism in heme-dependent cystathionine  $\beta$ -synthase.

**SAT-328****STRUCTURAL INFLUENCES OF CYANOBACTERIAL CIRCADIAN KAI C PROTEIN PHOSPHORYLATION MECHANISMS**

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Cyanobacterial circadian clock mechanisms represent a milestone in evolutionary history, which has allowed many organisms, from blue-algae to sunflowers, to adjust internal balances for maximum performance in daily activities. The underlying mechanisms have been mostly conserved throughout time and circadian protein interaction with DNA is now being intensively explored. In addition to being a model organism for circadian protein studies, *Synechococcus elongatus* provides a simple system that can be mimicked *in vitro* and is primarily defined by its phosphorylation pattern through a 24-hour cycle. Much of this system is still unknown as the mechanism by which activation takes place is still being extensively studied. Observation of the known mechanisms point to serine-threonine differences in chemical composition and placement on the protein. Hypothesized mutant forms of KaiC would have enhanced phosphorylation activity. Synthesis of mutant KaiC proteins required mutagenesis, FPLC protein purification, and densitometry for assessment of phosphorylation patterns *in vitro*. This presentation will discuss analysis of specific mutant forms of the KaiC circadian clock protein, their different phosphorylation patterns through oscillations, and the analysis of the underlying mechanisms for how previous literature determined the phosphorylation sites, perhaps leading to further investigations regarding KaiC phosphorylation, dephosphorylation, and DNA transcriptional regulation. A greater understanding of the cyanobacterial circadian clock system

may lead to enhanced strains for effective biofuel harvesting, carbon fixation, and oil production.

#### **FRI-322**

##### **INVESTIGATING THE CATALYTIC IMPORTANCE OF A CONSERVED NON-ACTIVE SITE RESIDUE IN TRIOSE PHOSPHATE ISOMERASE**

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Enzymes provide the enormous rate enhancements required to accomplish biological reactions on a time scale compatible with life. Understanding how enzymes work is a central goal of biology, as diseases are generally associated with alteration of enzyme function, most drugs act as enzyme inhibitors, and enzymes continue to play an ever increasing role in conducting industrial chemical reactions in environmentally friendly manners. While it is well known that enzymes position active site groups for catalysis, the extent and energetic importance of groups involved in this positioning are not well understood. In triose phosphate isomerase (TIM), glutamate residue 97 (E97) is conserved among all known TIM sequences and is not located in the active site. X-ray structures show E97 is situated adjacent to a catalytically important lysine residue (K13) and could help position the lysine for catalysis. To test the role of the glutamate in positioning, we are mutating glutamate and lysine individually and together to evaluate the energetic connectivity using double mutant cycles. Wild-type and mutant TIM enzymes are recombinantly expressed in *E. coli*, purified by chromatography, and analyzed by gel electrophoresis. The effects of mutations on enzyme activity and stability are being analyzed by Michaelis-Menten kinetics and fluorescence/circular dichroism. These studies will further our understanding of the catalytic importance of interaction enzymes use to position active site residues and may aid in incorporating these positioning features in the design of new enzymes to carry out green chemistry.

#### **FRI-314**

##### **DECREASING FERTILIZER USE BY OPTIMIZING PLANT-MICROBE INTERACTIONS FOR SUSTAINABLE SUPPLY OF NITROGEN AND PHOSPHOROUS FOR BIOENERGY CROPS**

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The elements nitrogen (N) and phosphorus (P) are essential elements for the growth and survival of plants. Yet plants are limited in their ability to fix elemental N from the atmosphere, as well as hydrolyze organic and inorganic phosphorous from insoluble compounds. To compensate for this shortcoming, plants form a mutualistic relationship with bacteria to obtain usable nitrogen and phosphate. Although the majority of plants that form nitrogen-fixing root nodules are in the legume family, new species of N<sub>2</sub>-fixing bacteria have been discovered in association with non-nodulating crops. The goal of this research lies in the identification of beneficial bacteria capable of fixing nitrogen and solubilizing phosphate. In this study, high-throughput isolation (HTI) was used to identify N-fixing and/or P-solubilizing bacteria from

tobacco (*Nicotiana tabacum*). Overall, 5 different phylogenetic orders were identified: Enterobacteriales, Bacillales, Actinomycetales, Rhizobiales, and Sphingobacteriales. The strain Kosakonia Oryzae ola 51 from the order Enterobacteriales, in particular, was identified as a nitrogen fixer by amplifying the *nifH* gene; those results were then confirmed by acetylene reduction assay. Ultimately, the goal of this research is to decrease fertilizer dependency by engineering plants to attract diazotrophic bacteria.

#### **SAT-325**

##### **FGF, BMP, SHH SIGNALING PATHWAYS REGULATE MORPHOGENESIS OF THE INNER EAR**

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The vertebrate inner ear forms from a region of thickened epithelial cells during embryogenesis. This epithelium invaginates, forming a cup-like structure on either side of the developing head that deepens and pinches off from the overlying ectoderm to form the hollow sphere of cells called the otocyst. This simple structure gives rise to the 2 major components of the ear, the vestibular and auditory chambers that sense movement and sound, respectively. The otocyst provides a unique system for analyzing the morphogenetic events that transform a simple epithelial embryonic rudiment into a highly complex three-dimensional organ such as the ear. Failure to undergo perfectly choreographed morphogenesis is a well-recognized cause of congenital hearing loss in humans. Bone morphogenetic protein (BMP), sonic hedgehog (SHH), and fibroblast growth factor (FGF) mediated-signaling are critical for many aspects of inner ear development. We hypothesize that these signaling pathways function both in parallel and via intersecting pathways to regulate a repertoire of epithelial cell behaviors, including changes in cell shape, location, division rate, and survival, and that these behaviors drive morphogenesis to ultimately sculpt the complex inner ear labyrinth. We have found several useful probes for BMP and SHH signaling and are testing a BMP reporter mouse, which we will use to examine the changes in BMP and SSH signaling in FGF-deficient otocysts. This work will provide insight into mechanisms underlying the morphogenesis of the inner ear and will ultimately be applied to diagnosis and treatment of patients with inner ear dysfunction.

#### **FRI-324**

##### **CHARACTERIZATION OF ALPHA-HELICAL CONTENT IN FLGM *AQUIFEX AEOLICUS* PEPTIDES**

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Intrinsically disordered proteins (IDPs) are known to have no well-defined secondary structure due to low hydrophobic residual content. Despite lacking stability of secondary structure, IDPs have several important biological functions such as gene expression, regulation, signaling, and binding to multiple partners. Our research focuses on FlgM, an IDP that acts as a negative regulator for flagella synthesis when binding to sigma-28 transcription factor. A previous study has characterized FlgM derived from *S. typhimurium* as lacking stable structure and existing in a mostly unfolded conformation in a dilute solution. In comparison, another variant of FlgM derived from the thermophilic organism *Aquifex aeolicus* has displayed alpha-helical structure

at 20 °C. As the temperature increased to 85 °C, optimal living condition for the organism, the structure of FlgM has a loss in its alpha helical content. We have been studying 7 truncated fragments of FlgM *A. aeolicus* to identify stable and unstable secondary structure in identified helical regions. Relative stabilization was studied with an increased gradient (0 to 50%) of 2,2,2-trifluoroethanol (TFE). Circular dichroism spectra were collected at 20 °C and 85 °C to give insight into how the local environment can change the nature of an IDP from an ordered to disordered state. Results have suggested the helices 2 and 3 are the structural units of *A. aeolicus* FlgM.

### **FRI-303**

#### **COMPUTATIONALLY GUIDED DRUG DISCOVERY OF HUMAN PROSTATE SPECIFIC MEMBRANE ANTIGEN (PSMA) INHIBITORS**

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Prostate cancer is the second leading cause of cancer death among men in the USA. The prostate specific membrane antigen (PSMA) is a metallopeptidase found in the human prostate, kidney, small intestine, liver, and brain. PSMA is overexpressed on prostate cancer cells, thus making it a candidate for prostate cancer imaging. This research project uses *in silico* methods to construct and examine 2 types of PSMA substrates and to determine what interactions are significant to enhance ligand binding. The study aims to examine 2 types of linker groups for determining the prime linker length required to reach the solvent interface. To do this, we attached either a polyethylene glycol (PEG) or aminohexanoyl moiety to a urea-based, dipeptidic template and varied the length of each type of linker group. The catalytic residue predictors, THEMATICS and POOL, verified the local region of activity for PSMA to aid in substrate positioning during local docking experimentation. The protein-substrate interactions were analyzed using binding energies and dissociation constants. We found that PSMA could not accommodate an inhibitor containing the PEG oligomer with more than 4 subunits. Additionally, PSMA could only bind an inhibitor with 1 aminohexanoyl group. The results highlight K699/Y700 of the S1' binding pocket that form the glutarate sensor, which aids in substrate recognition, and the importance of nonbulky linker groups to avoid steric clashes. These findings are limited and require further *in silico* studies. *In vitro* analysis will aid in determining the selected inhibitors' potential as prostate cancer imaging agents.

### **SAT-315**

#### **RAPID EVALUATION OF GENOME EDITING IN MALARIA**

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There are more than 200 million cases of malaria every year worldwide with over 600,000 resulting in death. Widespread administration of antimalarial compounds has largely been effective but has also led to the emergence of drug resistant parasites. Currently, there is an ongoing battle against malaria resurgence, where new antimalarial compounds are effective for only a limited time. The threat of resurgence underscores the need for more research on

malaria and rapid antimalarial drug discovery. One current problem is the limited and inefficient methods for generating mutations in the parasite. As a result, research has remained slow, greatly hindered by restriction to core techniques in molecular biology. To increase the rate of research, effective techniques for genome engineering must be developed. Here, we report the results of an ongoing investigation to better transfect and genetically engineer *Plasmodium falciparum*, the most deadly malarial parasite. Using droplet digital PCR, the results of direct transfections via electroporation of a Cas9 endonuclease were evaluated. Since Cas9 has been shown to be highly effective at creating cuts at a preprogrammed location, any successful transfection should be detectable through a high sensitivity assay like droplet digital PCR. Through a continued effort, there is hope that more effective transfection techniques will be developed to advance the rate of research and subsequent therapeutic discovery to better control malaria despite its acquisition of resistances.

#### **SAT-322**

##### **PORPHYRIN-INDUCED LASER DEACTIVATION OF TRYPSINOGEN-TRYPSIN CONVERSION**

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Pancreatitis is caused by inflammation of the pancreas. The digestive enzyme trypsin is activated from the precursor enzyme trypsinogen, causing auto-digestion and may lead to pancreatic cancer and fatality due to function loss. Addressing this problem is beneficial to human health. Our suggested solution for this problem involves stopping trypsinogen from forming trypsin by inducing conformational changes with a bound porphyrin dye and laser irradiation. Porphyrin dyes, composed of 4 linked heterocyclic groups forming a flat ring, are known to bind well with proteins. We will use spectroscopic techniques to analyze the binding affinity of specific porphyrins to trypsinogen and any conformation changes induced by irradiation. If conformational changes are detected, the trypsinogen will be tested for trypsin inactivation. The investigation could provide a way to reduce the damage caused by trypsin activation and could be further applied to other diseases using the same methods.

#### **SAT-311**

##### **CRYSTALLIZATION OF A P450 BM3 LIGHT-DRIVEN BIOCATALYST**

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Cytochrome P450 enzymes are important oxidative catalysts found in a variety of organisms. In nature, P450 enzymes rely on reductases as protein cofactors to supply electrons for the reactions they catalyze. We have recently shown that covalently attached ruthenium-II photo-sensitive labels can act as an efficient alternative for electron delivery. We hypothesize that electron delivery from the label is mediated by pi-stacking interactions with a key phenylalanine residue near the active site. In order to verify the model that led to this hypothesis, it is first necessary to grow crystals of the labeled protein and collect diffraction patterns to reveal the structure of the labeled protein. Using sitting-drop vapor crystallization, we have screened a variety of crystallization conditions to find protein and precipitant concentrations that result in



high quality crystals of the substrate-free, wild-type protein as well as the substrate-free, labeled protein. We will also present crystallization tests for the substrate-bound protein and diffraction studies for each variety of crystal. These studies will give us the first look into the structural basis of the labeled protein's efficiency, allowing us a glimpse into what it takes to make an effective, light-driven biocatalyst. (Supported by NSF-REU Grant DBI 1004350.)

### **FRI-313**

#### **BIOSYNTHESIS OF GRANATANE ALKALOIDS IN *PUNICA GRANATUM***

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The granatane and tropane alkaloids are structurally similar classes of bicyclic alkaloids, which have an uneven distribution across flowering plant families. Specifically, granatane alkaloids are found in the pomegranate plant (*Punica granatum*) where alkaloids are thought to be biosynthesized in the root and accumulate in the bark. It has been previously shown in the D'Auria lab that tropane alkaloid biosynthesis has evolved independently in different plant families. We are therefore interested in testing the hypothesis that the structurally similar granatane alkaloids also have an independent origin. A homology based *in silico* search was performed on a *P. granatum* transcriptome database in order to identify genes thought to be involved in alkaloid biosynthesis. Gene sequences used for this approach originated from known tropane alkaloid biosynthetic enzymes from *E. coca* or members of the Solanaceae family. Several putative biosynthetic enzymes were successfully identified during this initial basic local alignment search tool (BLAST) search. The genes encoding these enzymes were evaluated to determine whether or not they existed as open reading frames (ORFs), and primers were designed to isolate them from pomegranate tissue. Ongoing studies include the heterologous expression of these enzymes in a host such as *E. coli* or yeast. Furthermore, these enzymes will then be characterized via enzyme assay for their biochemical activities.

### **SAT-319**

#### **TISSUE SURFACE TENSION MEASUREMENT OF HYDRA EPITHELIAL TISSUES AND ITS ROLE IN DRIVING HYDRA REGENERATION FROM AGGREGATES**

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Hydra have the ability to regenerate their entire bodies from dissociated and reaggregated cells. A key step in the regeneration of hydra from cellular aggregates is the separation of cell types to form the 2 characteristic epithelialized body layers, endoderm and ectoderm. The 2 cell types segregate such that endoderm occupies the inside and ectoderm occupies the outside of the cell aggregate, corresponding to their proper arrangement in the animal. A popular theory, the differential adhesion hypothesis, suggests that cell types separate from each other because of differential interfacial tissue tension. For interacting tissues, the tissue with the higher surface tension should end up in the interior, and thus in the case of hydra correspond to endoderm. Using parallel plate compression, we can measure the surface tension of the 2 tissues thereby determining whether this theory alone can explain the cell

arrangement during hydra regeneration or whether additional parameters need to be considered. Regenerating hydra aggregates are a powerful system to study fundamental processes of pattern formation because they are accessible to quantitative physical measurements and undergo biologically relevant developmental processes.

#### **SAT-321**

##### **A DEEPER SLEEP AND A BRIGHTER DAY: DETERMINING THE STRUCTURE OF THE BMAL1 PROTEIN SWITCHING REGION**

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Mammalian circadian rhythms control the body's 24-hour cycle. Sleeping and waking, anabolic and catabolic processes all rely on the cellular mechanisms that keep them in alignment with each other and the external environment. The proteins CLOCK and BMAL1 form a heterodimeric transcription factor that promotes proper circadian function. The transcription activation domain (TAD) of BMAL1 contains a region critical to both activation and repression of circadian-driven transcription. The goal is to understand how the BMAL1 TAD controls this balance of activation and repression to generate the molecular circadian clock. BMAL1 has a region at the end of the TAD that takes on 2 different conformations like a switch (e.g., cis and trans) to control interactions with transcriptional regulators. In order to crystallize this protein, a trans-locked TAD will be used. A section of the *BMAL1* gene containing the TAD will be mutated to the trans form of the molecule, and the recombinant protein will be purified. The structure of the protein will be determined through X-ray crystallography in complex with the KIX domain of the transcriptional activator CBP. The structural determination of BMAL's TAD region will be a step forward in the quest for a mechanistic understanding of the circadian clock and the development of therapeutic agents to modulate circadian function in individuals.

#### **SAT-302**

##### **CYP2S1 INFLUENCES BANOXANTRONE-INDUCED GENOTOXICITY IN HUMAN BRONCHIAL EPITHELIAL CELLS**

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Cytochrome P450s are involved in about 75% of all drug metabolic reactions. This metabolism results in either bioactivation or inactivation of the drug. Cytochrome P4502S1 (CYP2S1) is a relatively new CYP and its function has not been fully elucidated. CYP2S1 exhibits considerable regulation in response to chemical cues. For instance, polyaromatic hydrocarbons and retinoic acid increase CYP2S1 expression, while glucocorticoids reduce expression. Interestingly, reduced oxygen levels also increase CYP2S1 expression, whereas most CYPs' expression is reduced. CYP2S1 expression is also elevated in a variety of epithelial-derived cancers. This expression pattern suggests that CYP2S1 may be poised as an important enzyme for bioactivation of banoxantrone (AQ4N). AQ4N is an anti-cancer prodrug which requires low oxygen and reduction to the bioactive metabolite, AQ4. Once metabolized to its active form, AQ4 intercalates DNA and also binds to and inactivates topoisomerase II. In heterologous

expression systems, CYP2S1 has been shown to metabolize AQ4N to AQ4. However, no one has demonstrated the impact of CYP2S1-mediated metabolism on AQ4-mediated genotoxicity in human cells. We hypothesize that regulation of CYP2S1 expression will influence the genotoxicity of AQ4N in human bronchial epithelial cells (BEAS2B). In order to test this, we performed a COMET assay, which examines genotoxicity in BEAS2B cells differentially expressing CYP2S1. BEAS2B cell depleted by approximately 75% CYP2S1 (i.e., 759 and 984) and cells over-expressing CYP2S1 (i.e., 2#3 and 2#1) were compared to their respective controls (i.e., SCRAM and pcDNA). Our results are consistent with a role for CYP2S1 in the metabolism of AQ4N.

#### **FRI-325**

##### **ANALYSIS OF DIFFERENT ATP RELEASE MECHANISMS INVOLVED IN THE ATTRACTION OF MICROGLIA TO NERVE LESIONS**

Roberto Diaz, Kenneth Muller.

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One important question following damage to the nervous system is how resting immune cells of the brain, the microglia, are activated and attracted to sites of injury. Evidence that microglia are similar across species from humans to invertebrates such as leeches and are useful in nerve repair makes microglia research in the leech relevant for understanding all microglia. The large glial cells and separate, visible microglia cells in leeches are experimentally useful. Nerve injuries induce glial calcium waves, which open pannexin/innexin channels to release extracellular ATP and cause microglia to begin moving. After a crush injury, calcium waves can spread several hundred micrometers away and can persist for at least an hour. From observations in mice and leeches, we hypothesize that ATP released through pannexin channels signals distant microglial cells, while ATP released through injured cell membranes at the lesion signals cells nearby. We will administer carbenoxolone to block ATP release through innexin/pannexin channels to test the hypothesis that nearby microglia will still move. Living microglial cells made visible with nuclear fluorescent dye will be tracked during 2 hours using time lapse photography and ImageJ. Then cell distribution will be measured in fixed tissue. Our experiments will show quantitatively how ATP has different effects on microglial cells' response to nerve crushes and thus may help improve treatment of central nervous system injuries.

#### **FRI-304**

##### **SYNTHESIS AND CHARACTERIZATION OF ISOCYANATE AMINO ACID-BASED SURFACTANTS**

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The purpose of this research is to synthesize and use chiral octyl isocyanate amino acid-based surfactants. A mixture of amino acid, sodium hydroxide, and isocyanates in acetone and water was mixed at room temperature for 1 hour. The product was easily separated from the reaction mixture by the addition of acid without any byproduct. Purity of the product was confirmed using HPLC and NMR spectroscopy. NMR water quenching studies in a largely basic solution showed both amide groups deprotonated, while a largely acidic solution showed both amide groups as protonated. This amino acid

isocyanate surfactant can be further investigated to determine how well the molecule performs as an antimicrobial agent with regards to the charge on the polar head of the surfactants.

#### **FRI-316**

##### **LASER MICROSURGERY TO INVESTIGATE THE BIOMECHANICS OF GERM-BAND RETRACTION IN HEAT-SHOCKED TISSUE**

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<sup>1</sup>*Southern Nazarene University, Bethany, OK,* <sup>2</sup>*Vanderbilt University, Nashville, TN.*

Germ-band retraction (GBR) is a developmental stage in *Drosophila* where two tissues, the U-shaped amnioserosa and surrounding germ band, move dramatically in concert as the amnioserosa contracts. However, when exposed to heat-shock, catastrophic holes emerge within the amnioserosa that result in GBR failure. The principal goal of this research was two-fold: to determine the biomechanical drivers of GBR and to then test our hypothesis that mechanical weakness was the cause of these fatal holes. To test this, a series of laser microsurgies was designed to ablate the dorsal aspect of the amnioserosa in both normal and heat-shocked tissue. By precisely ablating such a small region of interest, the injured tissue could then be imaged with confocal microscopy and post-ablation analysis could retroactively determine the pre-ablation mechanics. This was accomplished by algorithmically warping a pre-ablation image to resemble a post-ablation image, creating a vector field that quantitatively modeled this transformation, and applying this vector field transformation to a simple object, in our analysis a circle, from which numerical results could be obtained. With this approach, it was possible to calculate the aspect ratio (indicating the direction of the greatest tensions), radial strain (the magnitude of these tensions), and changes in cell shape/area in normal GBR and compare these values with identical experiments performed in heat-shocked tissue.

#### **FRI-330**

##### **EFFECTS OF TAU MUTANTS ON THE MECHANICAL PROPERTIES OF MICROTUBULES**

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*University of California, Santa Barbara, Santa Barbara, CA.*

Microtubules are dynamic cytoskeletal filaments that play important roles in intracellular transport and cell division. In cells, they are often stabilized by tau, a neural microtubule-associated protein that is critical for maintenance of a healthy nervous system. Several dementia disorders have been linked to mutations in the tau genes. In many cases, these tau mutants fail to bind to and stabilize microtubules, causing filament disintegration; however, there is a subclass of tau mutants that maintain strong microtubule binding, yet still cause neurological disease. The mechanical effects of this subclass are unknown. In order to gain a fundamental understanding in tau related neurological diseases, extensive studies on how tau proteins, particularly those mutants with strong binding, modulate microtubules are necessary. In this study, we focus on the changes in the mechanical properties of microtubules stabilized by different tau mutants. Using advanced microscopy, we will record movies of the fluctuations of fluorescently labeled microtubules subjected to thermal forces *in vitro* and determine their stiffness using spectral analysis of the microtubule shapes. To further study the interaction

between tau and microtubules, we will also label tau with fluorescent dyes and monitor the binding and the motion of tau proteins on microtubules with laser-induced fluorescence microscopy. We will measure the binding affinity, the cooperativity of binding, and tau diffusion coefficient using different tau mutants and under different chemical conditions. Taken together, our data will provide an improved understanding in how tau modulates microtubule mechanics and its effects in tau related neurological diseases.

#### **FRI-311**

##### **DETERMINING THE PROTEIN CONCENTRATION OF MALARIA VACCINE CANDIDATE ANTIGEN APICAL MEMBRANE ANTIGEN-1 (AMA1)**

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Nearly half of the world's population is estimated to be at risk for malaria, with pediatric populations in sub-Saharan Africa at highest risk for morbidity and mortality. Malaria is caused by protozoan *Plasmodium* species. *P. falciparum* causes the most severe form and is the major cause of malaria-related mortality. Developing a broadly protective vaccine holds great promise as a tool against malaria. Apical membrane antigen-1 (AMA1) is a leading *P. falciparum* blood-stage vaccine antigen, in part from observations that anti-AMA1 antibodies inhibit erythrocyte invasion. In a recent vaccine trial, a monovalent AMA1-based vaccine was found to have high allele-specific efficacy against clinical malaria, which is noteworthy as the first example of a blood-stage malaria vaccine with measurable protection against clinical malaria. However, limited information on the AMA1 epitopes associated with immune protection as well as extreme antigenic diversity of AMA1 highlight the need for new methods to study diverse AMA1 epitopes. An *E. coli* autotransporter, EspP, was engineered to display regions of AMA1 and variants of those regions; expressed proteins will be printed onto high-throughput protein microarrays. Our project is to develop a method for determining the concentration of AMA1-autotransporter proteins. Ultimately, human sera of individuals obtained pre- and post-malaria season and pre- and post-receipt of AMA1 vaccine FMP2.1/AS02A will be reacted with the protein microarrays. Information on seroreactivity to AMA1 epitopes will allow for identification of cross-protective epitopes. The knowledge of immunologically relevant regions of AMA1 is key to developing a broadly protective AMA1-based malaria vaccine.

#### **FRI-305**

##### **THE EFFECT OF ZINC ON THE GREEN COLOR OF ROASTED PISTACHIOS**

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Pistachios with an olive brown hue are thought to be of poorer quality and undesirable by the consumer. The pigment chlorophyll gives pistachios a bright green hue that is a desirable trait to consumers. Chlorophylls a and b are magnesium- ( $Mg^{2+}$ ) containing pigments that act as light-harvesting molecules, critical to photosynthesis in green plants. Heat treatment, such as roasting, causes the  $Mg^{2+}$  to be displaced from the porphyrin ring and replaced by two hydrogen ions, altering the color from bright green to an olive brown. The addition of other metals in a process known as re-greening can be

used to replace the  $Mg^{2+}$  and maintain green color. The 2 hydrogen ions can be displaced with zinc or copper ions to form either metal complex. The purpose of this study is to determine if the green color of pistachios can be maintained after roasting with the introduction of a zinc chloride ( $ZnCl_2$ ) dip. Pistachios were dipped in varying concentrations of  $ZnCl_2$  solution to expose the chlorophyll to the zinc ion. Once dipped, the pistachios were roasted at 138 °C. The chlorophyll and chlorophyll derivatives were then extracted from the heat-treated pistachios and further analyzed using UV/vis spectroscopy to determine the concentrations of chlorophyll in the pistachios and colorimetry to quantitate pistachio color. Increasing time in a  $ZnCl_2$  dip was found to increase the green color of roasted pistachios. Color analysis shows that  $a^*$  decreases as the time of dipping increases indicating more green pigment. Comparisons between  $H_2O$  dipped, 24-hour  $Zn^{2+}$  dipped, and raw, untreated pistachios showed that a 24-hour Zn dip was significantly greener than an  $H_2O$  dip and also showed similar results to the raw, untreated pistachio color analysis. We hypothesize that there will be a difference in the spectra of the  $Zn^{2+}$ -treated chlorophyll.

### **SAT-303**

#### **DETERMINING TITANIUM(IV) TRANSPORT FOR ITS POTENTIAL USE BY HUMANS**

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Titanium (Ti) is a metal compatible with human body tissue and is known for its hardness, its lightness, and its uses in biomedical applications. In humans, this metal is present in small but not insignificant concentrations and can be transported from the bloodstream into the cell by binding to a protein. It is characterized as being biocompatible due to it being immune to corrosion by body fluids and tissues. Titanium is found to be present in a wide variety of biomaterials and food, having access to our system, even though the method of entry into cells is still uncertain as is the acquisition by cells. The favored hypothesis is that titanium(IV) has the ability to bind to serum transferrin which transports the metal ion to the cells. The binding of Ti(IV) by transferrin induces conformational changes that may facilitate binding to the transferrin receptor for intracellular transport, and that is why it is of interest to determine the coordination of Ti(IV). For this, computational studies, protein docking experiments, and binding studies were used to determine the protein residues that were bound to the metal center of the active site. The data suggests that citrate plays an important role in the metal binding to the protein by serving as a synergistic anion and helping to transport the metal ion into cells.

### **FRI-328**

#### **INVESTIGATING A NEW MECHANISM FOR COMBATING FOODBORNE ILLNESSES**

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*Clostridium perfringens* is a pathogen linked to many common foodborne diseases that impact 1 in 6 people in the United States. It is a Gram-positive, anaerobic bacterium typically found in the human intestinal tract. Expression of an FAD-dependent enzyme called azoreductase (AzoC) is hypothesized to be responsible for antibiotic resistance and survivability of *C. perfringens*. The amino acid sequence of AzoC is less than 14% identical to homologs that have been

structurally characterized, which is too low for computational algorithms to predict its atomic structure. Consequently, we are using protein crystallography methods to determine experimentally its atomic structure. *C. perfringens* AzoC was expressed in *E. coli*, purified aerobically, and used to test a wide variety of crystallization conditions. We also tested *E. coli* expression, purification and crystallization conditions in an anaerobic chamber. The aerobic AzoC crystals were analyzed by single-crystal electronic absorption and Raman spectroscopies correlated with X-ray diffraction to 3.0 Å resolution. The optical spectra from a crystal of AzoC exhibit features typical of oxidized FAD ( $\lambda_{\text{max}} \approx 380, 450 \text{ nm}$ ). However, upon exposure to X-ray photons necessary for crystallographic analysis, the spectrum changes in dose-dependent manner that is consistent with a one electron reduction of the flavin moiety. Completion of the AzoC structure will require additional X-ray diffraction data to enable experimental phasing. The atomic structure AzoC in the presence of drug-like ligands will be an important step in developing new strategies to combat this pathogen.

### **FRI-310**

#### **KINETIC ANALYSIS OF FOLDING STRINGS BY LINEAR PATTERNS OF HYDROPHOBICITY**

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The self-assembly of linear sequences with alternating sticky regions into higher order structures is computationally challenging (an NP-complete problem), despite the fact that the process can occur readily in nature (e.g., protein folding). It has been algorithmically proven that any 2D or 3D shape can be made from a patterned string, although experimental data remains scarce. We have developed a means of fabricating mesoscale strings from flexible polydimethylsiloxane elastomers with defined patterns of hydrophobicity generated by ultraviolet ozone radiation. Simple hydrophobic sequences were verified using a mass balance to measure the surface tension while manipulating the water level around a partially submerged string. When strings are placed at the air-water interface, hydrophobic interactions promote conformations where hydrophobic regions are in contact with each other while minimizing bending. Kinetics suggest that energy is needed to induce bending of the string and surpass activation energies between conformations. Consistent folding motifs are observed after the system is stimulated with acoustic or vibrational energy. Tracking the energy added to the system and performing image analysis are helping to characterize the mechanism and kinetics of string folding in pursuit of generalizable folding design rules.

### **SAT-318**

#### **METAL ION SPECIFICITY OF AN UNUSUAL ABC TRANSPORTER SYSTEM**

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Transition metals are required for important biological processes including replication and electron transport, among others. ATP binding cassette (ABC) transporters are largely responsible for importing these essential elements and have been implicated as virulence

factors in a number of bacterial pathogens. In Gram-negative bacteria, ABC transporter systems are composed of three genes encoding a membrane-bound permease, cytoplasmic ATPase, and a periplasmic solute binding protein (SBP). The SBP specifically binds the relevant metal and shuttles it to the permease for translocation into the cytoplasm. In many bacteria, including human pathogens, a fourth gene of unknown function is found adjacent to ABC transporter genes specific for either Mn or Zn, suggesting a role for this gene in the import of these elements. Here we use *Paracoccus denitrificans* as a model system to investigate the role of this protein in transition metal import. *P. denitrificans* was grown in media replete with metals or lacking Zn, Mn, or Fe. Growth curves were measured to determine the degree to which metal starvation impairs growth. Transcript levels of the putative accessory factor (Pd98) and its associated SBP (Pd97) were measured under these conditions to determine the metal specificity of this system. These studies advance our knowledge of bacterial ABC transporter function, which has been implicated in the ability of pathogenic bacteria such as *Salmonella enterica* and *Yersinia pestis* to survive within the host.

#### **SAT-314**

##### **DETERMINING COLLAGEN ISOFORM RATIO AND STRUCTURE IN CEREBRAL PALSY PATIENTS**

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Cerebral palsy (CP) is caused by a neurological pathology and results in muscle stiffness (spasticity), poor muscle tone, and/or uncontrolled movements. It is now considered that abnormal extracellular matrix (ECM) content, specifically an increase in collagen concentration, may be causing the disruption of normal muscle mechanics. Our aim is to determine the specific collagen environment in CP muscles compared to typically developed (TD) muscles to elucidate the molecular basis of CP muscle stiffness. Collagen content was quantified using the combined efforts of ELISA and western blots. At this time, we have found that the 4 main functional collagen isoforms have a  $2.46 \pm 0.19$  fold increase in CP muscle. However, these increases are at a ratio proportional to concentrations found in TD, with type I found in the highest concentration. Further investigation is starting on the structure of collagen tendrils on the muscle, with more samples needed before making a proper conclusion. Imaging with a new 3D modeling system, 3View, will give a 3D reconstruction of the muscle and ECM environment. With these reconstructions, it will be possible to observe if the increased collagen is orientated uncharacteristically on the muscle fibers perhaps causing a change in the structural properties. Bearing in mind that muscle function is associated with ECM arrangement, these findings may suggest that the reduced movement and increased stiffness in CP patients could be due to irregular collagen remodeling. These findings may give new insight to a treatment regimen for these patients and patients with fibrosis.



### SAT-313

#### BACTERICIDE PROPERTIES OF AG-GQD NANOCOMPOSITES

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Functionalized silver (Ag) nanoparticles coated with graphene nanostructures, graphene quantum dots (GQD), were synthesized by laser irradiation of benzene-silver colloid. The functionalization of this Ag-graphene nanocomposite with polyethylene glycol provides stabilization and higher solubility in aqueous solution. The Ag-graphene nanocomposite was characterized by UV-Vis spectroscopy, transmission electron microscopy (TEM), Raman spectroscopy, X-ray photoelectron spectroscopy (XPS), field emission scanning electron microscope (FE-SEM) coupled with energy dispersive spectrometry (EDS), and Fourier transform IR spectroscopy (FT-IR). The antibacterial activity of Ag-graphene was tested using *Pseudomonas aeruginosa* and *Staphylococcus aureus* as model strains of Gram-negative and Gram-positive bacteria, respectively. The Ag-graphene nanocomposite solution exhibits strong antibacterial activity against both types of bacteria as tested using Kirby-Bauer assay disk diffusion and minimum inhibitory concentration (MIC) assay. By applying an external electric bias, a decrease in the bacterial inhibition time (less than 6 hours) can be attained. The success of this method allows us to propose a mechanism that describes the bactericide effect in terms of the ion transport in the solution when exposed to the bacteria. Taking advantage of the high biocompatibility of graphene and the antibactericidal activity of silver, the Ag-graphene nanocomposite is a nontoxic biomaterial suitable for numerous applications, such as self-sterile textiles, biomedical devices, coatings, and cosmetics.

### SAT-305

#### EVIDENCE OF THE PRESENCE OF AN ADDITIONAL COPPER UPTAKE TRANSPORTER IN THE PLASMA MEMBRANE OF MAMMALIAN CELLS

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Copper (Cu) is an essential trace element for all organisms as a co-factor for many enzymes/proteins supportive of life. Blood plasma proteins such as ceruloplasmin (Cp),  $\alpha$ 2-macroglobulin, and albumin are direct sources of Cu for mammalian cells. Copper transporter 1 (CTR1) is the only Cu uptake transporter known to date on the plasma membrane of cells that take up Cu from these plasma proteins. To determine whether Cu is taken up by an additional transporter, rates of uptake from the different Cu carrying plasma proteins and Cu-histidine were compared in cells that did/did not express Ctr1. We found siRNA knocked-down expression of CTR1 in human mammary epithelial and hepatic cell models, but had no effect on uptake of Cu(II) from the plasma proteins. Mouse embryonic fibroblasts that did not express Ctr1 took up Cu (II) bound to albumin or Cp almost as well as those expressing Ctr1. Uptake rates from mouse albumin reached a 2-4 fold higher Vmax (with a lower Km) than from human

albumin. Maximum uptake rates for Cu(I) versus Cu(II)-histidine were significantly higher, suggesting mediation by a reductase. Cp-<sup>64</sup>Cu(II) uptake decreased when excess Cu(II) was introduced, consistent with a competing effect for reduction of Cu(II) to Cu(I). These findings indicate that there is at least one additional unknown Cu transporter. Preliminary findings indicate that the unidentified transporter may be 250 kDa. It was captured by a cross-linking method involving biotinylation of the transporter upon exposure to the copper carrying plasma protein, followed by binding to streptavidin beads, SDS-PAGE, and sequencing.

#### **FRI-308**

##### **GENERATION OF BCL-2 AND BCL-XL RECOMBINANT PROTEINS TO BE USED IN ANALYSES OF THE PRO-APOPTOTIC ACTIVITY OF BMRP**

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Apoptosis is a physiological type of cell death that is essential for metazoans (animals). Apoptosis plays a critical role during development and for the normal functioning of an adult organism. Aberrant levels of apoptosis have been linked to the pathogenesis of numerous human diseases including cancer, disorders of the immune system, neurodegenerative diseases (such as Alzheimer's and Parkinson's), as well as cardiac arrest and stroke damage. Apoptosis is initiated upon activation of a group of cysteine proteases called caspases, which cleave cellular substrates at specific sites, triggering apoptosis. Bcl-xL, an anti-apoptotic member of the Bcl-2 family of proteins, has been identified as one of the substrates for caspase cleavage. Bcl-xL is cleaved at the C-terminus of the amino acid residues aspartate (D) 61, which converts Bcl-xL into a pro-apoptotic protein. Our laboratory has identified BMRP (Bcl-2 interacting mitochondrial ribosomal protein) as a novel Bcl-2 interacting protein with pro-apoptotic activity. We have generated a recombinant construct that drives the expression in mammalian cells of a mutant of Bcl-xL with enhanced anti-apoptotic activity (hBcl-xLD61A). We have also generated a recombinant construct encoding wild-type Bcl-2 fused to green fluorescent protein (GFP). These constructs will help us further our characterization studies of the pro-apoptotic function of the BMRP protein.

#### **BIOLOGY (GENERAL)**

#### **FRI-1011**

##### **PRODUCTION AND PURIFICATION OF THE RECOMBINANT VOLTAGE GATED CALCIUM CHANNEL $\beta$ SUBUNIT PROTEIN – A POTENTIAL TARGET OF THE ANTHELMINTHIC DRUG PRAZIQUANTEL**

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Voltage gated calcium channels regulate the movement of ions across biological membranes. Praziquantel (PZQ) is believed to disrupt Ca<sup>2+</sup> homeostasis in schistosome cells by interfering with the activity of these channels leading to a rapid influx of calcium ions. Despite its widespread use, the mechanism of action of the drug remains unknown. We hypothesize that

the molecular binding target of PZQ is to be found on one particular  $\beta$  subunit of schistosomes. The aim of this project is to produce recombinant  $\beta$  subunit proteins using a bacterial expression system and to use this protein as an antigen to raise antisera in rodents. The antisera will be used to detect the subunits in different schistosome tissues using light and confocal microscopy. A PZQ molecule synthesized with fluorophore will be used to visualize potential PZQ binding to the subunits.

#### **FRI-1002**

##### **INTER-INDIVIDUAL VARIATION IN METABOLIC RATES OF INTERTIDAL MUSSELS (*MYTILUS CALIFORNIANUS*)**

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The mussel *Mytilus californianus* exhibits inter-individual variation due to both inherent and environmental factors. Contributions of these factors to physiological and biochemical variation have yet to be thoroughly assessed. This study aims to quantify one aspect of variation by measuring whole animal metabolic rate before and after common gardening. Common gardening was used in an attempt to eradicate residual effects of environmental factors and to observe inherent inter-individual variation. Mussels were collected at Hopkins Marine Station (HMS) and transported to Loyola Marymount University (LMU) for common gardening. A second group was collected at HMS and common gardened on site. Individuals in this second group were collected from 2 different field sites, protected and exposed, which varied significantly in wave action, solar irradiance, and immersion duration. Metabolic rates of the LMU mussels were measured after 2 months of common gardening, then again 1 week later. Metabolic rates of the HMS mussels were measured one week after collection, then again after one month of common gardening. Metabolic rates were measured using a fiberoptic oxygen probe in a closed chamber respirometer. Metabolic rates decreased through common gardening, yet individuals' rank among the entire sample stayed consistent. In addition, mussels from the exposed site were observed to have faster metabolic rates than those from the protected site; this difference persisted throughout common gardening. Our results suggest that different metabolic rates of individuals are determined by both recent experience and fixed differences. This work is part of a larger, ongoing study to quantify biochemical and physiological variation among individuals.

#### **SAT-1019**

##### **EPIPHYTE DIVERSITY IN TREE TRUNKS OF TROPICAL FOREST FRAGMENTS**

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Epiphytes are plants that grow on other plants. It has been estimated that half of total plant species in montane forests are epiphytes. Because of their diversity, epiphytes also house and provide nutrients to insects, birds, and bats. This study serves to answer 2 main questions: Are there more types of trunk epiphytes in the primary versus secondary forest? And, is there a

different community of epiphytes in tree trunks among the studied forests? It is predicted that primary forests will have more epiphyte diversity than the logged and secondary forest because of differences in microclimate and population of animal species that inhabit them. Results showed that epiphyte diversity in selectively logged and primary forests were similar, and they had more epiphyte diversity than younger secondary forests.

#### **FRI-1017**

##### **HYPERINSULINEMIA INDUCES AUTOPHAGY IMPAIRMENT VIA REDUCTION OF LC3BI LIPIDATION IN EMBRYONIC CARDIOMYOCYTES**

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Insulin resistance is a major metabolic abnormality in the majority of patients with type-2 diabetes and it is due to impairment in insulin signaling. Autophagy is defined by protein degradation, organelle turnover, and nonselective breakdown of cytoplasmic components when introduced to stress or nutrient starvation. This is a vital cellular process; however, its fluctuation can be either adaptive or maladaptive depending on the context. Also, autophagy is known to cause insulin resistance in key metabolic organs such as the liver, skeletal muscle, and adipose tissue; however, little is known regarding autophagy in the heart. This study proposes that insulin resistance induces autophagy impairment in the heart. We observed autophagy reduction in TIRKO mice that lack the insulin receptor in the heart. Previous experimental results have shown that TIRKO hearts have significant reduction in ATG3 expression, defective LC3B-I lipidation, and p62 accumulation. To identify if hyperinsulinemia alone is responsible for the impairment of autophagy in embryonic cardiomyocytes (H9C2) cells were cultured in F-12 DEMEM containing 10% fetal bovine serum until they reached 80% confluence. Cell cultures were then exposed to high levels (7.6 IU/L) or physiologically relevant levels of insulin (3.8 IU/L) for 1 hour. Only high insulin resulted in a total ablation of LC3B-II levels. ATG3 levels were further reduced on cells exposed to high levels of insulin. The levels of p62 were reduced in both dosages. Taken together, the results show, for the first time, that hyperinsulinemia alone can induce autophagy reduction in embryonic cardiomyocytes.

#### **SAT-1003**

##### **THE ROLE OF TESTOSTERONE ON MALE MATING BEHAVIOR IN THE AFRICAN CLAWED FROG (*XENOPUS LAEVIS*)**

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Atrazine, the second most widely used herbicide in the United States, lowers testosterone levels in male African clawed frogs (*Xenopus laevis*). Reduced testosterone levels are associated with decreased mating behavior in males. Injecting castrated males with testosterone induced them to mate, suggesting that testosterone is both necessary and sufficient for mating behavior. In the current study, we administered human chorionic gonadotropin (hCG), which induces endogenous testosterone production, to intact males to determine if testosterone levels affect mating success in males. We predicted that high testosterone levels will result in

an increase in mating success. We injected different doses of hCG. Four experimental males were then placed in a pool with 4 control males to compete for 4 females. Males found copulating the next morning were considered successful. After mating sessions, blood samples were taken from the males for testosterone analysis by radioimmunoassay. Results showed more competitive mating in frogs injected with a 50 IU dose of hCG than injected with water, but had similar mating behavior when injecting a 200 IU dose of hCG compared to the full dose. These data suggest that hCG generates a testosterone surge that increases competitive mating behavior, but that all doses used so far may be above a threshold dose associated with mating success.

#### **FRI-1019**

##### **MONITORING THE EFFECT OF THE LOSS OF APC IN APOPTOSIS IN *CAENORHABDITIS ELEGANS***

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In mitosis, the spindle assembly checkpoint (SAC) ensures proper chromosome segregation by preventing the progression of the cell cycle if all chromosomes are not attached to spindles. The SAC prevents the transition to anaphase by blocking the action of the anaphase promoting complex (APC). In meiosis, control of synapsis depends on SAC genes, such as *MAD-1*, *MAD-2*, and *BUB-3*. It has been shown that unsynapsed chromosomes lead to apoptosis and this apoptosis also depends on *MAD-1*, *MAD-2*, and *BUB-3*. The hypothesis is that the APC plays a role in the synapsis checkpoint in meiosis. Metaphase to anaphase in phase 3 (MAT-3) mutations in the APC will be tested to see if they lead to apoptosis in meiotic cells. The nematode *C. elegans* in larval stage 4 (L4) will be observed microscopically and apoptosis scoping will be done at the bend of the germ line. The outcome of this research may help prevent cancer and improve genomic stability.

#### **SAT-1004**

##### **CONCENTRATION OF HALOGENATED ORGANIC COMPOUNDS IN CALIFORNIA MARKET SQUID**

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Halogenated organic compounds (HOCs) are found ubiquitously in the marine environment and have been shown to have negative biological effects such as neurotoxicity and endocrine disruption. A majority of these compounds are introduced to the oceans anthropogenically via pesticides or industrial processes, but a growing body of evidence suggests a biogenic origin for certain classes of HOCs. Some of these compounds bioaccumulate in marine organisms, and it is important to understand how they move through food webs and enter human diets. This study investigates concentrations of known biogenic HOCs (e.g., methyl and dimethyl bipyrrroles and polybrominated diphenyl ethers) in California market squid (*Loligo opalescens*). This species is important because squid are efficient consumers of lower trophic organisms and are common prey to apex predators. *L. opalescens* is also Southern California's largest fishery so, while serving as an economically important species, it also provides a direct link between

marine food webs and human populations. By investigating the concentrations of lesser studied, naturally produced HOCs present in the California market squid, we will increase our understanding of how these compounds move through the food web and levels of human exposure. Identification and quantification of target compounds in local squid populations will be accomplished by microwave-assisted extraction, gas chromatography/mass spectrometry, and electron capture detection.

#### **FRI-1006**

##### **WASMANNIA AUROPUNCTATA POPULATION TRENDS IN ADJACENT PRIMARY AND SECONDARY FORESTS AT THE LAS CRUCES BIOLOGICAL STATION IN COSTA RICA**

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*Wasmannia auropunctata*, also known as the little fire ant (LFA), is a cosmopolitan, economically important invasive ant found in Costa Rica. *W. auropunctata* thrives in disturbed habitats where it quickly displaces native species, thereby decreasing diversity in the areas it infests and disrupting ecosystem processes. However, the invasive behavior of LFA is not apparent within intact forests in its original home range. Within Costa Rica, the effect of LFA on the environment differs from that of disturbed habitats in other countries where LFA has been introduced. LFA in intact primary forest in Costa Rica appears to be a minor species, perhaps kept in check by competition and predation by other ant species. Previous studies at the Las Cruces Biological Research Station in southern Costa Rica have estimated LFA density in primary and secondary forests. The objectives of the present study are to examine population trends in LFA populations in primary and secondary forests to determine if LFA is invading primary forest from adjacent reforested areas. This is being accomplished by sampling LFA populations in leaf litter at several sites in primary and secondary forest and within the ecotone interface between these two habitats. LFA densities appear lowest in primary forests, and higher in the interface and within the secondary forest areas. This corroborates results from previous studies in the same area and suggests that biotic and abiotic factors, including other ant species, suppress LFA densities.

#### **FRI-1000**

##### **HOW CHOCOLATE CAN REDUCE FIBROSIS IN TYPE 2 DIABETES**

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Studies have shown that heart failure is among the top ten leading causes of death in patients suffering from type 2 diabetes (T2D). Mitochondrial dysfunction in diabetic hearts has been shown to lead to cardiac cell death and eventually fibrosis. Fibrosis is the buildup of collagen due to cell death, thereby decreasing the contractility and elasticity of the heart leading to heart failure. In this study, we looked at the effects of (-)-epicatechin (EPI), found in dark chocolate, on reducing the progression of type 2 diabetes and fibrosis *in vivo*. T2D was induced by feeding rats a high energy diet (HED) consisting of 10% lard and 20% glucose mixed with their normal chow. Animals were treated with EPI (1 mg/kg/day) or water by oral gavage daily.

Body weights and plasma glucose levels were measured weekly to monitor the progression of T2D. Our results demonstrated that the diabetic animals had significant weight gain (~44%) and increased blood glucose levels (519 mg/dL) compared to control animals (37% and 185 mg/dL, respectively). EPI significantly reduced changes in body weight (~33%) and blood glucose levels (351.2 mg/dL) compared to diabetic animals. Histological analysis using Masson's trichrome stain showed that diabetic hearts contained more collagen than the control hearts, which shows the progression of fibrosis. In addition, Nile-red data shows the presence of lipid droplets, further showing the progression of fibrosis in the hearts. In conclusion, our results demonstrate the ability of EPI to reduce body weight, plasma glucose levels, and fibrosis in T2D.

#### **SAT-1010**

##### **PRODUCTION AND CHARACTERIZATION OF A NOVEL PROTEASE FROM THE MARINE MICROBE *ERYTHROBACTER* SP. NAP1**

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This project involves the cloning, isolation, and biochemical characterization of a novel protease from a marine microbe *Erythrobacter* species NAP1. The long-term objective of this research is to determine if the protease has potential biotechnological applications including uses in the food industry, for bioremediation, as laundry additives, or in molecular biological studies. Using bioinformatics, a serine endopeptidase gene has been identified: *NAP1\_09782*, a hypothetical protein that has sequence similarity to a trypsin-like serine peptidase. The gene was amplified and cloned into a plasmid that was then introduced into 2 cell lines: one that allows for single step protein isolation and another that is optimized for periplasmic, cytoplasmic folding and toxic proteins. A nickel resin was used to isolate this protease. The linear protein is 760 amino acids long with a predicted molecular mass of 105.09 grams per mole, which can help define the structure and functional information and biotechnological applications. Understanding these characteristics will help move forward the study of protein-to-protein interaction within the science field to help improve other areas that involve medicine, waste management, and food science. The selected protease may be a good detergent additive because it may have the ability to break down protein stains in clothing at lower temperatures since it is from a cold-water environment. This would reduce the need for higher temperatures and could reduce costs.

#### **SAT-1021**

##### **STUDYING THE EFFECTS OF BEE SENSORY RECEPTORS WHEN TESTING FOR PROBOSCIS EXTENSION REFLEXION**

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Studying the proboscis extension reflex (PER) in bees serves as a way to understand their cognitive processing. The honeybee *Apis mellifera* has been a primary study in bee research,

but researchers are beginning to study other bee species to learn more about them. The objective of this research was to determine if other bee species, besides the honeybee, have a proboscis extension reflex (PER), and if so, where on the bee's body PER is triggered. When observing their foraging behavior, it was noticed that larger bees, such as *Xylocopa violacea*, would always grab the flower and land on it with their abdomen touching the flower, suggesting that for larger bees, PER could be triggered when rubbing their abdomen. Smaller bees, such as *Lasioglossum zephyrum*, grab part of a flower and insert their faces to retrieve nectar, suggesting PER could be triggered when touching their antennae. To test for PER, we replicated restraint methods based on the way the bees forage. The bees were first given sucrose and water as a control on real-like artificial flowers to observe their response. They were then tested with Q-tips to see if the bees would express PER in a lab setting. Eleven bee species were examined. The honeybee was used as a control. Out of the 11 species, 2 tested positive for PER.

#### **SAT-1012**

##### **ANTIBACTERIAL ACTIVITY OF COFFEEBERRY (*RHAMNUS CALIFORNICA*), A TRADITIONAL NATIVE AMERICAN HERBAL MEDICINE**

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Many bacteria are becoming resistant to current antibiotics due to improper usage and over-exposure. Plants have been used for centuries by traditional healers and may provide new antimicrobials to treat antibiotic-resistant bacteria. One such plant, coffeeberry (*Rhamnus californica*), has been used by the Kawaiisu to treat infected wounds. Our purpose is to investigate whether *R. californica* has antibacterial properties. Extracts (500 g/mL) of *R. californica* berries, leaves, bark, and flowers were prepared in methanol, ethanol, ethyl acetate, and water. The extracts were screened for antimicrobial activity against various skin pathogens including methicillin-resistant *Staphylococcus aureus* (MRSA), *Streptococcus pyogenes*, *Propionibacterium acnes*, *P. humerusii*, *Mycobacterium phlei*, and *Candida albicans* yeast using disk diffusion assays. The alcoholic leaf and bark extracts showed the most potent antibacterial activity. Zones of inhibition ranged from 11.0 mm (methanolic leaf extract) against Gram-positive cocci to 22.0 mm (ethanolic leaf extract) against *M. phlei*. The minimum inhibitory concentrations of ethanolic leaf and bark extracts ranged from 0.98 mg/mL against *M. phlei* to 600 mg/mL against MRSA. The minimal fungicidal concentrations are 250 mg/mL (ethanolic and methanolic leaf extracts) and 500 mg/mL (methanolic bark extract). MRSA's growth rate was 53% less in 500 mg/mL ethanolic leaf extract compared to the nutrient broth control. We are characterizing the method of action and are in the process of isolating the active compounds. These are valuable findings, as they may lead to development of plant-based, affordable antimicrobials to which bacteria do not show resistance.



**FRI-1010****NOVEL DEPOSITION OF NICKEL HEXACYANOFERRATE FILM AND ITS APPLICATION**

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This work presents a new, controllable deposition of nickel hexacyanoferrate (NiHCF) film onto various conducting substrates including pencil leads. The NiHCF was prepared by voltammetric scanning of the mixture containing nickel salts and ferricyanides at -1.0V - + 0.8V (vs. silver/silver chloride). Under this condition, the NiHCF film was *in situ* deposited; thus the film thickness could be controlled. The use of less expensive base electrodes is especially attractive for the easy implementation of functional films. As such, the NiHCF/pencil leads were examined extensively. Some environmentally significant species were found to have responses on the NiHCF film including thiocyanate and nitrite. Systematic studies showed these ions are oxidized with anodic scanning voltammetry, and NiHCF film enhances such oxidation, which showed the sensing potential. [This work was supported by NASA-TSGC-NIP, DoED-MSEIP, NOAA, and Welch Grant ( BJ-0027 ).]

**FRI-1016****CAN THE ADDITION OF ALGAE TO A SHEWANELLA FUEL CELL LED TO THE PRODUCTIVITY OF ELECTROGENIC CULTURES**

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In recent years, fossil fuel consumption has led to an increase in research toward renewable or clean alternate fuel sources. Bioenergy is a clean alternative to fossil fuels that has a small carbon footprint. In order to test and develop novel methods of bioenergy production, we established an experiment to test the electrical conduction potential of a bacterium (*Shewanella*) and an algae (*Chlamydomonas*) encapsulated in a silica sol-gel matrix. We hypothesized that the photosynthetic byproducts of the *Chlamydomonas* culture would supplement the carbon source needed for the respiratory functions of the *Shewanella* and also use the acetate produced by *Shewanella*. This would allow a photosynthetically enhanced electron production system that would be harnessed as electrical potential using a fuel cell schematic. Preliminary results indicate the production of electrical currents within the fuel cell for the single encapsulated *Shewanella* culture as well as the mixed culture.

**FRI-1003****FIRST DESCRIPTION OF DISCONTINUOUS RESPIRATION IN THE PRAYING MANTIS *HIERODULA PATELLIFERA***

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Unlike many vertebrates, insect respiration is unusual in that it is both irregular and discontinuous giving rise to discontinuous gas-exchange cycles (DGC). Gas movement through the respiratory system is regulated by abdominal pumping and the opening and closing of small orifices in the thorax and abdomen (spiracles) that are continuous with a network of tubules (trachea). Discontinuous breathing patterns have been described in a number of insects including cockroaches, beetles, and locusts by flow-through respirometry, video monitoring of spiracles, or abdominal movements. However, no such analyses have been done using praying mantises (Insecta, Mantodea). Here we used a custom designed, MatLab-based video analysis system to describe the respiration-related abdominal movements in the mantis, *Hierodula patellifera*. Analyses were conducted over periods ranging from 24-72 hours and under different feeding regimes. Overall, mantis respiration occurred in discrete 30-45 second bouts with inter-bout-intervals ranging from 50-60 seconds. Individual bouts consisted of three distinct phases: phase one was characterized by shallow, irregularly spaced breaths; phase two consists of a series of 15-20 rapidly occurring, deeper breaths collectively lasting 17-20 seconds; and phase three consisted of 3-5 very deep breaths, each lasting 18-20 seconds. The three phases were characterized by progressive abdominal elevation superimposed on the breathing-related oscillations. In addition, our preliminary data suggest there are post-feeding changes in breath rate which we hypothesize are associated with increased metabolic activity. These experiments represent important steps forward in our understanding of the complex patterning and regulation of respiration in this model system.

**FRI-1014****SURVEY OF DEMERSAL SPECIES IN PLANNED OFFSHORE WIND TURBINE SITES OFF THE COAST OF MARYLAND**

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Offshore wind power is relatively new to the marine environment, and creating these machines involves construction of turbines to be put atop the sea floor. These large solid structures may disrupt reproduction, feeding behaviors, and population dynamics of benthic species. Our aim for this research is to sample the benthic fauna off the coast of Maryland in prospective locations that would be affected by the structure of the turbines in the environment. An assessment of the organisms at the benthic level of the prospective sites was taken by using a towed camera sled and <sup>1</sup>/<sub>4</sub> inch mesh beam trawl in transects 10 nm from the coast on the Outer-Continental Shelf. The species surveyed from the assessment were enumerated and identified to better understand the sites. Initial trawling transects suggests that there are very homogenous species on the sea floor. The preliminary results propose that the presence of the

turbine will be affecting a small sample of species and not a large array. Using a camera sled and beam trawl transects to identify and detect benthic fauna at the prospective locations for offshore wind turbines will assist in determining suitable sites. Our research corresponding to wind power facilities will aid in developing an informed decision for siting wind turbines and maintaining low threat levels to benthic marine life.

#### **FRI-1007**

##### **IDEBENONE AMELIORATES MITOCHONDRIAL DYSFUNCTION IN AN ANGELMAN SYNDROME MOUSE MODEL**

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Angelman syndrome (AS) is a neurodevelopmental disorder, symptoms of which include microcephaly, epilepsy, impaired motor coordination, speech impairment, and intellectual disability. In 80% of cases, AS is caused by a deletion of the *E6-AP Ubiquitin E3 ligase (UBE3A)* gene on chromosome 15q11-13 on the maternal allele. Due to genomic imprinting of the paternal allele, *UBE3A* expression is silenced in regions of the brain, mainly the hippocampus and cerebellum. Previous studies of the maternally-deficient *Ube3a* AS mouse model revealed a structural mitochondrial defect and a significantly decreased level of complex III in the hippocampal region. In our study, we analyzed the effects of a coenzyme Q<sub>10</sub> (CoQ<sub>10</sub>) analog, idebenone, in the mouse model. We hypothesized idebenone would improve the flow of electrons in the electron transport chain (ETC) and alleviate the symptoms of AS. To analyze whether there were any coordination or behavioral changes after treatment, we conducted a rotarod assay to measure motor coordination and a marble burying assay to assess activity in novel environments. From these assays, we found an improvement in motor coordination and increased activity in novel environments with idebenone treatment. Secondly, immunohistochemistry (IHC) and western blot were performed to investigate the effects of idebenone on expression levels of mitochondrial complexes in the hippocampus. Results revealed increased expression of complex III and COX IV in the hippocampus of idebenone-treated mice. These results suggest that treatment with a CoQ<sub>10</sub> analogue such as idebenone may potentially alleviate symptoms in patients with Angelman syndrome.

#### **FRI-1021**

##### **REDUCED MATING BEHAVIOR IN ESTROGEN EXPOSED *XENOPUS LAEVIS* MALES**

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Atrazine reduces testosterone (T) and increases estradiol (E2) production in male African clawed frogs (*Xenopus laevis*). Atrazine also inhibits male reproductive behavior. In the current study, we examined whether the loss of male mating behavior was due to increased E2 and/or decreased T, and assessed whether E2 inhibited male reproductive behavior by decreasing endogenous T. Immersion in E2 or 17 $\alpha$ -ethinyl estradiol (EE2) and E2 implants were used to elevate estrogen levels and examine effects on male reproductive behavior. E2-treatment by

immersion was ineffective. T levels in treated males were reduced dramatically 24 hours after exposure but shortly returned to normal. Treatment with EE2, which has a longer half-life, reduced male reproductive behavior. Males treated with EE2 were out-competed by control males 3 to 1. E2 implants also reduced male reproductive behavior. Control males out-competed treated males 11 to 2. E2 levels ranged from 13 - 42 ng/ml in implanted males, but T levels were not affected in an earlier study, and current analysis will determine hormone levels in animals used in breeding studies. Both E2 and EE2 decreased reproductive behavior, but possibly independent of any effects on endogenous T.

#### **SAT-1018**

##### **INVESTIGATION OF ROLES FOR CELLULAR FACTORS IN HUMAN CYTOMEGALOVIRUS NUCLEAR EGRESS**

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Human cytomegalovirus (HCMV) is a member of the herpesviridae family of DNA viruses. Like other DNA viruses, HCMV replicates its genome in the host cell nucleus. The genomic DNA is packaged and assembled into viral nucleocapsids that translocate into the cytoplasm. Since HCMV nucleocapsids are too large to pass through the nuclear pore complex, the virus utilizes a complex multi-step process, nuclear egress, to exit the nucleus. During this process, the nucleocapsids gain access to the inner nuclear membrane (INM) following disruption of the underlying nuclear lamina. This is followed by the budding of the nucleocapsids into the perinuclear space. Finally the enveloped nucleocapsids fuse with the outer nuclear membrane (ONM) to be released into the cytoplasm. The key players in this process include two conserved viral proteins that form the nuclear egress complex (NEC). In HCMV, these proteins are the membrane-bound protein UL50, and its nucleoplasmic partner UL53, and both of these proteins are essential for viral nuclear egress. We have tried to explore the possibility that the virus recruits cellular factors for this step. One of them was Alix, a member of the cellular endosomal sorting complex required for transport (ESCRT) family of proteins. We are interested in testing the roles for Alix and TSG101 during HCMV replication and nuclear egress. We are using dominant negative (D/N) mutants of both Alix and TSG101 to reduce the functions of the endogenous proteins in human fibroblasts.

#### **SAT-1017**

##### **INCREASING ACCRUAL TO STUDIES OF HIV/AIDS PATIENTS WITH CANCER**

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Despite living with a compromised immune system and the side effects of long term use of HIV/AIDS medication, people living with HIV/AIDS (PLWHA) are now reaching the decades when the incidence of age-related diseases increases. Cancer is one of the most common life threatening diseases of the aging process, and its treatment places additional challenges on the body. The goal of this research is to examine why PLWHA are difficult to recruit for participation

in research studies when cancer develops. Institutional review board (IRB)-approved flyers and word-of-mouth were used in clinic and community settings to recruit 45 PLWHA to the study's focus interviews, of which 25 participants were also coping with cancer. Eligible participants were at least 18 years old, had a diagnosis of HIV/AIDS, and spoke English. Interviews were transcribed, coded with Dedoose software, and analyzed. Subsequently, participants were invited to join focus groups to discuss the findings and develop strategies for expediting participant accrual to studies for PLWHA and cancer. Of the focus interview participants, 15 joined the focus groups, thereby providing continuity juxtaposed with new participants' fresh perspectives. This paper will describe the summative data gathered during the focus interviews, the study promotion strategies that evolved from the focus interview data, and the focus group members' evaluations of, and recommended revisions to, those promotion strategies. Those strategies are ready for testing in a definitive study focused on PLWHA and cancer.

### **SAT-1007**

#### **THE IMPACT OF GENE DUPLICATION AND DIVERGENCE ON THE FORMATION OF PROTEIN COMPLEXES**

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The process of organ identity is relatively well understood in *Arabidopsis*, where the ABC model explains the genetic basis of floral organ identity. The ABC model contains A, B, and C genes, which are expressed in overlapping fields to produce floral organs: sepals, petals, stamens, and carpels. In this model, A genes are responsible for sepal identity, A + B genes for petal identity, B + C genes for stamen identity, and C alone for carpel identity. These genes are members of the *MADS-box* transcription factor family, which function together in protein complexes; however, it remains unknown how evolutionary conserved these *MADS-box* genes are amongst disparate plant species. To address this, we are interested in studying the process of floral organ identity determination in the lower eudicot *Aquilegia* (columbine). This new model system is unique in possessing 5 types of floral organs rather than the typical 4. Previous experiments using virus-induced gene silencing (VIGS) in *Aquilegia* have shown that while some duplicated *MADS-box* genes have inherited portions of the ancestral functions (subfunctionalization), others have evolved entirely new functions related to the fifth type of floral organ (neofunctionalization). Yeast two-hybrid and three-hybrid screening will be conducted to determine physical interactions occurring between different *Aquilegia* *MADS-box* proteins. Understanding the process of flower development in *Aquilegia* offers an important reference point for evolutionary comparisons between different species of flowering plants. Furthermore, it will help us elucidate the genetic basis for the evolution of floral novelty.

**FRI-1015****OBESITY: CORRELATION BETWEEN BODY-MASS INDEX (BMI) AND LEPTIN**

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Over the past decade, obesity has been a growing epidemic. According to the Center for Disease Control and Prevention, more than one third of U.S. adults (34.9%) are obese. In 2008, the estimated annual medical cost of obesity in the United States was \$147 billion. In this study, we focused our attention on leptin, known for its role in indicating to the brain that food satiation has been reached. If we could find a mutation in this gene, it could lead to insight and validity in implicating that not only diet is a factor that contributes to obesity, but genes as well. Using a human subject informed consent form, questionnaire, weight scale, and tape measure, Qiagen buccal genomic DNA extraction kit, primers for human leptin gene *exon 3*, PCR kit, and agarose gel electrophoresis, we used BMI values and diet to establish trends in different racial groups and correlated them with DNA changes, if any. Findings from this study revealed no mutations, but variations and gaps were found in the intronic region. Overall, our findings may expand our understanding of the role of leptin in correlation with BMI. However, our sample size was not large enough to draw conclusions.

**SAT-1015****ATTENTION INCREASES V1 NEURONAL FIRING RATES IN MICE**

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Visual attention increases the firing rates of V1 neurons. However, it is not well understood how V1 neurons gain their tendency to fire more action potentials (APs) as well as how they interact with each other to increase their firing rates. Here, we investigated the mechanism of V1 APs gain when an animal is paying visual attention. Calcium imaging with the synthetic calcium indicator GCAMP6 was used to measure neuronal spiking and synaptic input across populations of neurons *in vivo*. A viral vector carrying the *GCAMP6* gene was transduced into V1 neurons of wild-type mice. Next, the mice were trained both to pay and ignore visual attention. A two-photon calcium imaging experiment was performed to measure V1 neuronal spiking activities. Our preliminary data suggests that V1 neurons increase their firing rates through a tonic depolarization, and their spiking activities were higher when the animals were paying attention as compared to when attention was ignored. Our findings are important since visual attention was found to deteriorate in many neuronal diseases, and its mechanism needs to be understood to create future treatments.

**FRI-1009****A NOVEL MOUSE MODEL TO STUDY CHRONIC PROGRESSIVE MULTIPLE SCLEROSIS**

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Multiple sclerosis (MS) is an inflammatory autoimmune disorder affecting the central nervous system (CNS) which affects over 400,000 Americans and over 2.5 million people worldwide. Although most patients are initially diagnosed with relapsing remitting MS, the majority of these patients later develop a chronic progressive form of MS for which there is no well-established mouse model. The most common genetic factors associated with genetic susceptibility to MS are played by the human leukocyte antigen (HLA) genes which reside within the major histocompatibility complex (MHC), in particular the HLA-DR2b haplotype. Additionally, tumor necrosis factor (TNF)- $\alpha$  signaling through the TNFR2 receptor has been shown to have an important role in the remyelination process, and mice deficient for TNFR2 have been shown to have increased disease severity. The aim of this project is to evaluate TNFR2-/- mice, transgenic for the MS-associated HLA-DR2b haplotype, for their potential use as a model for chronic progressive MS. Our data indicates that the disease observed in TNFR2-/- HLA-DR2b closely mimics the pathology and clinical phenotype observed in chronic-progressive MS. Currently, we are further investigating the mechanisms that contribute to the disease phenotype in these mice. Thus, TNFR2-/- HLA-DR2b mice can be used to study chronic/progressive MS and illuminate some of the mechanisms which are involved in the pathology of this disease.

**SAT-1013****FTIR STUDY OF ANAPLASTIC SARCOMA OF THE LIVER IN MICE**

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Anaplastic sarcoma is a rapidly dividing cancer of the bone, cartilage, fat, muscle, blood vessels, and other connective or supportive tissues. A standard treatment for anaplastic sarcoma has yet to be made due to its resistance. The most common treatment has been nephrectomy. The other cancer treatment option is resection. Although the morbidity and mortality rates of resection have improved over the years, this method still remains invasive and does not guarantee the complete removal of cancer. The goal of this research aims to develop a method to detect cancer and differentiate between normal tissue, cancerous tissue, and the margin by using infrared spectroscopy. The infrared spectrum of the tissue was used to select chemical absorption vibrational bands that are different in the cancer segment and normal segment of the tissue. These differences allowed us to develop biomarkers. When plotted against each other, the biomarkers produced 2D plots, histograms, and contour images that highlighted possible cancerous regions, normal regions, and marginal regions. To ensure the validity of our method, our results were compared to an H&E of the tissue. Thereby, one of the future medical applications of this cancer study is to construct a fiber optic probe that could produce a spectral

image of a patient's tissue in real time during surgery. As a medical tool, the probe could signal the surgeon what tissue to incise and aid in the process of successfully removing all cancerous tissue, including the intermediate tissue, in order to decrease the chance of recurrence.

#### **SAT-1002**

##### **EFFECTS OF JNK ACTIVITY ALTERATIONS ON THE DEVELOPMENTAL RESPONSE TO ETHANOL EXPOSURE**

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Fetal alcohol syndrome (FAS) causes a variety of detrimental phenotypes in humans including reduced birth weight, decreased survival, developmental delays, and learning and memory defects. Although this disorder is preventable, the number of individuals affected by FAS has not decreased in 30 years. Therefore, a better understanding of ethanol (EtOH) response pathways during development could provide possible treatments or cures for the disorder. We use *Drosophila melanogaster* to study developmental ethanol effects. When exposed to EtOH during development, *Drosophila* exhibit many of the same deleterious phenotypes seen in humans, including lower survival. We have previously shown that the insulin-receptor pathway is involved in mediating the effects of developmental EtOH exposure and exerts its effects in part through regulation of the response to oxidative stress. In addition, we have shown that expression of genes in the Jun kinase (JNK) pathway is reduced in ethanol-exposed larvae. We therefore hypothesize that signaling through the JNK pathway, which is known to regulate oxidative stress resistance, is suppressed by developmental ethanol exposure. We will expose flies mutant for basket (*bsk*, encodes JNK), kayak (*kay*, encodes JNKK), and puckered (*puc*, encodes a JNK phosphatase) to developmental EtOH and compare survival rates and development times, to those of controls. We predict that *bsk* and *kay* mutants, which have reduced JNK signaling, will be sensitive to ethanol, while *puc* mutants, which have increased JNK signaling, will be resistant. (This research was supported by the National Science Foundation NSF-REU Grant# DBI 1004350.)

#### **SAT-1016**

##### **NESTMATE RECOGNITION IN *POLYBIA***

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Social insects can often distinguish between kin and non-kin. Recognition cues appear to be chemical, through cuticular hydrocarbon signatures. *Polybia* is a genus of social wasps belonging to the tribe Epiponini. There is little scientific knowledge about nestmate recognition in *Polybia* wasps. This research will increase our knowledge of kin recognition mechanisms by adding more information on Epiponini wasps. This research was conducted at Las Cruces Biological Station in Coto Brus County, Costa Rica. Because neighboring colonies tend to be more closely related than distant colonies, we hypothesized that *Polybia* wasps would be more likely to reject individuals from distant colonies. To test nestmate recognition we will remove 10 individuals from the study nest (main nest) for a certain period of time and reintroduce



these individuals back to their nest. To test the effect of introducing non-nestmate kin, we will remove 10 individuals from 2 neighboring nests and introduce them to the main nest. We will do the same using individuals from 2 distant nests. We expect the results to show a significant difference between nestmate recognition and non-nestmate recognition from neighboring and distant colonies. Therefore, we expect to conclude that *Polybia* wasps do reject unrelated non-nestmates with more frequency than non-nestmate kin.

#### **SAT-1006**

##### **ASSESSING MICROBIAL BIOREMEDIATION IN A WOODCHIP BIOREACTOR FOR POLLUTANT REMOVAL**

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The Monterey County Farm Bureau states that Monterey County's agricultural community is among the most productive in the world. This productivity is coupled with heavy use of pesticides, herbicides, and fertilizers. Current regulations require the agricultural industry to reduce pollution and allow for this to be done using treatment systems. The goal for this project is to establish data to promote the construction of woodchip bioreactors adjacent to agricultural fields as a way to protect coastal habitats as well as reduce the environmental damage to marine waters that receive agricultural runoff. An over-ground woodchip bioreactor will be used in this study. A water quality test will be necessary to check for turbidity, pH, temperature, salinity, dissolved oxygen, and phosphate and nitrate concentrations. A colony count will be done to determine the concentration of bacteria in the woodchip bioreactor at the inflow, middleflow, and outflow. Bacteria colonies will be picked to axenic cultures. Polymerase chain reaction (PCR) will be run to identify the presence of nitrate reductase genes and organophosphate degradation genes in bacteria. If the data shows a reduction in the amount of nitrate and phosphate in the drainage, then it may also be effective for bioremediation of other pollutants like pesticides, herbicides, and pathogens. An over-ground woodchip bioreactor could be an option for farmers to reduce pollution because it does not use a lot of land and its efficiency may be improved by existing environmental conditions.

#### **FRI-1013**

##### **HUNT FOR GENES REGULATED BY CONTACT-DEPENDENT GROWTH INHIBITION SYSTEMS**

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Bacteria engage in communal behavior, capable of communicating among the colony. One example of such interactions is contact-dependent growth inhibition (CDI), whereby bacteria touch neighboring, competing cells, inhibiting their growth. It is known that CDI is mediated by large, cell surface proteins bearing toxic tips. These tips are auto-cleaved on contact with cell surface receptors on the neighboring cell. The focus of this work is to determine which genes are up- or down-regulated in isogenic cells capable of engaging in CDI orchestrated by a type V secretion system. Through transposon mutagenesis, the *lacZ* gene was randomly inserted into a chromosome of *E. coli* strain K12 and fused to virtually every gene therein. This identifies cells

where gene regulation (transcription and translation) is altered by the CDI system. The CDI gene is introduced into these cells via electroporation. IPTG, a *lac* operon inducer, is added to media, inducing CDI on the plate. Xgal binds to the *lacZ* product,  $\beta$  galactosidase, and causes blue coloration in the bacteria. The *lacZ* expression between CDI+ and CDI- cells is compared directly by the intensity of the blue color of each colony. This work would be the first in which bacteria have been shown to communicate via CDI. These studies are directly relevant to understanding how bacteria interact with one another in the real world, for example, in the human intestinal microbiome. Further, these results could be applied to the development of drugs that block communication between pathogens, or enhance communication and growth between beneficial strains.

#### **FRI-1020**

##### **ENVIRONMENTAL CHARACTERIZATION FOR A SWINE TRANSPORT ASSESSMENT**

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Transportation of animals has potential impacts on the humane treatment of animals and the safety of both the animals and the people involved. This study will review outdoor weather conditions and ASHRAE annual records to determine if there are correlations among the various data sets and aspects. The swine industry recognizes that problems occur during transport that result in dead or down pigs and supports research focused on trailer management to improve challenging environmental conditions. A year-long monitoring study was completed for assessing the thermal environment during pig transportation over a wide range of outdoor weather conditions. During this study, the trailer was managed according to industry practices (Transport Quality Assurance Program of the National Pork Checkoff). A weather data set of hourly outdoor temperatures that correspond to the geographical trailer location was generated using the GPS coordinates and the data from the nearest local National Oceanic and Atmospheric Administration (NOAA) weather station. Indoor environment and outdoor weather data was summarized into an overall distribution to represent the outdoor conditions and indoor conditions over the complete study. This distribution will be compared to geographical distributions within the United States, based on ASHRAE records, to represent applicability. Additionally, correlations were assessed between the inside and outside environmental data to identify trends, specifically floor temperature, skin temperature, and overall temperature during extreme hot and cold conditions. Results of this study have the potential to identify management areas for reducing the number of dead or down pigs. Analysis is ongoing and complete results will be presented.

**FRI-1008****SOIL CHARACTERISTICS OF A RAINFOREST HIKING TRAIL AT THE VOLCAN TENORIO NATIONAL PARK, COSTA RICA**

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Volcán Tenorio National Park in northwestern Costa Rica received 35,000 visitors in 2012, a substantial increase over previous years; many came to enjoy the Rio Celeste (Sky-blue River). The river and waterfall are accessed by a single trail with various types of surfaces: unimproved bare soil, tree roots, concrete blocks, logs, or other materials. In order to assess the impact of trampling by hikers, soil conditions were analyzed during the rainy season along the trail in areas with and without soil coverings. At each point, path width was measured. Soil pH, percent moisture, resistance to penetration, total dissolved solids (TDS), and conductivity were tested. Values were compared at 3 positions at each sampling site: the center of the trail, the edge of the trail and the nearby forest interior 3 m from the trail edge. Soil characteristics were similar for all trail types; bare soil did not differ from other soil coverings. Soil pH (range 4.5- 6.8) and soil moisture (range 20-70%) did not vary with respect to either position or trail type. Resistance to penetration was greatest at the center of the trail. TDS and conductivity differed between the trail and the adjacent forest interior. Under present levels of use, trampling appears to have caused minimal damage in soil conditions, without substantial degradation of the trail.

**SAT-1000****LORAZEPAM IS A SAFER ALTERNATIVE TO ANTIPSYCHOTICS FOR ATTENUATING BRAIN INJURY-INDUCED AGITATION**

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Traumatic brain injury (TBI) affects 10,000,000 people worldwide and 1,700,000 in the United States, making it a significant health concern. In addition to motor and cognitive dysfunction, TBI also induces aggression and agitation, which hampers acute care and rehabilitation. To attenuate these behavioral dysfunctions, antipsychotic drugs (APDs) are administered. Studies from our laboratory have shown that chronic administration of APDs impedes the acquisition of spatial learning. Despite the negative effects, some form of sedation is necessary so that physicians can treat disruptive patients. Hence, the goal of this study was to evaluate the effects of lorazepam, a benzodiazepine, on motor and cognitive outcome after TBI. Twenty-eight anesthetized adult male rats received either a cortical impact (2.8 mm deformation at 4 m/sec) or sham injury and then were randomly assigned to 4 groups where a TBI and corresponding sham group received either lorazepam (1.0 mg/kg; i.p.) or saline vehicle (1.0 mL/kg; i.p.) once daily for 19 days. Motor function and cognition were assessed using established tests on days 1-5 (beam-walk) and 14-19 (water maze), respectively. No significant

motor and cognitive differences were revealed between the TBI+lorazepam and TBI+vehicle groups ( $p = 0.60$  and  $p = 0.09$ , respectively). These results suggest that daily administration of lorazepam (1.0 mg/kg) does not impair motor and cognitive outcome after TBI, which is unlike that reported for APDs. Hence, lorazepam should be considered as an alternative treatment to control clinical TBI-induced agitation and aggression. Ongoing studies are determining the range of doses that can be safely administered.

#### **FRI-1005**

##### **CARDIAC REPAIR IS ENHANCED BY NOTCH SIGNALING IN CARDIAC PROGENITOR CELLS**

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Cardiovascular disease is the number one cause of death in the United States. Current therapies for heart disease target preservation of function but do not support tissue regeneration to pathological challenge. The notch signaling pathways play a critical role in cardiac development. It guides cardiac cell fate decisions that underlie myocyte and vessel differentiation. In the adult heart, notch plays a regenerative role after pathological injury. When notch is reactivated in the damaged myocardium, overexpression of the intracellular domain either by genetic or exogenous means lessen destructive effects of hypertrophy and ischemia. Adult cardiac progenitor cells express the notch receptor and respond to notch activity by proliferating and differentiating into transient amplifying myocytes, reinforcing the importance for this signal in cardiac repair. The level and duration of notch activity determine whether progenitors continue to proliferate or exit the cell cycle and commit to an adult cardiac cell phenotype. We demonstrate that elevated notch signaling promotes growth, survival, and differentiation of cardiac progenitor cells into smooth muscle lineages *in vitro*. Transfer of cardiac progenitor cells engineered to express activated notch (CPCeK) into infarcted myocardium results in better cardiac function and smaller infarct size compared to hearts receiving control cells (CPCe). Levels of phosphorylated Akt and ribosomal S6 are elevated in CPCeK, suggesting a mechanistic basis for the improved growth, survival, and cardioprotection in these cells. These findings reveal further potential for exploiting the notch pathway as a therapeutic target in the treatment of cardiac disease.

#### **FRI-1001**

##### **COMPARISON OF EPISTAXIS SEVERITY SCORE AND EPISTAXIS FREQUENCY IN HEREDITARY HEMORRHAGIC TELANGIECTASIA (HHT) AND THE GENERAL POPULATION**

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Hereditary hemorrhagic telangiectasia (HHT) is an autosomal dominant disease characterized by external and internal arteriovenous malformations (AVM). AVMs are vascular malformations that result in a high pressure artery connecting directly to a vein. Life threatening consequences of HHT include complications of brain, lung, and liver AVMs. Externally, one sign of HHT is small AVMs called telangiectases. These telangiectases also cause epistaxis (i.e., nosebleeds). Because these telangiectases can form in the thin tissue of the nose, any slight trauma can

initiate bleeding. Telangiectases, epistaxis, and family history of HHT are used in diagnosis of HHT. Individuals with HHT require screening protocols to look for solid organ AVMs using MRI and echocardiogram technologies. However, the diagnosis is often uncertain in individuals with mild phenotypes and the screening procedures are costly. To better diagnose HHT it is especially important to understand the range of severity of epistaxis in the general population. We have and are continuing to collect data on epistaxis using the epistaxis severity score (ESS), a validated questionnaire in the population diagnosed with HHT. We used this same questionnaire to assess the phenotypic variability in the general population. To date, we have collected 98 individuals from the general population and are in the process of collecting additional individuals. By collecting ESSs and frequencies of epistaxis in the general population we can use this information as a control to determine thresholds for who requires genetic testing and AVM screening. This will also allow for a more cost-effective approach to diagnosis and management.

#### **FRI-1004**

##### **THE INFLUENCE OF POLLINATOR ANATOMY ON COMMON MILKWEED POLLINATION**

Adriana Roman, Aaron Howard.

*Northeastern Illinois University, Chicago, IL.*

Flowering plants require vehicles, such as wind or animals, to move pollen between plants. From the plant perspective, it is important that the vehicles fit well with flowers, so that pollen movement and plant reproduction are efficient. For this study, we investigated the relationship between insect pollinator (animal vehicle) anatomy and the pollinator's ability to remove pollen from flowers of the common milkweed plant (*Asclepias syriaca*). We collected 200 insects after they visited flowers of common milkweed plants found on the campus of Northeastern Illinois University and preserved them in a freezer for further analysis. Then, using a dissecting microscope and Imagej, we estimated the amount of pollen each pollinator carried along with the size of various anatomical features. The western honey bee (*Apis mellifera*) carried significantly more pollen than either native bumblebees or lepidopterans (butterflies and moths). This may be due to the fact that, across traits, western honey bees are smaller in size than native bumblebees and more similar in size to native Apids (e.g., *Anthophora abrupta*) that were more abundant pre-European settlement. Through this study, we hope to gain a better understanding of the pollination system of the common milkweed and conserve it for organisms, like the monarch butterfly, that rely on it as a host.

#### **SAT-1011**

##### **AT THE HEART OF MICROTUBULE NUCLEATION: ELUCIDATING THE INTERFACE BETWEEN ALPHA- AND GAMMA-TUBULINS**

Luis Gonzalez<sup>1</sup>, Erin Turk<sup>2</sup>, Tim Stearn<sup>2</sup>.

<sup>1</sup>*University of California, Los Angeles, Los Angeles, CA,* <sup>2</sup>*Stanford University, Stanford, CA.*

Microtubule nucleation and assembly are accomplished via the interplay of 2 factors: the *alpha/beta*-tubulin heterodimer, which polymerizes to form microtubules, and the *gamma*-tubulin ring complex (gTuRC), which nucleates microtubule formation. Based on structural

studies of microtubules and the gTuRC, microtubule nucleation is proposed to occur by a direct interaction of *gamma*-tubulin with *alpha*-tubulin; however, this interaction has never been experimentally confirmed. To show definitively that *gamma*-tubulin and *alpha*-tubulin interact, and identify the residues involved in their interaction, we make use of the yeast two-hybrid system. We used site-directed mutagenesis of key residues in *Xenopus gamma*-tubulin proposed to be involved in this interaction (T175R, V179R, D176A, E177A, and S179A). Additionally, we used error-prone PCR to make random mutations and thus discover additional residues that may be involved in this interaction. We then used the yeast two-hybrid system, in which we have shown that *gamma*-tubulin and *alpha*-tubulin interact, to test which mutants of *gamma*-tubulin were still capable of interaction with  $\alpha$ -tubulin. By identifying the domains in *gamma*-tubulin required for interaction with *alpha*-tubulin, further studies can be conducted to specifically address how disruptions in microtubule nucleation affect cell physiology and division.

#### **SAT-1020**

#### **THE RECORDING OF MONOPHASIC ACTION POTENTIALS SIMULTANEOUSLY FROM THE EPICARDIAL SURFACES OF PORCINE HEARTS**

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Monophasic action potentials (MAPs) are electrical signals that represent the focal depolarizations and repolarizations of cardiac myocytes. The detection of MAPs via applied catheters may aid in determining both characteristic waveforms as well as the relative viability of the underlying cardiac tissue. Such detection would be beneficial in cases of atrial fibrillation, where ablative therapies are used to kill the cells triggering the arrhythmia. Recording MAPs at the trigger site post-ablation, the success of the treatment can be assessed immediately, and corrected if necessary. The purpose of the study was to collect and compare signature epicardial MAPs from isolated hearts. Hearts from swine were re-animated using previously described Visible Heart® methodologies: each heart was functioning in a normal sinus rhythm. Modified 7 Fr mapping catheters, with 4 ball electrodes and 2 ring electrodes each, were placed on the epicardial surface while another was inserted into the heart. The catheters were arranged such that both recorded from the same approximate anatomical location. Epicardial MAPs, along with the ECG, were recorded using a multichannel recorder. MAPs were recorded from both atrial and ventricular locations on the right side of the heart. In cases of atrial fibrillation an ablation may be performed either epicardially on the myocardium to attempt to make induced lesions transmural. The detection of MAPs using a MAPs catheter can be used to determine the relative, acute, viability of cardiac tissue in a specific area, which can lead to a higher rate of success for the treatment of atrial fibrillation.

## **FRI-1012**

### **CATEGORIZING BACTERIOPHAGES FOR TREATMENT OF ISOLATED MRSA STRAINS USING PCR ASSAY**

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When treating methicillin-resistant *Staphylococcus aureus* (MRSA) infections, vancomycin is commonly used. Vancomycin is traditionally administered systemically for 2 weeks, but can result in adverse effects, including nephrotoxicity. Phage therapy, i.e., the use of bacterial viruses to kill target bacteria, is an alternative method used to treat antibiotic-resistant bacterial infections. Because of their specificity, bacteriophages are less likely to alter the patient's microbiome when compared to antibiotics. There are 2 types of bacteriophages. Temperate bacteriophages can incorporate their DNA into the host's genome by using integrases. This involves the lysogenic cycle – the prophage (i.e., integrated phage DNA) stays dormant until it enters the lytic cycle. Obligately lytic bacteriophages can only undertake the lytic cycle by lysing their hosts, using the host's internal mechanisms to replicate and propagate. This characteristic makes these types of bacteriophages a favorable organism of alternative antibacterial agents for therapeutic purposes due to their inability to cause horizontal gene transfer. This study will characterize a group of newly isolated bacteriophages, which may be used as antibacterial agents to treat MRSA infections. Using a multiplex PCR assay we will identify integrase genes in the bacteriophage DNA as a means of differentiating between obligately lytic and temperate bacteriophages. The genes we will be searching for are: *Sa1int*, *Sa2int*, *Sa3int*, *Sa4int*, *Sa5int*, *Sa6int*, and *Sa7int*. These bacteriophages will be further tested to determine their effectiveness at lysing clinical MRSA strains.

## **SAT-1014**

### **EFFECTS OF ESTROGEN ON THE GONADAL DEVELOPMENT OF ESTROGEN SENSITIVE AND INSENSITIVE CROSSBRED *XENOPUS LAEVIS* TADPOLES**

Cara He, Tyrone Hayes, Xuan (Susan) Luong, Flor Gowans, Faye Pon, Alejandra Cabrera, Karen Jiawen Zhang, Maggie Tsang.

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When genetically male larval African clawed frogs (*Xenopus laevis*) are exposed to estrogen, they develop into female frogs phenotypically. In addition, temperature affects growth and development and potentially sex differentiation of tadpoles. We examined interactions between estrogen and temperature on sex differentiation across 2 populations of *X. laevis* that differ in their sensitivity to estrogen. We raised tadpoles from both populations at 17 °C and 27 °C to compare differences in growth and gonadal development. After metamorphosis, we dissected the frogs and examined their gonads to determine their sex and compute sex ratios. The sex ratio differences between the 2 temperatures were less than 5%. The 2 populations differed greatly in estrogen sensitivity when exposed to 3 ng/ml estrogen. An insensitive population was 17% female at 17 °C and 9% female at 27 °C, while the sensitive population was 90% female at 17 °C and 86% at 27 °C. We are currently studying hybrid offspring between

these two populations. We crossed the male from the sensitive population to the female from the insensitive population (and vice versa) to create the hybrids. The current study will determine whether the estrogen sensitivity is heritable through the maternal parent, paternal parent, both, or neither.

#### **SAT-1009**

##### **PATTERNS OF HERBIVORY WITH RESPECT TO LEAF CHARACTERISTICS IN RAINFOREST SPECIES AT VOLCAN TENORIO NATIONAL PARK COSTA RICA**

Ana Nunez Castrejon<sup>1</sup>, Juan Cerda Herrera<sup>2</sup>, Diana Lieberman<sup>2</sup>.

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Insects are the most significant herbivores in the tropical rainforest. In this study, we asked whether herbivory in rainforest plants is related to variation in leaf characteristics. We predicted that insects should feed most on plants with thin leaves and high moisture content. Herbivory patterns were analyzed in 4, co-occurring, closely-related understory species at Volcán Tenorio National Park in northwestern Costa Rica. Leaves of comparable age were sampled from *Dieffenbachia* sp., *Spathiphyllum* sp., *Philodendron* sp. (Araceae), and *Peperomia* sp. (Piperaceae). Types of damage, in order of frequency were: holes in the leaf blade (45.0% of leaves); chewed edges (42.2%); scraped leaves (11.5%); and leaf mines (1.2%). All types of herbivory were distributed independently of each other on the leaves. Epiphyll frequency was highest in *Peperomia* (66.7% of leaves). Leaf area loss was greatest in *Peperomia*, followed by *Dieffenbachia*, *Philodendron*, and *Spathiphyllum*. The distribution of types of damage was the same in all 4 species. The species differed in leaf size, thickness, weight per area, moisture content, and rate of water loss. Herbivory was highest in species with fast rates of water loss. There was no simple relationship between herbivory levels and leaf thickness, leaf moisture content, or leaf weight per area, nor was herbivory associated with presence or absence of epiphylls.

#### **SAT-1001**

##### **CHARACTERIZATION OF GENES ASSOCIATED WITH ABSENCE OF GERM LINE CELLS IN ZEBRAFISH (*DANIO RERIO*)**

Carina Ramos, Kellee Siegfried.

University of Massachusetts Boston, Boston, MA.

Zebrafish is a crucial animal model to study early development and gene function in vertebrates. We are using zebrafish to identify and study genes that are necessary for germ line development. Our goal is to understand the role played by two genes in the germ cells: *C17orf104* (named *moto*), and *slc34a1a* (named *vacant*) in zebrafish. By comparing the gene sequence of *c17orf104* and *slc34a1a* from diverse species, we learned they are highly conserved in vertebrates, including *Homo sapiens*. Also, they are highly expressed in the reproductive system. Although, there is still a lack of information about the function of these 2 genes in germ cells. Our histological studies have shown mutations affecting these 2 genes in zebrafish, both ultimately resulting in sterile males. The mutation on *C17orf104* is presumed to



be responsible for a failure in meiosis. The mutation affecting *slc34a1a* leads to loss of all germ cells. In this study, we are testing how the genetic mutation at each locus affects the development of the germ line cells in zebrafish. To confirm that each of our original mutations is the cause of the observed sterility, we are generating new mutations in each. To this end, the CRISPR - associated proteins (Cas) system was used as a targeted genome mutagenesis tool. Furthermore, functional elements may be recognized on the basis of their evolutionary conservation.

#### **SAT-1008**

##### **METHYLGLYOXAL CAUSES NEURONAL CELL DEATH VIA OXIDATIVE STRESS**

Astrid Trujillo, Steven Keys, Sue Mungre.

*Northeastern Illinois University, Chicago, IL.*

Uncontrolled diabetes can lead to several serious complications such as kidney failure, atherosclerosis, and neuropathy. Diabetic neuropathy causes a burning, tingling sensation in the extremities; alternately it might lead to loss of sensation. This is believed to be due to impairment and eventual death of neurons. However, the mechanisms by which neuronal death occurs are not yet clear. Earlier studies have shown that methylglyoxal (MG), a metabolite of glucose, is present in high levels in diabetic patients. MG is reported to bind to proteins and alter their functions. The goal of our study was to determine whether MG treatment causes death of neuronal cells. We observed that 40 mM MG caused 60% death of neuronal PC12 cells within 24 hours. MG also increased the activity of inducible nitric oxide synthase (iNOS) and caspase-3, suggesting that MG causes apoptotic cell death via oxidative stress. This was supported by our observation that glutathione, a known antioxidant, and curcumin from the spice turmeric alleviated the effect of MG. We hypothesized that these conditions may lead to an increase in the level of Bcl2, a mitochondrial protein that protects cells from apoptosis. We are in the process of determining the expression of Bcl2 in the presence of MG. The findings will eventually help decipher why diabetic conditions lead to loss of neuronal function.

#### **SAT-1005**

##### **DEVELOPMENT OF A HIGH THROUGHPUT ASSAY FOR SCREENING DRUGS TARGETED AGAINST GPCRS**

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G protein-coupled receptors (GPCRs) are the largest class of receptor proteins and an important target for therapeutic intervention. GPCR signaling is responsible for a vast range of physiological processes like behavioral regulation and homeostasis modulation. Because of the complexity behind GPCR signaling, assays which target specific pathways or cellular events are often limited by lack of knowledge of receptor biology. This gives rise to a need for assays that target general features of receptor response to agonism/antagonism that can be applied to many GPCRs. We have developed a high throughput assay based on fluorogen activating peptide (FAP) technology in order to measure GPCR binding and internalization. FAPs are genetically encoded reporters that exhibit fluorescence in the presence of particular fluorogens

and can be used to tag GPCRs. By using two FAP fluorogens and measuring cellular fluorescence, receptor binding, internalization, desensitization and resensitization can be monitored. Measurements were made using Intellicyt's iQue HD Screener, a high throughput flow cytometer. We have demonstrated performance of this assay in 384-well plate format using the  $\beta_2$  adrenergic receptor as a model system. Our results thus far demonstrate reproducibility and consistency of the desensitization/resensitization assay. We will further develop the assay with agonists and antagonists, measure the fluorescence of each channel before and after addition of agonist/antagonist to analyze receptor internalization and recycling. By validating the use of GPCR and FAP technology within high-throughput screening environment, drug research and development companies will be able to apply this technology to observe the general response of receptors to a compound.

## BOTANY

### SAT-1023

#### CHARACTERIZATION OF BIOMASS-RELEVANT TRAITS IN THE C4 GRASS SPECIES *SETARIA*

Rebekah Figueroa<sup>1</sup>, Bryan Penning<sup>1</sup>, Robert Sykes<sup>2</sup>, Mark Davis<sup>2</sup>, Steve Decker<sup>2</sup>, Nicholas Carpita<sup>1</sup>.

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There is a growing need to more completely understand the genetic composition of the C4 grass species, the main crop grown as biomass feed stocks, in order to develop the most efficient means for biofuel production. The compact size, short life cycle, large seed production, and close genetic synteny with major bioenergy crops, such as maize, sorghum, switch grass, and *Miscanthus* make *Setaria italica* (foxtail millet) an ideal genetic model to investigate C4 bioenergy grasses. Gene discovery of important biomass relevant traits in *Setaria italica* are directly translatable to improving the use of energy feed stocks. Toward this goal, we are classifying into large, multi-gene families cell-wall related genes in *Setaria italica* using rice, sorghum, *Arabidopsis*, and maize as backbone sequences. In addition, 200 recombinant inbred lines of the parent plants *Setaria italica* (B100) with *Setaria viridis* (A10) were crossed and given to us in order to map relevant biomass traits using quantitative trait locus (QTL) analysis. Pyrolysis molecular beam mass spectroscopy (PyMBMs) will be used to chart relative lignin abundances in this population. A saccharification assay will be performed in order to better understand the digestibility of the population. This investigation found that comparisons with the Phenylpropanoid, Csl, and CesA maize gene families show numerous orthologs with *Setaria italica*. Preliminary findings from this study show *Setaria italica* may be a valuable model for biomass relevant traits in C4 grasses.

**FRI-1023****COMPARING SEED VIABILITY AND HARVEST CONSISTENCY ACROSS SITES AND YEARS FOR THE FEDERALLY ENDANGERED PLANT *ERIASTRUM DENSIFOLIUM* SPP. *SANCTORUM***

Ignacio Vera Jr., Darren Sandquist.

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The Santa Ana River woolly star, *Eriastrum densifolium* spp. *sanctorum*, is a federally listed, endangered plant species native to the Santa Ana River floodplain in Redlands, CA. Woolly star has a specific habitat preference for young sand deposits that develop after periodic flooding. A major reason for its protection is the lack of such flooding from the Santa Ana River due to regional flood control measures. Suitable woolly star habitat is now significantly reduced and only supports small populations. A seed reserve of approximately 77,000 viable woolly star seeds was collected as part of a larger project that will simulate a small flood in an attempt to artificially generate new woolly star habitat. Seed collections involved formalizing a method for harvesting, sorting, counting, testing viability, and storing the seeds. The methods were tested at three sites and across two years with slightly lower than normal precipitation (2012 and 2013). Our objective was to achieve consistent and reproducible seed recovery across years and sites. Variation across sites was larger than expected, but recovery between years was consistent. Our results indicate that the harvest method appears to be reliable for consistent seed recovery, but that seed production differs significantly between sites.

**SAT-1025****RELATIVE IRON CONCENTRATIONS IN THE LEAVES OF *CHAMAESYCE MULTIFORMIS* (EUPHORBIACEAE), A TRADITIONALLY USED ENDEMIC HAWAIIAN MEDICINAL PLANT**

Maria Petelo, Lindsey Watanabe, Michael Ross.

*Kapiolani Community College, Honolulu, HI.*

*Chamaesyce multiformis* is a plant endemic to the Hawaiian Islands. In Hawaiian it is known as 'Akoko (refers to blood) and traditionally used to treat women's health. The natural maturation of 'Akoko leaves cause the pigmentation to progress through phases: from blue, to green, yellow, orange, and finally red, before the leaves abscise. The yellow to red colored leaves of 'Akoko are made into a tea to treat women's health. Traditional preparation methods are performed by the Kahuna Lā'au Lapa'au (practitioner) when preparing the tea, which include specific consideration of time of day and month. In general, Kahuna tend to collect medicinal plants in the early morning of a lā'au moon phase. During the lā'au moon, medicinal plants are believed to be most potent; therefore, medicine prepared from these plants would be most effective in treating health problems. More specifically, 'Akoko tea is used to treat women's menstrual pains and pregnancy-related debilities. Many of these types of problems are known to be caused by iron deficiencies. Therefore, we hypothesize that the yellow to red leaves of 'Akoko are higher in iron than that of any other color phase. In this study, the leaves of each color phase were collected and prepared traditionally, and the concentration of iron was analyzed using spectrophotometric methods. Preliminary results suggest that iron is highest in yellow to red leaves collected during the morning hours of a lā'au moon.

**SAT-1024****NITRATE UPTAKE AND ROOT HYDRAULIC PROPERTIES OF *PHASEOLUS VULGARIS* AND *ZEA MAYS***

Stefan Ortega, Kristy Duran.

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To be successful within their habitat, plants must alter their physiology to accommodate changing soil conditions. Plants require nitrogen in the form of nitrate which they acquire from their roots. Nitrate concentration in the soil is variable and often the limiting factor in plant growth. To be successful, plants should maximize their nitrate uptake. Previous studies have shown that plants are capable of altering the hydraulic properties of sections of their roots in response to soil nitrate levels to absorb water from areas of high nitrate concentration. This experiment reports the differences in this physiological change in a grain, *Zea mays*, and in a legume, *Phaseolus vulgaris*. A split root experiment was used to illustrate differential uptake of varying nitrate solutions. The results showed a trend in *Zea mays*: root hydraulic conductivity was increased in a nitrate-rich solution and decreased in a low nitrate solution. On the other hand, the results showed a decrease in root hydraulic conductivity in nitrate-rich solution and an increase in a low nitrate solution in *Phaseolus vulgaris*. This result was statistically significant. The difference between the two plant species can be explained by the symbiotic relationship legumes share with nitrogen fixing *Rhizobia*. Legumes may avoid nitrogen toxicity by decreasing root hydraulic conductivity in high nitrate conditions. Grains, on the other hand, must compensate for the lack of a symbiotic relationship with nitrogen fixing organisms by increasing their nitrate uptake by their roots.

**FRI-1025****THE EFFECTS OF DIFFERENT MOON PHASES ON THE MEDICINAL PROPERTIES OF *CHAMAESYCE MULTIFORMIS* (EUPHORBIACEAE)**

Lindsey Watanabe, Maria Petelo, Michael Ross.

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In traditional Hawaiian medicine (Lā'au Lapa'au), it is believed that healing properties accumulate in plants at night. Therefore, moon phases are given special consideration by traditional medical practitioners (Kahuna Lā'au Lapa'au). These practitioners generally collect medicinal plants in the early morning of a lā'au moon phase. During lā'au moon phases, medicinal properties are thought to be at their highest potency (mana), therefore medicinal plants would be gathered and prepared at that time. 'Akoko, *Chamaesyce multiformis*, is an endemic medicinal Hawaiian plant used to treat female debilities. The leaves of this plant are known to be high in iron. Thus, we hypothesized that 'Akoko leaves collected on lā'au moon phases will be higher in iron than leaves collected on any other moon phase. In this study, iron levels were compared between the 'Akoko leaves collected on a specified lā'au moon phase versus another general moon phase. The levels of iron were analyzed using spectrophotometric methods. Preliminary results suggest that leaves collected on a lā'au moon are higher in iron than leaves collected on any other moon phase.

**FRI-1024****FITNESS IMPACTS OF MYCOHETEROTROPHY IN *CORALLORHIZA STRIATA* (ORCHIDACEAE), *PINUS PONDEROSA* (PINACEAE), *PSEUDOTSUGA MENZIESII* (PINACEAE), AND *TOMENTELLA FUSCOCINEREA* (THELEPHORACEAE)**

Anita Enriquez, D. Lee Taylor.

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Mycorrhizal symbioses are ubiquitous in the plant kingdom and impact the growth, community composition, and responses to stress and climate change of vegetated terrestrial ecosystems. All mutualistic symbioses are susceptible to cheating that can produce a range of evolutionary impacts including disintegration of the symbiosis. While most plants make their own food by photosynthesis, some plants have evolved mechanisms that allow them to parasitize fungi for their energetic needs. The fitness impacts of this relationship, mycoheterotrophy, are unknown. *Corallorhiza striata* is an obligately mycoheterotrophic orchid that possesses no chlorophyll and must interact with a fungus. This fungus, *Tomentella fuscocinerea*, forms mycorrhizae with surrounding trees, the ultimate source of the carbon used by the orchid. The fungus provides the orchid with carbohydrates and minerals; however, the relationship is unreciprocated and possibly detrimental to the host fungus and the linked tree. We will compare the abundance of fungi and tree growth in systems with and without *C. striata*. *Pinus ponderosa* and *Pseudotsuga menziesii* will be germinated in rhizotrons and inoculated with the accommodating fungus cultured from *C. striata* rhizomes. Half of the seedlings will receive viable *C. striata* seeds while the other half will receive seeds sterilized by autoclaving. Understanding the impact of cheating can shed new light on mycorrhizae, the most abundant symbiosis on land.

**SAT-1026****EARLY LAND PLANTS TODAY: TREE OF LIFE EXTENDS ITS BRANCHES TO EDUCATION AND CITIZEN SCIENCE**

Anthony Carmona<sup>1</sup>, Lauren Hasan<sup>2</sup>, Justyna Drag<sup>2</sup>, Charlie DeLavoie<sup>2</sup>, Brendon Reidy<sup>1</sup>, Jonathan Scheffel<sup>2</sup>, Juan Larrain<sup>2</sup>, Matthew Grief<sup>2</sup>, Thomas Campbell<sup>1</sup>, Matt von Konrat<sup>2</sup>.

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Many people may be surprised to learn that the Earth is currently undergoing the sixth mass extinction period in its history. Spurred by global climate changes and pollution, many species are diminishing in number and diversity, some even to the point of extinction. One such group of organisms that are exquisitely sensitive to these changes is the Bryophytes (liverworts, hornworts, and mosses.) Liverworts (*Marchantiophyta*) are a particularly diverse and evolutionarily significant group of plants found worldwide which can be used to monitor and measure environmental changes. However, due to their cryptic nature and small size, liverworts are often overlooked and can be very difficult to describe and classify. Therefore, it is imperative that we be able to identify these precious species before it is too late. To this end, we have designed an engaging online citizen science project in partnership with Zooniverse.org. This allows amateur scientists, the public, to engage in meaningful research to measure and classify various liverwort species. A large portion of this project is conducted behind the scenes, collecting and preparing samples for the website. To date, we have received over 35,000

measurements from over 3,000 participants. Here, we report on using this novel citizen science approach as a tool to help accelerate the process of biodiversity discovery and documentation.

#### **SAT-1028**

##### **QUANTIFYING GENETIC EXPRESSION OF DEFENSE RESPONSE HORMONES IN SELENIUM HYPER-ACCUMULATOR SPECIES *STANLEYA*: A NOVEL INTER-SPECIFIC APPROACH**

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The quantified differences in gene expression within the species *S. pinnata* and *S. elata* may lead to discovery of the levels of gene regulation needed for Se hyperaccumulation in *Stanleya*, thereby advancing phytoremediation, agriculture, and medicine. Variances in gene expression were statistically quantified within the biological pathways for salicylic acid, jasmonic acid, and ethylene, which are active in stress response to selenium (Se) in the genus *Stanleya* (Brassicaceae). Transcription rates from three bioreplicates of two *Stanleya* species (hyperaccumulator *S. pinnata* and non-accumulator *S. elata*), consisting of individual plant samples with specified growing conditions of +Se and -Se, were compared for hormone biosynthesis processes, transcription factors, and stress response. Sequences were aligned and confirmed following a flow of bioinformatic tools: TAIR, MAFFT, BLASTn, and Mesquite. Up and down regulation was segregated and quantified in Microsoft Excel where a t-test of the averaged bioreps was performed to quantify expression rate between species and treatments. Flow charts were created to designate positions of enzymes in hormone synthesis and show their expression differences. We found several genes producing significantly different ( $p < 0.05$ ) expression rates between *S. pinnata* and *S. elata* while other sequences were similarly expressed or completely absent in one transcriptome or the other. Expression variances ranged widely. ICS2, a salicylic acid biosynthesis enzyme, expressed at 162 RPKM (reads per kilobase per million) in *S. pinnata* root +Se vs. 9.3 RPKM in *S. elata* root +Se ( $P = 1.92 \times 10^{-6}$ ) while transcription factor MYB29 displayed little variance under the same conditions at 6.19 RPKM vs. 8.46 RPKM respectively ( $P = 0.005$ ).

#### **FRI-1027**

##### **INVESTIGATING *ARABIDOPSIS* CELL WALL MUTANTS' SALT TOLERANCE CAN LEAD TO FUTURE UNDERSTANDING OF HOW TO IMPROVE DROUGHT TOLERANCE FOR OTHER CROPS**

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Drought will increasingly become more devastating to agriculture as the effects of global warming continue to develop. Recent studies have found that by mid-century, 1,100 counties in the United States will face even higher risks of water shortages. Finding a way to increase drought tolerance in crops can help counties that are at high risk of drought reduced crop yield loss. The plant cell wall regulates water porosity and also elongation of roots. Therefore, we are investigating if a change of cell wall composition leads to greater resistance to drought conditions. We are examining the weight of cell wall mutant seedlings after treatment in media with various salt concentrations (0, 100, 130, and 160 mM NaCl) compared to wild type to

determine water retention after salt treatments. Additionally, we will be measuring root length after salt treatment. This ongoing project may show mutants have better water retention and root elongation by finding they have more seedling weight and longer roots after treatment. Exposure of *Arabidopsis* cell wall mutants to salt stress conditions tests resilience of their unique cell wall that can help further the understanding of the biological mechanisms used in combating substantial drought conditions. Ultimately, the findings in *Arabidopsis* can be applied to other crop plants to improve their tolerance to drought as it is an excellent model species for all plants.

#### **FRI-1026**

##### **ANTIMICROBIAL PROPERTIES OF A TRADITIONAL MEDICINAL PLANT *MIMULUS AURANTIACUS***

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Within the last two decades, the rise in bacterial resistance to antibiotics has increased, sparking a search for novel solutions to infections. *Mimulus aurantiacus* (Sticky Monkey Flower) is used in traditional Miwok medicine to treat intestinal and skin infections. The aim of our work is to isolate and characterize the antimicrobial compound(s) in *M. aurantiacus*. *M. aurantiacus* leaves, roots, and flowers were ground and mixed separately in methanol, ethyl acetate, and water (400 mg/mL). These extracts were screened against methicillin-resistant *Staphylococcus aureus* (MRSA) in agar diffusion assays. The methanolic leaf extract was most effective against MRSA producing an average zone of inhibition (3 mm) greater than methicillin (0 mm) and comparable to vancomycin (4 mm). The antimicrobial chemical does not cause bacterial lysis and does not appear to be a protein. We are currently determining the method of action of the methanolic leaf extract. From these experiments, we determined that the Sticky Monkey Flower leaves contain a potential antibiotic.

#### **FRI-1022**

##### **CHARACTERIZATION OF THE *ARABIDOPSIS THALIANA* GENE *PBL13***

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Plants are attacked by various pathogens which can cause huge losses in agriculture. In response, plants have evolved to recognize pathogen-associated molecules that trigger a defense response by reprogramming gene expression. Kinases help relay signals by attaching phosphate groups to proteins, thereby changing their structure and function to influence their interactions with other proteins. Because of its homology with known kinase coding genes, the *Arabidopsis* gene *PBL13* has been identified as a receptor-like kinase involved in plant defense signaling. To better understand the function of *PBL13*, its promoter region, which controls gene expression, will be fused to the marker gene  $\beta$ -glucuronidase (*GUS*). *GUS* codes for an enzyme that reacts with glucuronosides to produce a visible color in a process known as *GUS* staining. Next, *Agrobacterium* will be used to transform *Arabidopsis* plants with the aforementioned promoter-*GUS* fusion. After obtaining transgenic lines from these plants, *GUS* staining will be performed to reveal the location and timing of *PBL13* expression. By revealing this aspect of *PBL13* function, this project will provide a better understanding of plant defense signaling which can help in implementing better control strategies for pathogens.

**SAT-1027****MICRO CLIMATES WITH MACRO IMPLICATIONS: HOW BRYOPHYTES HELP DEFINE THE WORLD AROUND US**

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Bryophytes (liverworts, hornworts, and mosses) play important roles both ecologically and economically in ecosystems worldwide, yet their role in community interactions remains widely unknown. Their small sizes allow them to fill essential niches within the food webs to which they belong. Bryophytes also contribute to global carbon and nitrogen fixation capacity, absorb large quantities of water, and release organic acids which can decrease decomposition rates within their communities. Their unique physiology makes them particularly vulnerable to climatic variations as well as to changes in soil and water pH. Given their acute sensitivity and reliance upon environmental conditions, their presence in the ecosystem has the potential to indicate broader trends in forest health. To examine bryophyte and forest community interactions in particular, we are conducting a multisite survey of bryophyte species between high and low quality oak woodlands within the northeastern Illinois area. We chose two areas of high quality as judged by invasive frequency, canopy trees, history of the woodland, presence of streams, and decorticated wood and two areas of low quality defined by these same standards, but at a lower level overall. We then compared the areas for bryophyte diversity. Furthermore, we correlated these species distribution patterns with soil and climate data. From this study, we hope to determine the relative utility of using bryophytes as an indicator of overall forest health in Illinois.

**SAT-1022****SYSTEMATICS, PHYLOGEOGRAPHY, AND SPECIES DISCOVERY IN THE AUSTRALIAN ANGIOSPERM GENUS *GONOCARPUS* (HALORAGACEAE)**

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The angiosperm genus *Gonocarpus* (Haloragaceae) is a relatively poorly known group with high levels of local endemism throughout its range. It occurs primarily in Australia (34/37 spp.) with 6 species ranging into New Zealand and/or Asia. Much of *Gonocarpus* diversity is found in the southwest Western Australia International Biodiversity Hotspot where several species are considered rare or of priority concern. The most recent taxonomic treatment for the genus was based on morphology only and included very few specimens as collections were limited until recently. This genus also has a high level of morphological plasticity, and several species are described as highly variable. Here, we use a molecular phylogenetic approach to aid in our understanding of species limits, evolutionary relationships, and biogeographic origins. DNA data was collected from the nrDNA internal transcribed spacer (ITS) region for 91 accessions. Chloroplast DNA (cpDNA) data was collected from intron region trnL – trnF for 82 accessions for comparative analyses. Sequences were analyzed to construct a phylogenetic hypothesis,



determine times of divergence, and infer ancestral distribution. Results from phylogenetic analyses of both ITS and cpDNA show high molecular variability among species and have uncovered cryptic species in southwest Western Australia. Analyses support an origin of the genus in Western Australia approximately 50 mya with dispersal east and multiple events leading to dispersal into Asia. These results will be used to help define new species of *Gonocarpus*, inform conservation efforts, and provide further evidence regarding phylogeographic patterns in Australia.

## CANCER BIOLOGY

### FRI-1046

#### IDENTIFICATION OF PAN-RESISTANT *BCR-ABL/T315* MUTATIONS THAT ARE SENSITIVE TO AXITINIB

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Chronic myeloid leukemia (CML) is a hematologic malignancy caused by the *BCR-ABL* fusion gene. *BCR-ABL* is a constitutively active tyrosine kinase, contributing to leukemogenesis by phosphorylating substrates that activate signaling pathways, ultimately affecting growth and differentiation of hematopoietic cells. Therefore, *BCR-ABL* is a critical target in CML therapeutics. Imatinib was the first targeted small molecule tyrosine kinase inhibitor (TKI) that achieved a clinical response, but 30% of patients are intolerant or acquire *BCR-ABL* mutations that confer drug resistance. Second- and third-generation *ABL* inhibitors were later developed, and they are largely effective against most imatinib-resistant mutations. However, the *T315I* mutation remains resistant to all *ABL* TKIs, except for ponatinib. Other amino acid mutations have also been recently detected at this residue in CML patients, so in order to better characterize the potential spectrum of *T315* mutations in *BCR-ABL*, this study examined the sensitivities of all possible *T315* mutants to approved TKIs. Our goal is to provide a comprehensive profile for clinical application to predict the most appropriate agents for cases associated with these mutations. We sought to generate all possible amino acid mutations at *T315* and measure their sensitivities to TKIs using biologic and biochemical assays. This investigation is still ongoing, but preliminary data suggest that some mutations which are resistant to all of the approved *ABL* TKIs may be sensitive to axitinib, which is presently approved for treatment of other cancers. Complete results and their clinical implications will be presented.

### SAT-1046

#### SYNTHETIC LETHAL INTERACTION BETWEEN TUMOR SUPPRESSOR RAD17 AND CHK1 KINASE IN HUMAN CANCER CELLS

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Cancer cells often have impaired tumor suppressors. Although current drugs can target cells with gain-of-function oncogenes, targeting cells with loss-of-function tumor suppressors is

problematic. However, performing synthetic lethal (SL) screens for proteins that are essential only in the context of specific cancer-causing alterations can reveal “druggable” proteins within cells that have “undruggable” genetic alterations. Two proteins are SL if the loss of either one is viable to the cell, but the suppression of both is lethal to the cell. So, targeting a protein that is SL to tumor suppressors should destroy only cancer cells that have altered tumor suppressors and spare normal cells. This study elucidates such SL interactions of Rad17, a tumor suppressor, and Chk1 kinase (Chk1) in humans. We find that cells that have loss-of-function of Rad17 exhibit sensitivity to suppression of the Chk1 kinase. We also find that the mechanism underlining the Rad17-Chk1 SL interaction seems to be P53 dependent, but cell cycle independent.

#### **SAT-1039**

##### **MITOTIC SPINDLE REORIENTATION THROUGH ESTROGEN BINDING TO GPER AND ER $\alpha$**

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Breast cancer afflicts many people and is studied extensively, but little is known about estrogenic factors that may cause development and progression of breast cancer. Tumor progression in breast cancer may be promoted by estrogen binding to estrogen receptors. The binding of estrogen to the G-protein-coupled estrogen receptor (GPER) and the estrogen receptor  $\alpha$  (ER $\alpha$ ) leads to increased proliferation and altered morphology of mammary duct structures. Since the direction a cell divides can lead to different duct morphologies that cause uncontrolled cell growth within the lumen, we suspect mitotic spindle reorientation is linked to morphological changes and tumorigenesis in mammary structures. Therefore, we hypothesize that mitotic spindle reorientation as a result of estrogen binding to GPER and ER $\alpha$  can affect ductal morphology. We will culture human non-tumorigenic MCF10A cells in 3-dimensional culture on a reconstituted basal lamina and treat them with estrogenic compounds along with endocrine-disrupting chemicals that act as estrogen-receptor agonists or antagonists (tamoxifen, genistein, and methoxychloride). Mitotic spindle reorientation will be assessed by immunofluorescence microscopy using anti-tubulin antibodies to detect mitotic spindles and DAPI to label nuclei. Since estrogen alters morphology of mammary duct structures in MCF10A cells that do not express ER $\alpha$ , we believe that GPER is the likely receptor to cause a shift in mitotic spindle orientation. Identifying mitotic spindle reorientation will improve scientists’ understanding of tumor progression in breast tissue and its direct relation to estrogen. These studies may lead to treatments such as reducing cells’ estrogen affinity in people who have these receptors.

**SAT-1037****TARGETING CANCER METABOLISM: THE EFFECTS OF A NOVEL MITOCHONDRIAL PEPTIDE ON CANCER PROGRESSION**

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In the early 1920s, Nobel laureate Otto Warburg hypothesized that cancer is a metabolic disease, specifically a mitochondrial dysfunction, based on his observation that cancer cells consume significantly more glucose, an observation now commonly referred to as the Warburg effect. It stands to reason that a potential target for cancer treatment would be related to the mitochondria, the organelle central to a cell's proliferation through their generation of cellular energy as well as biosynthetic precursors that serve as building blocks for a dividing cell. However, the precise metabolic regulatory mechanisms of this essential organelle are not fully understood. Most of current biology has focused on how the cell communicates to the mitochondria to modulate cellular metabolism, but relatively little is known about how mitochondria influence the cell. The recent discovery of mitochondria-derived peptides (MDP) positions mitochondria as a proactive and influential organelle that regulates cellular metabolism. In this study, we examined the effects of a particular MDP called MOTS-c on the progression of various cancer models through proliferation assays both *in vitro* and *in vivo*. Our results in various cancer cell lines (22Rv1, PC3, LnCAP) as well as animal models (BALB/c, NOD SCID) show a profound anti-proliferative effect with MOTS-c treatment, an effect which appears to stem from the mitochondrial peptide's manipulation of powerful metabolic pathways. This study portrays the possibility of retarding the proliferation of cancer by targeting cellular metabolism, as well as the potential role of the mitochondria as a significant communicator in the progression of cancer.

**FRI-1047****IDENTIFICATION OF BREAST CANCER BIOMARKERS IN PREPUBERTAL RAT MAMMARY EPITHELIA**

Joyce Tam, Ignacio Camarillo.

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Breast cancer, the most prevalent cancer among women, is also the second leading cause of cancer-related death among women in the United States as reported by the American Cancer Society. Evidence has shown a link between obesity and higher cancer risk. Many studies have suggested a positive relationship between exercise and reduced risk of cancer development. Physical activity may lead to reduced levels of certain factors such as estrogen, leptin, and insulin-like growth factor in the body. A further study reveals that the relationship between physical activity and reduced cancer risk is also present in offspring of mothers who engaged in exercise during pregnancy. To better understand the mechanisms in this relationship, it is important to evaluate how exercise influences the molecular markers associated with breast cancer. ER- $\alpha$  proteins are nuclear receptors that play a key role in proliferation. Contrastingly, ER- $\beta$  has a role in inhibiting cell proliferation. Loss-of-function p53 promotes tumor formation in that abnormal cells are allowed to progress through the cell cycle. The protein marker ki67 is

used to observe proliferation in cells and tissue. Given the roles of these markers, we expect to see reduced expression of ER- $\alpha$  and an increased expression of ER- $\beta$  and p53 in exercised rats. We also expect to see reduced proliferation measured by ki67 in exercised rats because we expect to see less undifferentiated epithelial cells. Our overall aim is to better understand what effects maternal-fetal programming has on offspring and how it offers tumorigenesis protection.

#### **FRI-1045**

##### **COASTAL SEDIMENT-DERIVED GRAM-NEGATIVE BACTERIA AS A SOURCE OF NEW NATURAL PRODUCTS**

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Natural products (NPs) are the chemical compounds produced by natural sources such as animals, plants, and microorganisms. NPs are a good choice for drug discovery since historically some have a pharmacological or biological activity that can be used in drug discovery or design. The goal of this study was to identify bacteria that produce NPs. Our research group at University of California, Santa Cruz collected sediment samples from the Northern California Coast. Gram-negative bacteria (GNB) were isolated from these samples. The bacteria were then grown in liquid cultures, extracted, and analyzed by liquid chromatography mass spectrometry (LCMS). Chemically prolific strains identified by the screening procedure were then grown in a large scale bioreactor. Compounds from the large scale culture were isolated and their structures were elucidated through advanced spectroscopic methods such as nuclear magnetic resonance (NMR). Extracts were also evaluated for biological activity through biomap screening at the University of California Santa Cruz Screening Center.

#### **SAT-1042**

##### **INHIBITION OF RABBIT MUSCLE ALDOLASE, ENOLASE, LDH, AND PK BY A TRADITIONAL CHINESE MEDICINE, EPIGALLOCATECHIN GALLATE**

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Several traditional Chinese medicines (TCM) have been used as cancer chemotherapeutic agents. The explanations for their effectiveness have varied. We propose the hypothesis that some of these reported chemotherapeutic cancer reagents may inhibit glycolysis since cancer cells depend on glycolysis as an energy source. The main focus of the study was to determine the inhibitory effects of epigallocatechin gallate (EGCG), a TCM, on the glycolytic enzymes enolase, aldolase, pyruvate kinase (PK), and the enzyme lactic dehydrogenase (LDH). The data show that EGCG inhibited enolase, aldolase, PK, and LDH. All inhibitions were reversible of the reversible type. The Ki values for the EGCG inhibitions of enolase, aldolase, PK, and LDH will be determined in future projects. We conclude that the inhibition of these glycolytic enzymes and LDH by EGCG is related to the inhibition of cancer cell growth.

**FRI-1035****THE ROLE OF CDK6 IN CHEMO-RESISTANCE IN SMALL CELL LUNG CANCER**

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Small cell lung cancer (SCLC) patients often develop resistance against cisplatin and/or etoposide chemotherapy and less than 5% survive for over 5 years. There is a need to develop new and efficient drugs for patients and identifying the mechanisms responsible for chemotherapy resistance is crucial toward discovering new drug targets. Studies have discovered mutations in resistant clones as well as up-regulation and down-regulation of a number of proteins compared to levels in sensitive cell lines. This project takes a genetic approach to test the necessity and/or sufficiency of the gene *CDK6* (cyclin dependent kinase 6) to promote drug resistance. This gene is found to be up-regulated in drug resistant clones of SCLC cells. We first tested if *CDK6* is sufficient to promote drug resistance in 3151T1 lung cell lines derived from mouse models. *CDK6* was cloned into a PIG viral vector and was grown in ampicillin resistant *E. Coli* cells to facilitate confirmation of successful PIG-CDK6-HA cloning. A *CDK6* containing retrovirus was then prepared by transfecting the construct into 293T cells, to which necessary virus-packaging components gag/pol and VSVG were provided. Parental cell lines 3151T1 were infected with the *CDK6* retroviruses, treated with various concentrations of cisplatin and etoposide drugs, and cell titer glo assays were used to determine the number of viable cells after treatment. Results indicated that *CDK6* was not sufficient for drug resistance on its own. We are now investigating the necessity of *CDK6* for drug resistance by knocking down the gene in resistant cell lines.

**FRI-343****CURCUMIN-REGULATED EMT IN LEPTIN TREATED HUMAN BREAST ADENOCARCINOMA CELLS**

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Breast cancer is a growing health concern and there is reason to believe that obesity may be a driving force behind it. Overexpression of leptin, an adipocyte-derived hormone responsible for regulating appetite and energy homeostasis, may contribute to the development of metastatic breast cancer by regulating several signaling pathways that stimulate proliferative and migratory properties of cancer cells. Conversely, curcumin, an active component of the Indian spice turmeric, has been shown to regulate cell proliferation and potentially reverse epithelial-mesenchymal transition (EMT). This investigation explores the effects of increased leptin levels on the migratory abilities of rat mammary adenocarcinoma cells (MDA-MB-231) and curcumin's ability to inhibit leptin-induced invasive, migratory properties. To evaluate curcumin's efficacy we conducted a series of comparative treatments involving MDA-MB-231 cells cultured in minimal essential media (MEM) (serum-free or supplemented with 10% fetal bovine serum (FBS) or 1% FBS) and treated with curcumin (30 ug/ml), leptin (100 ng/ml) or a combination of the two. We then tracked the directionality of cell movement in response to different

treatments via live cell imaging using MDA-MB-231 cells seeded in 3D nanoculture dishes and an inverted light microscope. At this point, final results and conclusions have not yet been generated. However we anticipate decreased cell mobility and reversed EMT following treatment with curcumin. Curcumin's capacity to reverse leptin-enriched EMT *in vitro* is a trait that may be applicable to the development of chemotherapeutic treatments for obesity-induced breast cancer.

#### **FRI-1033**

##### **INVESTIGATION OF T-CELL RECEPTORS INTERACTING MOLECULE (TRIM) ON NATURAL KILLER CELLS IN MICE**

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Natural killer (NK) cells are large, granular, cytotoxic lymphocytes that have a critical role in the innate immune system. NK cells contain viral infections in the earliest stages of infection and can play a regulatory function in the activation of adaptive immunity. T-cell receptor interacting molecules (TRIM) represent a TCR-associated polypeptide involved in the recruitment of intracellular proteins to the plasma membrane in the activation of the T cell and are involved in a vast range of biological processes, which include cancers, genetic disorders, and neurological disorders. TRIM is expressed on T cells as well as NK cells. The purpose of this experiment was to determine the role of TRIM on NK cells using wild-type and TRIM knock-out mice. Two cell lines were used, RMA and RMA-S which were grown in *in vitro* tissue culture and injected into the mice. RMA cells have major histocompatibility class I molecules (MHC I) on their plasma membranes whereas RMA-S cells are MHC I deficient, which makes them ideal for this study because NK cells kill pathogens that are foreign to the host. This report will essentially highlight the difference, if any, in the killing of the RMA-S cells between the wild-type and TRIM KO mice. The p-value will also be calculated to determine any statistical significance.

#### **FRI-1039**

##### **DETERMINATION OF ANTICANCER EFFICACY OF COMPONENTS FROM PEARL GARLIC USING BREAST CANCER CELLS *IN VITRO***

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One of the promising strategies for cancer prevention today is chemoprevention. A growing body of research has demonstrated that certain components from regular garlic possess chemopreventive properties against cancer. Isolation and characterization of biologically active anticancer agent(s) from different types of garlic such as pearl garlic have not yet been reported. Previously, crude extracts from pearl garlic have shown anticancer activity *in vitro*. Further studies are required to evaluate the safety and efficacy of pearl garlic in cancer treatment. Pearl garlic contains components with high medicinal values. The main purpose of this study is to isolate and characterize anticancer agents from pearl garlic and test their efficacy *in vitro*. In the current study, pearl garlic cloves were crushed in methanol and acid-

methanol and extracted for 24 hours at room temperature, then filtered and incubated at 37 °C for 48 hours. During this incubation period, aliquots were collected every 3-4 hours and components were identified using thin layer chromatography. Progressively, the concentration of ajoene was increasing in different aliquots. The collected samples were then freeze dried, and are now being tested for their anticancer efficacy on breast cancer cells *in vitro*. The components from the aliquots will also be purified using silica gel column chromatography. Subsequently, these will be eluted using solvents with varying polarities, freeze dried and tested for their anticancer efficacy on breast cancer cells *in vitro*.

#### **FRI-1036**

#### **BREAST CANCER AWARENESS AND PREVENTION: GENETIC COMMUNICATION AND MULTIPLEX TESTING PREFERENCE FOR WOMEN AT MODERATE TO HIGH RISK OF BREAST CANCER**

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Women have a 12% lifetime risk of being diagnosed with breast cancer. A family history is a major risk factor accounting for approximately 5-10% of breast cancers. BRCA 1/2 are from autosomal dominant transmission and associated with 45-65% lifetime risk. The remaining hereditary breast cancers are due to moderate and low risk gene mutations. Identifying women at increased risk for hereditary breast cancer is important for personalized health care and may help prevent and control the disease. The Utah Risk Education Assessment Cancer Heredity Study assessed knowledge, attitudes, and beliefs about familial breast cancer, relevant health care practices among women who had a first-degree relative with the disease, tested negative for a BRCA1/2 mutation, and were considered at moderate to high risk. Surveys by mail or telephone were administered to 166 women and assessed their genetic risk communication preferences, cancer worry, risk perceptions, sociodemographics, and interest in multiplex genetic testing. Descriptive statistics and logistic regression models were used to identify factors linked to genetic risk communication and multiplex testing preferences. A similar study is currently underway in New Mexico to assess differences in Hispanics. Participants preferred receiving genetic information from health professionals rather than the internet. Cancer worry levels were low. Most participants believed their risk was the same or higher than women their age and that their lifetime risk was about 50%. High cancer worry was found to be associated with greater interest in counseling. There was a high level of interest in cancer risk communications and multiplex genetic testing.

**FRI-1031****PEDF INDUCES THE MIGRATION, DIFFERENTIATION AND PHAGOCYTTIC ACTIVITY OF MACROPHAGES**

Dalia Martinez-Marin, Thomas Nelius, Stephanie Filleur.

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Macrophages have been described as one of the main inflammatory components involved in prostate cancer (PCa) initiation, progression, and metastases formation. PEDF (pigment epithelium-derived factor) is an anti-angiogenic factor and was recently suggested as an immune-modulating factor. PEDF expression has been shown to be down-regulated in PCa compared to normal tissues. In previous studies we've demonstrated that PEDF re-expression in PCa cells curbs tumor growth and significantly prolongs the survival of tumor-bearing mice. Others have shown that PEDF expression increased the recruitment of tumor-cytotoxic macrophages into orthotopic rat prostate tumors suggesting a link between PEDF and inflammation in PCa. However, while the role of PEDF in inflammation has been suggested, the precise modes of action of PEDF on macrophages remain unknown. We've demonstrated that PEDF stimulates the migration of monocytes/macrophages, and that PEDF directly induces the differentiation of macrophages toward a M1/tumor-cytotoxic pathway. We are currently investigating the molecular pathways by which PEDF induces the migration, differentiation, and phagocytic activity in macrophages. We are also investigating the PEDF-derivative synthetic 18-mer peptide (AA39-57) and its mechanism of action on macrophages. P18 blocks growth and angiogenesis in prostate cancer. Finally, we will assess PEDF gene therapy using bone marrow-derived macrophages (BMDMs) as a novel therapeutic modality for advanced PCa. Our central hypothesis is that PEDF expression will induce the migration and differentiation of BMDMs into a tumor-cytotoxic phenotype and, as a corollary, will block tumor growth and metastases formation, and prolong survival. This project may lead to development of improved therapeutic approaches to treat PCa.

**SAT-1044****PHOSPHORYLATION OF T146 ON LINKER HISTONES AFTER DNA DAMAGE INDUCED BY MITOMYCIN C**

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Linker histones are previously thought to be involved only in the formation of higher-order of chromatin structure. Novel functional roles of linker histones, such as their dynamic interaction with DNA, involvement in protein-protein interactions and involvement in gene regulation, have recently begun to become apparent. It is believed that these functions may be regulated by histone posttranslational modifications. Phosphorylation of H1 isoforms at threonine 146 (T146) has been reported to have a crucial role in repressing p53 activity and ultimately regulating p53-dependent transcription. In this project, phosphorylation of linker histones at the site of T146 is observed after treatments of Mitomycin C at time intervals of 0, 15, 30, and 60 minutes to look for a trend in the phosphorylation. Cells from human breast cancer cell line



MDA-MB-231 are grown in an optimal environment prior to treatment. Following the treatment, the cells are harvested and the linker histones are extracted along with other core histones used as a control group. Extracted protein samples are run on SDS-PAGE gels, transferred to nitrocellulose and probed with anti-H1 phospho T146 and anti-histone H4 antibodies. Based on previous studies conducted by other researchers, phosphorylation of H1 at T146 is expected to rise at minute 15 followed by decrease as a function of time. Our results confirm the change in phosphorylation of H1 at T146 after DNA damage induced by mitomycin C and will further our mechanistic understanding of the use of H1 phosphorylation as a biomarker in breast cancer.

#### **FRI-1040**

##### **GENE EDITING EFFICIENCY OF THE CRISPR/CAS9 SYSTEM IN CANCER CELLS**

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Glioblastoma multiforme (GBM) is the most frequent and aggressive primary brain tumor with the average survival time of 12 months. Our group has combined human patient-derived GBM models with the power of clustered regularly interspaced palindromic repeats (CRISPR/Cas9) technology to identify novel candidate GBM therapeutic targets and cancer specific vulnerabilities. CRISPR/Cas9 uses an RNA containing a 20-nt target sequence to facilitate a targeted double stranded break, which results in an insertion/deletion (indel) and knockout of the targeted gene. Previously, our lab used CRISPR to target KIF11, an essential microtubule-motor protein, to evaluate the CRISPR system in primary GBM cells. Unexpectedly, we observed a small population of viable cells containing the CRISPR/Cas plasmid following 21 days of outgrowth. Through the experiments proposed here, we hope to better understand why the CRISPR/Cas technology is not effectively killing all GBM cells. One possible reason is that Cas9 has been silenced, which will be evaluated through western blot. If Cas9 is expressed, it is possible that it has generated in-frame mutations, the frequency of which will be evaluated through sequencing. Furthermore, previous work demonstrated that knock out of KIF11 does not result in immediate cell death or arrested cell division. Thus, we will present data that demonstrates the length of delay between CRISPR gene editing and the KIF11 phenotype in cancer cells. Overall, these experiments will provide insight into why some cells survive following introduction to the CRISPR system, as well as the timespan between CRISPR/Cas 9 targeted gene inactivation and the resulting phenotype.

**FRI-1034****THE WNT10B/ $\beta$ -CATENIN PATHWAY DRIVES SELF-RENEWAL, INVASIVENESS OF TRIPLE-NEGATIVE BREAST CANCER BY CHANGING CHROMATIN STATE VIA AN HMGA2 AND EZH2 MECHANISM**

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Wnt10b/ $\beta$ -catenin signaling is active in triple-negative breast cancers (TNBC) which includes basal-like, mesenchymal-like, and mesenchymal stem-like breast cancers. However, in TNBC lung metastasis, the mechanistic role of Wnt/b-catenin activity is not fully characterized. We provide evidence that the Wnt10b/ $\beta$ -catenin/HMGA2 signaling axis mediates lung metastatic events *in vivo*. Absence of HMGA2 in both mouse and human TN cells blocks *in vivo* lung metastasis, loss of core epithelial-to-mesenchymal transition (EMT) genes, and concurrent restoration of CDH1. Mechanistically, ChIP analysis uncovered that HMGA2 occupancy at the promoters of *Wnt* and *EMT* genes is necessary for epigenetic maintenance of both histone and DNA methylation events. Silencing of HMGA2 in MDA-MB-231 cells alters histone 3 lysine 4 trimethylation (H3K4me3) of *Wnt*-targets, and decreases *EZH2* and *DNMT3A* occupancy, concurrent with loss of CpG-island DNA methylation at the *CDH1* promoter. QPCR verifies open vs. closed chromatin confirmation for either *Wnt* and or *EMT* markers, establishing “rules” for “active” chromatin. Future ChIP analysis of H3K27me3 and histone acetylation markers H3K9Ac and K3K18Ac will reveal further insights to the “rules” governing invasiveness and self-renewal driven by the Wnt10b/ $\beta$ -catenin/HMGA2 signaling axis. The insights gained from our studies will reveal potential novel therapeutics targeting epigenetic events in TNBC patients.

**SAT-1030****CISPLATIN INDUCED ACTIVATION OF THE EPIDERMAL GROWTH FACTOR RECEPTOR AS A MECHANISM FOR EPIGENETIC SILENCING IN OVARIAN CANCER CELL PLATINUM RESISTANCE**

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Resistance to platinum compounds in ovarian cancer imparts a major obstacle to increasing patient survival. The epidermal growth factor receptor (EGFR) plays a role in the regulation of growth and differentiation in normal cells and proliferation in malignant cells. It is known that dysregulation of the EGFR pathway, including prolonged receptor activation, is associated with platinum resistance in cellular models, and our lab revealed a novel mechanism by which constitutive EGFR activation regulates DNA methyltransferase (DNMT) activity and DNA methylation. Platinum resistance is associated with epigenetic downregulation (via DNA methylation) of genes involved in platinum drug response, particularly genes important for drug uptake. Given the established link between platinum resistance and alterations to DNA methylation, our studies investigated the effects of acute cisplatin treatment on EGFR activation and DNMT activity. We hypothesized that acquired chemoresistance resulting from

cisplatin treatment is initially triggered by cisplatin-induced EGFR activation and subsequent alterations to DNMT activity. We show activation of EGFR upon treatment of OVCA433 cells with cisplatin. Functional EGFR activation following cisplatin treatment was also observed by evaluating activation of downstream targets Jak2 and Akt. Hence, cisplatin facilitates activation of EGFR and its downstream signaling pathways. Our observations unmask a potential mechanism by which initial exposure to cisplatin can activate EGFR signaling and cause epigenetic alterations that may contribute to the development of platinum resistance. By understanding the underlying mechanism for development of platinum resistance and discovering targets of methylation, we may be able to enhance sensitivity to platinum-based chemotherapeutics.

#### **SAT-1045**

##### **LACTATE DEHYDROGENASE EXPRESSION IN AFRICAN WOMEN WITH TRIPLE-NEGATIVE BREAST CANCER**

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The incidence of breast cancer in African American women (AAW) is lower than that of their Caucasian counterparts. However, the age-adjusted mortality rates are much greater (77%) for AAW compared to Caucasian American women (CAW). These differences in survival were attributed to socioeconomic factors and access to health care. Genetic and immunohistochemical studies revealed that biological variations may account for this disparity too. These studies have suggested a higher prevalence of basal-like tumors in premenopausal African American women and low prevalence of luminal tumor as a causative. These are characterized by being high-grade aggressive tumors that are estrogen receptor negative (ER-), progesterone receptor negative (PR-), human epidermal growth factor receptor-2 (HER-2) +/- . We proposed that the phenotypic diversity of breast cancer might be accompanied by a corresponding diversity in protein expression patterns that we could reveal using proteomic technologies. We hypothesized that in addition to ER- and PR- expression and the absence in expression of HER-2, the protein composition of triple-negative tumors varies between AAW and CAW. Two-dimensional gel electrophoresis, mass spectrophotometry, and data analysis of protein from breast cancer tissues were used to identify differentially expressed proteins from AAW and CAW. We have found that many proteins were differentially expressed in AAW breast cancer tissues compared to CAW. One of these is lactate dehydrogenase, which was found to be overexpressed in tissues from AAW. Western blot of luminal and TNBC cell lines confirmed expression.

#### **SAT-1047**

##### **SIGNALLING EFFECTS FROM THE INHIBITION OF CNKSR1 PH-DOMAIN IN CANCER CELL LINES**

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Kirsten rat sarcoma viral oncogene homolog (*KRAS*) is found to be mutated in 25% of cancers and is central to the development of cancer. Mutant-*KRAS* (mut-*KRAS*) is also involved in the

resistance to many cancer therapies. The connector enhancer of kinase suppressor of *RAS1* (CNKSR1) is a protein found to be associated with and is critical for the activity of mut-*KRAS* but not wild-type *KRAS*. Thus CNKSR1 is an important target for cancer therapy. PHusis Therapeutics has developed small molecule inhibitors with high affinity for CNKSR1 using its *in silico* modeling system. Our goal is to optimize these compounds through surface plasmon resonance spectroscopy, synthetic chemistry, and drug design. We evaluate our leads *in vitro* for the effects of *KRAS* signaling by western blot and immunoprecipitation. This project involved evaluating target inhibition by novel potent inhibitors of mut-*KRAS* cell line growth that showed binding to the isolated CNKSR1 PH-domain. Three compounds were evaluated for direct target inhibition in both mut-*KRAS* and wt-*KRAS* cell lines in culture for the active form of RAS and its downstream effectors. Cells were treated with varying concentrations of the compounds for 24 hr and assessed for target inhibition. Data will be presented to show the cellular effects on growth and target inhibition by the three novel CNKSR1 inhibitors. The conclusions from this work are that the inhibition of CNKSR1 by small molecules leads to inhibition of the active form of RAS and to the inhibition of cancer cell growth that is driven by mut-*KRAS*.

#### **SAT-1032**

##### **A BIOLOGICAL UNDERSTANDING OF POTENTIAL SIGNALLING PATHWAYS ELICITED THROUGH MAXIMUM CORRELATION IN LUNG AND CERVICAL CANCER: INITIAL RESULTS**

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Statistical correlation among pairs of genes has been useful for building models of biological networks. Determining whether a sequence of events or gene expression tendencies lead to the onset of diseases, such as lung or cervical cancers, could prove to be imperative for finding better treatments for these diseases and possibly cures. In our research group, a mathematical network optimization model known as the travelling salesman problem (TSP) has been used to create potential signaling pathways in lung and cervical cancer. This study focuses on establishing if the resulting pathways are biologically viable and if a cause-effect relationship can be determined with this method. Should this be successful, further biological studies could be carried out to solidify knowledge of these proposed pathways for their future use in the fight against cancer.

#### **SAT-1040**

##### **HIGH EXPRESSION OF EMT MARKERS AS EARLY DETECTION FOR TRIPLE NEGATIVE BREAST CANCER**

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Breast cancer represents the second most commonly diagnosed cancer type among women in the United States. Triple-negative breast cancers (TNBC) are aggressive and frequently metastasize to the lung and brain leading to a poor prognosis. Here, we aim to identify

properties of non-malignant breast lesions that predict progression to metastatic TNBC. We hypothesize that TNBCs with metastatic potential arise in response to activation of Wnt/beta-catenin signaling. Secretable Wnt ligands from activated basal-epithelial stem cells elicit either autocrine and or paracrine cellular responses and thereby promote epithelial-to-mesenchymal-transitions (EMT), invasion, and metastasis. To investigate the role of Wnt/beta-catenin signaling, we have collected samples of the earliest identifiable breast lesions (atypical hyperplasia) from African American women at high risk to develop TNBC. We determined the expression pattern for known markers of the Wnt/beta-catenin signaling pathway (*BMI-1*, *HMGA2*, and *WNT10B*) in normal, atypical hyperplasia, and TNBC samples by immunohistochemistry. Preliminary results revealed a higher expression of *BMI-1*, *HMGA2*, and *WNT10B* in atypical hyperplasia and TNBC than observed in normal tissue. These results are promising and reveal that the presence of these markers may lead to earlier detection of TNBC in women who are at high risk to develop TNBC. Innovative therapeutics to prevent metastasis for TNBC patients based on these EMT markers can be developed and increase the survival rate of patients with TNBC.

#### **FRI-1032**

#### **THE IMPACT OF A CD40 AGONIST ON *GLUT1* AND *GLUT2* EXPRESSION IN THE TUMOR MICROENVIRONMENT OF PANCREAS CARCINOMA**

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Glucose metabolism is frequently increased in many solid malignancies. We previously showed that an agonist CD40 monoclonal antibody (mAb) can decrease glucose metabolism in pancreatic ductal adenocarcinoma (PDA). Here, we examine the impact of an agonist CD40 mAb on the regulation of glucose transporter (*GLUT*) expression in the tumor microenvironment of PDA using the *Kras*G12D/+; *Trp53*R172H/+ *Pdx-1*Cre mouse model of PDA. The expression of *GLUT1* and *GLUT2* within the tumor microenvironment was analyzed by immunofluorescence microscopy. Tumors were examined 1 and 14 days after treatment with a CD40 mAb and compared to untreated tumors. We found that *GLUT1* was highly expressed in tumor cells within the tumor microenvironment of PDA, and that tumor cell expression of *GLUT1* was modulated by treatment with a CD40 mAb when compared to untreated tumors. Specifically, *GLUT1* expression was observed to transiently increase in tumors cells after one day of treatment and return to baseline by day 14. In contrast, we found an absence of *GLUT2* expression in untreated tumors that was upregulated beginning one day after treatment with a CD40 mAb. By day 14 post treatment, both tumor cells and stromal cells were found to express *GLUT2*. In conclusion, our findings suggest that immunotherapy with an agonist CD40 mAb can alter glucose transporter expression in the tumor microenvironment of PDA.

**FRI-1037****IDENTIFICATION AND VALIDATION OF POTENT NATURAL PRODUCTS AGAINST PEDIATRIC MALIGNANCIES**

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Terrestrial natural products have been a source of therapeutic agents throughout human history. Plants can rapidly produce hundreds of useful secondary metabolites; however, identification and structure elucidation is labor intensive and difficult to replicate. Recent progress in bio-guided screening has allowed us to rapidly screen hundreds of natural product fractions from the American continent. The main objective of this study was to identify and quickly validate the most potent natural product hits against pediatric malignancies and build a cataloging system based on their bioactivity. We hypothesized that bioactive natural products that were tested in preliminary cytotoxic studies using a limited cellular cancer panel, namely hepatocellular carcinoma (HepG2), human embryonic kidney (HEK293), human skin cell (BJ), and B-cell lymphoma (Raji), would demonstrate activity against our stable blood cancer cell line panel derived from acute lymphoblastic leukemia (ALL). Fractions that demonstrated high activity in the initial cytotoxic panel within a reasonable therapeutic window were screened against UOCB1 and NALM06. From both studies, fractions were evaluated using the proliferation CellTiter-Glo assay in a high throughput setting. This cellular assay measures the ATP concentration of viable cells as a direct indicator of proliferation inhibition induced by certain naturally occurring cytotoxic compounds. The raw data from these studies was used to compile a database of all bioactive fractions. Compounds were purified by column chromatography and elucidated using NMR spectroscopy and mass spectrometry techniques. As a proof of principle, our pilot study highlights 2 natural product fractions and our promising findings.

**SAT-1031****RHODIOLA CRENULATA INHIBITS WNT SIGNALING IN MDA-MB-231 TRIPLE NEGATIVE BREAST CANCER CELL LINES**

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Breast cancer is a leading cause of cancer death in women, second to lung cancer. Triple negative breast cancer (TNBC) tumors are the most aggressive form of breast cancer that does not express Her2/Neu receptor and estrogen and progesterone receptors. The Wnt pathway is a signaling pathway that is essential in normal cell development and has been implicated in breast cancer where it plays a role in cell invasion and cancer stem cell maintenance. *Rhodiola crenulata* (RC) is a Tibetan mountain-dwelling plant, commonly used in Eastern alternative medicine as an adaptogen. Previously, we have shown that RC inhibits migration and invasive behaviors of TNBC cell lines and increases cell death. In this study, we demonstrate the inhibition of WNT target gene activation in MDA-MB-231 cells upon treatment with RC. We

performed a  $\beta$ -catenin reporter luciferase assay and qPCR for WNT target genes. Our results demonstrate an inhibition of  $\beta$ -catenin transcriptional activation as well as a decreased expression of canonical WNT target gene expression. These data suggests that RC inhibits WNT signaling in this triple negative breast cancer cell line and hints to a possible mechanism for how *Rhodiola* provides protective effects on triple negative breast cancer subtypes.

#### **FRI-1038**

##### **PRO-APOPTOTIC GENE EXPRESSION COMPARISON BETWEEN RECOMBINANT DISINTEGRINS R-MOJ-DA, R-MOJ-DN, AND R-MOJ-DM-TREATED SK-MEL-28 CELLS**

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Disintegrins are small, non-enzymatic peptides that bind and activate integrins. Integrins can initiate signal transduction pathways leading to cell migration, survival, and apoptosis. Previous studies have shown that three mutated recombinant mojastin peptides (r-Moj-DM, r-Moj-DN, and r-Moj-DL) induce apoptosis of SK-Mel-28 cells. Three other recombinant mutants with a second aspartate, carboxyl to the RGD (r-Moj-DA, r-Moj-DG, and r-Moj-DV) failed to induce apoptosis of treated SK-Mel-28 cells. Additionally, RNA sequencing data of SK-Mel-28 cells treated after 6 hr with r-Moj-DM showed significant upregulation and downregulation of 40 genes. In the present study, we compared the expression of several pro-apoptotic genes after treatment with two apoptotic-inducing peptides (r-Moj-DM and r-Moj-DN) and one non-apoptotic peptide (r-Moj-DA). We hypothesized that gene expression of seven pro-apoptotic genes will be significantly higher in r-Moj-DM and r-Moj-DN treated cells. SK-Mel-28 cells were treated for 1, 2, 4, and 6 hrs with either 5  $\mu$ M of r-Moj-DA, r-Moj-DM, or r-Moj-DN peptides. Following treatment, mRNA was isolated from treated cells and cDNA synthesized using a Qiagen Reverse Transcriptase Kit. Quantitative (Q) PCR was used to examine gene expression levels and compared to expression levels of untreated cells. Our results from r-Moj-DA-treated cells indicate that expression levels of the seven pro-apoptotic genes tested showed a non-significant upregulation as compared to the expression of the same genes from r-Moj-DM-treated cells. In the next weeks, we will be examining the expression of the same seven pro-apoptotic genes in r-Moj-DN-treated cells.

#### **FRI-1044**

##### **THE EFFECTS OF MASS SPECTROMETRY ANALYSIS OF LIPIDOMICS IN CIRCULATING TUMOR CELLS**

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Circulating tumor cells (CTCs) are cells that have shed into the vasculature from a primary tumor and circulate through the bloodstream, and they are thought to cause metastatic disease. Even though CTCs are present in low numbers in the blood, their characterization, specifically finding a unique signature of phytosterols (PS) and cholesterol lipid profiles as compared with the lipid profiles of primary tumor and metastasis, will potentially provide information to understand if lipids in CTCs influence the metastatic process. In a proof-of-concept study, we began creating a protocol to extract the lipids from the primary tumor, CTCs, and metastasis. Through the use of density gradient centrifugation of the blood, the CTCs and

peripheral blood mononucleated cells (PBMCs) were isolated from cancer and healthy patients' blood. The density gradient centrifugation gives a combination of the CTCs and PBMCs sampled. Therefore, a modified Blight and Dyer method for lipid extraction is currently being tested to see if only the lipids from CTCs can be extracted and analyzed using a triple stage quadruple mass spectroscopy (TSQ-MS) machine. Results presented in this work will serve as a starting point to define possible PS and cholesterol biomarkers that can reveal metabolic pathways with potential for novel drug cancer therapy.

#### **SAT-1034**

##### **CLINICAL UTILITY OF NEGATIVE ZIRCONIUM-89-J591/PSMA POSITRON EMISSION TOMOGRAPHY SCAN IN THE EVALUATION OF MEN WITH LOCALIZED PROSTATE CANCER**

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We have previously described that Zirconium-89 (<sup>89</sup>Zr)-labeled J591 monoclonal antibody-based positron emission tomography (PET) scan can identify clinically significant localized prostate cancer (PCa). We therefore wanted to assess whether <sup>89</sup>Zr -J591 PET could also be used to delineate between clinically significant and insignificant localized PCa. Monoclonal antibodies J591 labeled with <sup>89</sup>Zr target prostate-specific membrane antigen. Eleven patients were injected intravenously with <sup>89</sup>Zr -J591 followed 5-7 days later by *in vivo* whole body PET scans. Radical prostatectomy was performed the day after imaging, and prostate specimens were submitted for *ex vivo* microPET imaging and histologic evaluation. For the purposes of this study, clinically insignificant lesions of PCa were defined as having a Gleason score ≤ 6. Histopathology maps were created for each prostatectomy and were compared to both *in vivo* and *ex vivo* PET images. In 8 out of 11 patients, a total of 14 lesions with Gleason score 6 were identified in histologic evaluation. None of these lesions were visible in the *in vivo* PET images. One focus measuring 6 mm was visible on the *ex vivo* microPET imaging study. By comparison, Gleason ≥ 7 lesions of similar size were visible on both *in vivo* and *ex vivo* PET scans. This pilot study yields preliminary evidence to suggest that the absence of any visible lesions on <sup>89</sup>Zr-J591 PET scan may point to the absence of any prostate cancer of Gleason score ≥ 7. In doing so, this may have the potential to distinguish between clinically significant from insignificant localized PCa.

#### **FRI-1030**

##### **DEVELOPING THERAPIES TO INHIBIT T CELL ACUTE LYMPHOCYTIC LEUKEMIA FROM ENTERING THE BRAIN USING THE CRISPR/CAS9 SYSTEM**

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Thirty percent of children who develop T cell acute lymphocytic leukemia (T-ALL) will relapse within two years of chemotherapy treatment and die. Relapse has shown to be attributed to the migration of the leukemic T cells past the blood brain barrier (BBB) and into the central nervous system (CNS) where the leukemic cells can evade the effects of chemotherapies. It has previously been shown that C-C chemokine receptor 7 (CCR7) aids in the leukemic cells invasion



past the BBB in response to its ligand CL19. We have preliminary data that shows CCR7-positive T-cells enter the brain, and we are investigating the distribution of CCL19 to determine the site of entry. We propose that blocking expression of CCR7 will inhibit the movement of leukemia into the brain. We are developing a panel of RNA-guided, DNA-cleaving nucleases that use the endonuclease Cas9 to delete genomic *CCR7* in human T-ALL. This system uses the type II clustered, regularly interspaced, short palindromic repeats (CRISPR)-associated Cas9 pathway taken from the prokaryote *Neisseria meningitidis*. In this system, Cas9 is guided by short RNA molecules that are homologous to a specific target of DNA to cleave this region of interest. The panel of CRISPR/Cas9 enzymes we are creating use RNA specific to the *CCR7* gene to guide Cas9. We anticipate the CRISPR/Cas9 system will lead to a potential therapy that can inhibit T-ALL from entering the brain.

#### **FRI-1028**

#### **TARGETED CANCER NANOTHERAPEUTICS BY ADOPTIVE TRANSFER OF MONONUCLEAR SPLENOCYTES**

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Breast cancer chemotherapeutics rely on blood vessels to deliver drugs to tumors by passive diffusion. However, the poor vasculature, altered extracellular matrix, and reduced lymphatic drainage of tumors limit diffusion, compromising drug efficacy. Additionally, most chemotherapeutics cause adverse systemic side effects because they are not specific to cancerous cells; rather, they target all rapidly dividing cells. Nanotechnology shows potential in optimizing drug targeting and limiting toxicity due to the enhanced permeability and retention effect which allows nanoparticles to passively enter and accumulate in the tumor vicinity. Porous nanoparticle-supported lipid bilayers (protocells), which can be modified with diverse molecules, are especially adept at optimizing cargo capacity and stability. However, protocells remain prone to the limitations of passive diffusion and rapid clearance by the liver. Therefore, we proposed a method of active delivery in which circulating mononuclear cells (MCs), which naturally infiltrate tumors, could effectively deliver protocells to their targets. MCs were extracted by density gradient from the spleens of immunocompetent polyomavirus middle T (PyMT) transgenic mice. Ectopic expression of the PyMT oncoprotein results in epithelial mammary tumors that mimic human breast cancer progression. MCs loaded with DOPC (1, 2-dioleoyl-sn-glycero-3-phosphocholine)-coated protocells, further modified with PEG (polyethylene glycol), DOPS (1,2-dioleoyl-sn-glycero-3-phosphoserine), or DOTAP (1,2-dioleoyl-3-trimethylammonium-propane), were injected into PyMT mice. We observed the biodistribution of directly-injected protocells versus protocell-loaded MCs through fluorescence microscopy of cryosectioned tumors and flow cytometry of digested tumors. Our results demonstrate that MC-mediated delivery enhances localization of protocells to mammary epithelial tumors compared to freely circulating protocells.

### **SAT-1035**

#### **ANALYSIS OF P70 S6 KINASE PHOSPHORYLATION IN BRAF<sup>V600E</sup>-MUTATED MELANOMA CELLS**

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One of the most common genetic alterations in melanoma is a substitution of valine for glutamic acid at position 600 encoding BRAF<sup>V600E</sup>. This constitutively active protein leads to sustained activation of the ERK1/2 mitogen-activated protein kinase (MAPK) signaling pathway. BRAF<sup>V600E</sup>-expressing melanocytes frequently cooperate with the phosphoinositide 3-kinase (PI3K) signaling pathway in order to progress to melanoma. Cooperation of these pathways has been recently shown to regulate the phosphorylation of p70 S6 kinase (p70<sup>S6K</sup>) and its downstream target, ribosomal protein S6. Moreover, MAPK inhibition resulted in a significant inhibition of p70<sup>S6K</sup> phosphorylation, whereas PI3K inhibition had no effect on p70<sup>S6K</sup> phosphorylation. Although PI3K inhibition had no effect on p70<sup>S6K</sup> phosphorylation, MAPK and PI3K inhibition decreased ribosomal protein S6 phosphorylation. The differential effects of MAPK and PI3K inhibition on p70<sup>S6K</sup> phosphorylation could be attributed to the phospho-specific antibody which recognizes analogous phosphorylation sites of both the p70 (Thr389) and p85 (Thr412) isoforms of S6 kinase as well as S6 kinase II (Thr401). Thus, we wanted to determine the phosphorylated S6 kinase isoforms detected with the phospho-p70<sup>S6K</sup> (Thr389) antibody using inhibitors of the MAPK and PI3K pathways and BRAF<sup>V600E</sup>-mutated melanoma cells. Preliminary data reveals that the antibody recognizes a 70 kDa phospho-protein inhibited by MAPK inhibition, but insensitive to PI3K inhibition and a 60 kDa phospho-protein not present in all BRAF<sup>V600E</sup>-mutated melanoma cells. The work conducted in this study will help us identify what isoforms of S6 kinase proteins are detected by the phospho-p70<sup>S6K</sup> (Thr389) antibody in BRAF<sup>V600E</sup>-mutated melanoma cells.

### **FRI-1029**

#### **SGTα A NOVEL THERAPEUTIC TARGET FOR PROSTATE CANCER**

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Steroid hormone receptors (SHRs) are essential for the regulation of developmental, reproductive, and physiological homeostasis in eukaryotes. SHRs belong to the nuclear receptor superfamily and comprise the androgen (AR), glucocorticoid (GR), progesterone (PR), mineralocorticoid (MR), and estrogen (ER) receptors. Understanding their regulation is critical for the development of novel therapeutic strategies for SHR-mediated diseases such as prostate cancer and fertility issues. The heat shock protein (Hsp) 90/70 kDa is vital for the dynamic chaperone complex that drives SHRs folding. Different chaperones and co-chaperones allow the receptor to be either positive or negative regulated. The recently identified co-chaperone human small, glutamine-rich TPR-containing protein alpha (SGTα) has been associated to Hsp70 and Hsp90 binding to antagonize the AR transcriptional activities. Interestingly, we have demonstrated that SGTα can also regulate GR and PR using functional yeast and mammalian reporter assays. On the other hand, another TPR-containing protein,

FKBP52, has the ability to positively regulate the same receptors. When we co-expressed SGTα and FKBP52 in yeast and mammalian systems, SGTα continued to abrogate receptors' transcriptional activities. Although both proteins bind Hsp90's MEEVD motif through their TPR domain, our data suggests that SGTα activity is not solely due to a competition for binding Hsp90, but it may have some role at the transcriptional or translational level. Additionally, the mutant K160A SGTα which is within the TPR domain has a decreased affinity to bind the Hsp70/90 assembly, losing ability to regulate the receptor.

#### **FRI-1042**

##### **INVESTIGATING THE ROLE OF THE NATURAL PRODUCT NI-07-INDUCED AUTOPHAGY IN KILLING BREAST CANCER CELLS**

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Recent studies in our lab have demonstrated that the green product NI-07 has strong anti-cancer properties including water solubility and the ability to target malignant cells across various cancer cell lines while remaining nontoxic to the normal cells. However, little information is known about the mechanism behind NI-07's ability to aggress cancer cells and the manner in which NI-07 induces cell death. Previously, we observed morphological changes and vacuolization in NI-07-treated breast cancer cells consistent with autophagy-induced programmed cell death (PCD). Autophagy is a type of PCD involving three distinct pathways that degrade and recycle cellular components using a combination of autophagosomes and lysosomes. Based upon preliminary data from our lab, autophagy occurs at 24 hours. However, we hypothesized that autophagy was initiated earlier. To test this hypothesis and the role of autophagy in NI-07-induced programmed cell death, breast cancer cells and normal cells were grown cultured and treated with 36.6 mM NI-07 for 24 hours. The cell lines were then analyzed by XTT to measure the changes in metabolism. Viability and cytotoxicity were determined by trypan blue exclusion. To determine the importance of autophagy in cell death, cells were analyzed using the Cyto-ID autophagy detection kit. We further investigated which autophagic pathway predominates by analyzing changes in heat shock factor 1 (HSF1) downstream targets using western blotting against HSF1, heat shock protein 60 (HSP60), and heat shock protein 90 (HSP90).

#### **SAT-1041**

##### **ANALYSIS OF HER2 AND CD44 TURNOVER RATES IN TWO BREAST CANCER CELL LINES USING FLUORESCENCE MICROSCOPY**

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Cancer stem cells (CSCs) are a select group of tumor cells believed to be responsible for recurrence, metastasis, and therapy resistance. In breast cancer, HER2<sup>+</sup>/CD44<sup>+</sup>/CD24<sup>-/low</sup> cells have been shown to be more tumorigenic, aggressive, and therapy resistant. MCF7-Clone 6 is a breast cancer cell line derived from wild-type MCF7 cells that survived long-term fractionated

ionizing radiation treatment, and CSC-like phenotype (HER2<sup>+</sup>/CD44<sup>+</sup>/CD24<sup>low/-</sup>) is enriched in these cells. SKBR3 cells are a well-established breast cancer cell line that over-expresses HER2 and is positive for CD44. In this study, we sought to determine the turnover rates of HER2 and CD44 in SKBR3 and MCF7-Clone 6 cell lines in order to better understand protein dynamics in these particular cell lines. We analyzed HER2 and CD44 turnover rates by using fluorescence microscopy and quantified them by using ImageJ software. Determining the turnover rates of these two surface proteins in the two breast cancer cell lines is critical to the long term goals of our lab to develop novel metallic nanoparticles tagged with HER2 and CD44 antibodies. These nanoparticles could be used to continuously image cancer cells over multiple cell cycles and therefore help increase our understanding of breast cancer cell proliferation as well as breast cancer stem cell maintenance and differentiation.

#### **FRI-1043**

#### **COMPARISON OF ANTICANCER EFFICACY OF COMPONENTS FROM SAFFRON STICKS AND STEM**

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Breast cancer is the most common cancer in women. The United Kingdom and United States have the highest incidence rates worldwide. Therefore, it is a priority for these countries to focus on breast cancer awareness and the development of new strategies to eradicate this devastating disease process. One of the promising strategies for cancer prevention today is chemoprevention. A growing body of research has demonstrated that saffron extract itself and its main constituents, the carotenoids, possess chemoprevention properties against cancer. Isolation and characterization of biologically active anticancer agents from saffron have not yet been reported. Further studies are required to evaluate the safety and efficacy of saffron in cancer treatment. The main purpose of this study is to isolate and compare anticancer agents from saffron sticks and stem and test their efficacy *in vitro*. In previous studies, it was reported that the partially purified methanol fractions of saffron using cation exchange chromatography showed a 70-80% inhibitory effect on breast cancer cells (MCF7) growth but had no effect on the growth of normal epithelial cells (MCF10A). In the current study, anticancer components from saffron flower sticks and stem were extracted in five different solvents (dichloromethane, ethyl acetate, hexane, methanol, and water), partially purified using silica gel column, and the efficacy of fractions containing saffron components was tested on breast cancer cells (MCF7) *in vitro*. The anticancer activity was exclusively associated with methanol, ethyl acetate, and water extracts. These fractions are now being further purified and characterized structurally.

**FRI-1018****CHARACTERIZATION OF THE SIGNALING NETWORKS INVOLVED IN THE ANTICANCER EFFECTS OF THE MOST BIOLOGICALLY ACTIVE RECOMBINANT MOJASTIN MUTANT DISINTEGRINS**

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Previous studies have shown that disintegrins induce anti-cancer effects in multiple cancer cell lines through interactions with integrin receptors. Ligand interactions with integrin receptors affect many cellular functions, such as cell adhesion, cytoskeletal organization, cell growth, differentiation, migration, angiogenesis, and apoptosis. Our studies have shown that recombinant (r) Mojastin disintegrins exert anti-cancer effects in multiple cell lines at varying degrees depending on their amino acid (AA) composition flanking the RGD integrin-binding motif. Interestingly, r-Mojastin D-mutant disintegrins (r-Moj-D\_) evoke the most prominent phenotypes in apoptotic induction, cell proliferation inhibition, and cell migration inhibition of human SK-Mel-28 cells. However, the key integrin-dependent signaling cascades used in these cellular responses are not known. To illuminate critical signal transduction pathways, we used a functional genomics approach, including: whole-transcriptome RNA sequencing (RNA-SEQ), qRT-PCR gene expression studies, RNAi, and immunocytochemistry. Our RNA-SEQ results show differential expression of 40 genes (10 up, 30 down) in SK-Mel-28 cells treated with r-Moj-DM, which was validated by qRT-PCR. Of the 10 up-regulated genes, only 1 was identified as a pro-apoptotic gene using the Database for Annotation, Visualization, and Integrated Discovery tool (DAVID). Confocal microscopy was used to study localization of this pro-apoptotic protein. Additionally, lentiviral shRNAs were used to silence this pro-apoptotic protein to determine its role in r-Moj-D\_ induced apoptosis. Future studies will include protein analysis of the focal adhesion complex and related integrin-dependent signaling networks. These results will elucidate the signal transduction pathways affected by Mojastin mutant disintegrins and are important for cancer therapy innovation.

**SAT-1038****THE ROLE OF CTGF IN THE BONE MARROW MICROENVIRONMENT OF PRE-B ACUTE LYMPHOBLASTIC LEUKEMIA**

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Precursor B-cell acute lymphoblastic leukemia (pre-B ALL) is the most common hematological neoplasm in children, accounting for 85% of pediatric ALL. Despite an 80% increase in 5-year event-free survival over the last 50 years, approximately 20% of children with ALL relapse for reasons that have not yet been determined. Several studies have indicated the significant role of the bone marrow microenvironment (BMM) in mediating pre-B ALL therapy resistance. The gene encoding connective tissue growth factor, *CTGF*, has been identified as one of several signature genes regulating cell signaling and interaction in the bone marrow. However, the mechanism by which *CTGF* contributes to this interaction is unknown. Here, we hypothesized that *CTGF* overexpression promotes adhesion of leukemic cells to the BMM. RNA was extracted from 15 primary pre-B ALL patient samples and 5 cell lines to perform RT-PCR, followed by

qPCR to determine *CTGF* expression levels. We confirmed that both pre-B ALL patient samples and cell lines differentially express *CTGF* as compared to healthy human B-cells. In order to evaluate the role of *CTGF* in mediating adhesion in the BMM, 697 and RS4;11 pre-B ALL cells overexpressing *CTGF* were transiently transfected with *CTGF* shRNA, followed by cell-cell and cell-extracellular matrix adhesion assays. The level of adherent cells was reduced by ~30% in samples exhibiting *CTGF* knockdown. Our data demonstrates that *CTGF* is involved in adhesion of pre-B ALL cells to fibronectin and HS-5 stromal cells. This could have significant implications on the role of *CTGF* in leukemia cell survival and chemoresistance.

#### **FRI-1041**

##### **PERTURBING HEMATOPOIETIC STEM CELL MIGRATION THROUGH A VASCULAR ENDOTHELIAL BARRIER BY BLOCKING VCAM1 ADHESION**

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Hematopoietic stem cells (HSCs) have been used clinically for over half a century; however, the mechanisms regulating HSC trafficking through vascular barriers remain unclear. We seek to further understand the intricate mechanisms of HSC binding to vascular endothelial cells (VECs) and the impact of blocking these mechanisms on HSC migration toward the chemokine CXCL12. One such mechanism involves vascular cell adhesion marker-1 (VCAM1), which is expressed both on the surface of HSCs and VECs. It is involved in binding of leukocytes to the VECs as an integral component in the migration of leukocytes through the vascular endothelial tissue *in vivo*. Previous *in vitro* data from our lab suggests that blocking integrin- $\alpha$ -4 (VLA-4), VCAM1's binding partner, on VECs blocks the migration of HSCs, progenitors, and B-cells through the VEC layer toward CXCL12. We next pursued whether the reciprocal is true; whether HSC migration through VECs is perturbed by blocking VCAM1 on VECs. We tested this by using 2 different blocking antibodies targeting VCAM1 in an *in vitro* VEC migration assay. VECs were cultured on transwells and grown to confluency prior to adding anti-VCAM1 blocking antibodies to the VEC layer. Lineage-depleted bone marrow cells were then allowed to migrate toward CXCL12 for 2 h. The effects of blocking VCAM1 were quantitatively measured using flow-cytometry (BD LSRII). Our hypothesis was that by blocking VCAM1 on ECs, HSCs would have perturbed migration through VEC transmembranes as seen with the blockage of VLA-4 in previous studies. Understanding HSC migration mechanisms may lead to innovations in HSC transplants.

#### **SAT-1043**

##### **FOCAL ADHESION KINASE (FAK) IS REQUIRED FOR CSPG4-DRIVEN CELL SURVIVAL AND AKT PHOSPHORYLATION IN RESPONSE TO DABRAFENIB**

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The resistance of melanoma to chemotherapeutics, such as the RAF inhibitor dabrafenib, is associated with the activation of cell surface proteins (e.g., integrin) and receptor tyrosine kinase (RTK) pathways. Chondroitin sulfate proteoglycan 4 (CSPG4) is a transmembrane proteoglycan found in high concentrations in melanoma cells. This proteoglycan leads cellular

functions that drive tumorigenesis by the activation of the integrin signaling pathway through focal adhesion kinase (FAK), and RTKs. We have previously found that CSPG4 is responsible for increasing AKT phosphorylation (P-AKT) and cell survival in response to dabrafenib. This project consists of 2 parts. In the first part, we hypothesized that FAK is required for P-AKT in response to dabrafenib. We inhibited FAK pharmacologically, and found that P-AKT decreased, but using it in combination with dabrafenib could not decrease the P-AKT. In the second part, we hypothesized that the loss of CSPG4 would re-sensitize dabrafenib-resistant cells to dabrafenib. CSPG4 was knocked down using siRNA, and cell survival analysis was used to generate a dose-response curve to SB590885, a dabrafenib parent compound. It was determined that the cells with CSPG4 knockdown were more vulnerable to the drug. However, only a partial knockdown was obtained, therefore the experiment will be repeated using viral infection to increase knockdown efficacy. These results suggest that targeting CSPG4 could improve melanoma treatment using a combination of therapies.

#### **SAT-1142**

##### **INVESTIGATING DASATINIB TREATMENT RESISTANCE IN ALL WITH SYSTEMS BIOLOGY AND ShRNAs**

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Treatment of acute lymphocytic leukemia (ALL) with standard-of-care, dasatinib and/or chemotherapy is currently unsuccessful for approximately 20% of children and 60-80% of adults. Thus, advances are needed in order to increase the proportion of patients gaining a successful outcome. Our approach is to employ computational systems analysis of experimental data from shRNA perturbations of ALL B-cells, with the goal of identifying genetic regulators of dasatinib response. In an initial *in vivo* screen, ALL B-cells were infected with a 20,000-shRNA library and then tail-vein injected into mice; we determined how the number of cells with specific shRNAs remaining in circulation changed following drug treatment. An increase in cells expressing a given shRNAs from pre-treatment to post-treatment indicated resistance to treatment at these targeted loci, whereas a decrease indicated the shRNAs sensitize cells to treatment. Clustering and mutual information analyses identified targets that both promote disease progression and confer resistance to therapy. Particular targets were then tested for validation *in vitro*, including ubiquitin-conjugating enzyme E2Q, ADP-ribosyltransferase 4, FAT Tumor suppressor 1, and Claudin 12. The validation results will ascertain whether these genetic targets confer resistance or sensitivity to dasatinib in ALL.

## CELL/MOLECULAR BIOLOGY

### SAT-1079

#### INTERACTION BETWEEN THE LUNG PATHOGEN, *CHLAMYDIA PNEUMONIAE*, AND EPITHELIAL CELLS FROM THE ORAL CAVITY

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*Chlamydia pneumoniae* (*C.pn*) is an intracellular bacterium that affects the respiratory tract and causes lung infections. *C.pn* can be transmitted by person-to-person by respiratory secretions and can go through numerous transformations during its life cycle such as monocytes, macrophages, and endothelial cells. Studies showed *C.pn* is present in the oral microbiota of normal subjects. However, little is known about whether *C.pn* can cause oral disease. Chlamydia infections are usually characterized through inflammation, which is an innate immune response. A variety of pathogens and endogenous danger signals activate inflammasomes, which are multiprotein complexes containing an adaptor protein, a protease called caspase-1, and a sensor such as NLRP3. Once the NLRP3 is stimulated, it triggers the secretion of proinflammatory cytokines, acting as a defense against infection. The human oral cavity contains numerous different bacterial, viral, and fungal species. The gingival epithelial cells (GECs) are the first line of defense against numerous oral pathogens, but it is not known whether GEC cells can be infected with *C.pn* and eventually lead to activation of the NLRP3 inflammasome. The hypothesis of this research is to determine whether *C.pn* can infect GECs and activate the NLRP3 inflammasome in GECs. The results from this study raise the possibility that under certain conditions, *C.pn* could cause inflammation in the oral cavity.

### FRI-1088

#### MINOR THINGS IN LIFE: EVOLUTION OF U12 INTRONS

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Many genomes contain 2 distinct types of introns: U2 (major) introns which are spliced by the U2spliceosome and U12 (minor) introns which are spliced by the U12spliceosome. Although the major and minor spliceosomes splice distinct introns, their structure and snRNPs are highly similar to one another. U2 introns make up more than 99% of introns in all characterized genomes, with U12 introns making up less than 1% of introns. Although the quantity of U12 introns are minuscule and some species have lost U12 introns altogether, the last remaining U12 introns appear to be highly evolutionarily conserved. The evolution of the major and minor spliceosome remains a mystery, with no clear evidence as to whether U2 or U12 introns arose before the other. The reasons for the last remaining U12s to remain so highly conserved is also cryptic. We sought to build software to perform genome-wide identification of U12 introns, and to apply it to diverse eukaryotic genomes. U12 and U2 introns have splice sites motifs, with particularly strong conservation of motifs in U12 introns, allowing for distinguishing U12 and U2 intron. We implemented a position weight matrix which quantitatively analyzes the probability that an intron is either more U2- or U12-like based on its splice site sequences. Preliminary



results using this program show that U12s are present in various distant and newer species and that U12s are not properly represented in many current genome annotations. This method will be leveraged to elucidate the evolution of the major and minor spliceosomes.

#### **SAT-1067**

##### **C. ELEGANS MODEL OF AMYOTROPHIC LATERAL SCLEROSIS: UNDERSTANDING THE ROLE OF TDP-43 EXPRESSION ON HSN MOTOR NEURON FUNCTION**

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Neurodegenerative diseases are often characterized by a continual loss of neuron abilities. Amyotrophic lateral sclerosis (ALS), also known as Lou Gehrig's disease, is a progressive neurodegenerative disease affecting nerve cells that are important for locomotion. When motor neurons atrophy, due to their lack of regenerative ability, muscle control is severely impaired. Some individuals with ALS carry mutations in a gene called TDP-43. It is hypothesized that mutations in TDP-43 cause TDP-43 to aggregate leading to motor neuron degeneration. We have generated a nematode *C. elegans* model for ALS. This model was made by cloning the human version of the TDP-43 gene under the control of a pan-neuronal promoter. Taking advantage of the transparency of *C. elegans*, the human TDP-43 was tagged with a YFP (yellow fluorescent protein) to provide visual representation of its aggregation during development and aging. Egg laying assays were performed as an indication of neuronal function, specifically, to monitor TDP-43 and the effect of its aggregation on HSN motor neurons which are responsible for vulval muscle contraction and thus the reproductive success of *C. elegans*. Preliminary data suggests there is a 55% decrease in progeny production in animals expressing TDP-43. Furthermore, TDP-43 expressing animals have a 30% decrease in egg laying rate compared to wild-type animals. Taken together, our data indicates defects in HSN motor neurons. Our studies using this *C. elegans* model will continue to enhance our understanding of the connection between TDP-43 and motor neuronal defects associated with ALS.

#### **SAT-1053**

##### **REGULATION OF CELL ADHESION IN THE EARLY EMBRYO**

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Cell adhesion molecules hold cells together and help establish apical-basal polarity. In the early embryo, there is an increase in cell adhesion with successive divisions such that blastomeres transition from a spherical to epithelial cell morphology. While it is known that calcium-dependent cadherins mediate cell adhesion, it is unclear what signals trigger junction formation in the early embryo. The small GTPase Rac has been implicated in regulating cell adhesion in some cell types, and preliminary data indicates that activated mutants of Rac can trigger precocious cell-cell junction formation in sea urchin embryos. We hypothesize that the transition from spherical to epithelial cell morphology is mediated by the activation of Rac through the guanine exchange factor, TIAM1. Towards these ends, we isolated the *PH-CC-Ex* domain of sea urchin TIAM1, which can act as a dominant-negative mutant that disrupts

endogenous TIAM1 activity. This domain will be expressed in sea urchin embryos, which will be followed by timelapse microscopy. If Rac is, indeed, required for the establishment of cadherin-based adhesion, then expression of the *PH-CC-Ex* domain should inhibit cell adhesion and epithelialization. If successful, this will be the first evidence for a G protein-mediated pathway regulating cell adhesion during the first stages of development.

#### **FRI-1070**

##### **AMYOTROPHIC LATERAL SCLEROSIS IN *C. ELEGANS*: THE EFFECTS OF TDP-43 EXPRESSION ON NEURONAL HEALTH**

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TDP-43 is an RNA-binding protein that has been linked to neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS). TDP-43 becomes inappropriately cleaved and accumulates in the cytoplasm of affected cells forming aggregates. To study the effects of TDP-43 on neuronal function, we generated a *C. elegans* model for ALS by cloning the human wild-type *TDP-43* gene tagged with a yellow fluorescent protein (YFP) under a pan-neuronal promoter. Animals expressing *TDP-43* have severely limited motor neuron capabilities. To explore whether these motor deficits are a result of neurodegeneration, we introduced a red fluorescent protein reporter into GABAergic motor neurons. Microscopy was used to visualize and compare the neuronal health of motor neurons in transgenic animals to those in wild-type animals. In addition, the subcellular localization of TDP-43::YFP was assessed in order to determine whether cytoplasmic accumulation was contributing to motor deficits. Preliminary data revealed that animals expressing *TDP-43* show signs of neurodegeneration and neuronal abnormalities. Deciphering whether neurodegeneration and/or TDP-43 mislocalization and accumulation lead to motor neuron dysfunction may reveal candidate cellular processes that could be targeted for therapeutics.

#### **SAT-1063**

##### **INVESTIGATING THE RELATIONSHIP BETWEEN INTRON BRANCH SEQUENCE AND SPLICING INHIBITION BY PLADIENOLIDE B**

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An essential step in gene expression is RNA splicing, which is the removal of non-coding intron sequences and ligation of the remaining exon sequences in pre-mRNA gene transcripts to produce a mature mRNA. This process is catalyzed by a complex macromolecular machine called the spliceosome. Understanding spliceosome activity is important because changes in splicing are associated with several human diseases. For example, mutations of the core splicing factor SF3B1 are associated with cancer. A key role of SF3B1 is to stabilize U2 snRNP, a small nuclear ribonucleoprotein, in the spliceosome and identify the intron branch sequence. The anti-tumor drug pladienolide B (PB) targets SF3B1 and inhibits splicing of some but, surprisingly, not all pre-mRNA transcripts. Therefore, we hypothesized that splicing inhibition by PB depends on the strength of intron branch sequences. We predict that, compared with stronger intron

branch sequences, weaker intron branch sequences will be inhibited more easily by PB. To test this hypothesis, we will use an *in vitro* splicing assay with a pre-mRNA containing different intron branch sequences and will compare PB inhibition. Our results will inform future studies looking at the effect of SF3B1 and PB on splicing of introns in cancer cells. These studies will also impact efforts to use PB as a chemotherapeutic.

#### **SAT-1062**

##### **USING LIVE ZEBRAFISH LARVAE TO ELUCIDATE THE ROLE OF ENDOCYTIC TRAFFICKING IN INTESTINAL CHOLESTEROL ABSORPTION**

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Cholesterol is an essential dietary lipid that contributes to membrane integrity and hormone biosynthesis. However, its dysregulation in humans is associated with increased cardiovascular disease and subsequent adverse cardiac events. Although 50% of the dietary cholesterol entering the intestinal lumen is absorbed, the mechanism by which this occurs has not been elucidated with sufficient detail from a cell biology standpoint. While there are numerous studies in cultured cells describing the intracellular trafficking of cholesterol, few were performed *in vivo*. We hypothesized that dietary cholesterol absorption can be imaged in live zebrafish using a fluorescent cholesterol analog; absorption proceeds via known endocytic pathways; and mutations in the endocytic machinery of the intestine will alter the rate of cholesterol absorption. We developed transgenic zebrafish lines that express Rab markers for specific endocytic compartments (early, late, or recycling endosomes) as well as Rab mutant lines with altered endocytic activity. Larvae from these lines were fed a high-fat diet supplemented with fluorescent cholesterol and imaged using live confocal fluorescent microscopy. We found that fluorescent cholesterol absorbed by the intestine colocalizes with early and recycling endocytic compartments suggesting that dietary cholesterol is being absorbed via endocytosis. Mutations in the endocytic machinery result in morphological changes to the endocytic compartments, but their effects on cholesterol absorption have yet to be determined. Taken together, our studies establish the larval zebrafish as a model for live imaging of dietary cholesterol endocytosis.

#### **FRI-1062**

##### **ANALYSIS OF B LYMPHOCYTE DEVELOPMENT DURING AGING IN SCLEROSTIN-DEFICIENT MICE**

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When sclerostin (SOST), a glycoprotein that is essential for proper bone formation, is absent, hyperactive bone growth occurs concomitant with a decrease in bone marrow (BM) cavity size. SOST-knockout (KO) mice consequently display increased bone densities due to dysregulated bone growth and hyperactive Wnt signaling in osteoblasts. In addition, we have observed that the BM cavities in 10-16-week old KO mice contain deficiencies in growth factors that adversely affect B lymphocyte development. We hypothesized that B cell populations would be further altered in the KO mice as they age. Peripheral blood was analyzed monthly to quantify mature

and immature B cell populations in KO and control wild-type B6 mice up to 1 year of age. A noticeable decrease in B cell expression in the older KO mice was observed. Current studies are underway in young KO mice to determine the exact age when B cell development in the BM is affected. Future studies will examine the B cell populations in the lymphoid organs of the older mice and test B cell responses to immune challenge. Knowing how SOST functions to regulate B cell development and immune response could provide information on how to sustain robust immunity in patients suffering from defects in bone homeostasis and prevent age-related decline in immunity in individuals. Furthermore, a significant reduction in B cell numbers or function in KO mice could indicate that the use of anti-SOST antibodies for treatment of osteoporosis may have unintended effects on B cell immunity in those patients.

#### **SAT-1069**

#### **MEXICAN FREE-TAILED BATS: A POSSIBLE TRANSMISSION VECTOR FOR WHITE-NOSE SYNDROME**

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*Pseudogymnoascus destructans* (Pd) is a fungus responsible for causing white-nose syndrome (WNS), a newly emerging disease that has killed at least one million hibernating bats since 2006. Despite its dramatic impact on global bat populations, little is known about the mechanism of transport or transmission of this fungal pathogen. The Mexican free-tailed bat, *Tadarida brasiliensis*, is a non-hibernating, long-distance migrant that congregates in roosting sites shared by hibernating bats susceptible to Pd. Given their large migratory range and frequent contact with other bat species, *Tadarida* may serve as an important vector in the transmission of Pd; however, because spore dispersal via *Tadarida* has not been studied, this possibility is difficult to evaluate. The purpose of our study is to determine whether *Tadarida* is a transmission vector for cold-tolerant fungi including Pd. We sampled *Tadarida* from the Orient Mine in south-central Colorado in June and August of 2014. In this process, body surfaces of *Tadarida* were swabbed for fungal spores, and spores were cultured at 20 °C and 6 °C to determine viability. Our preliminary results indicate that at least 10 unique fungal species are transported on *Tadarida* capable of growing at 20 °C. We have also identified 2 fungal species cultured at 6 °C, which is considered to be the optimal temperature for Pd growth. These results demonstrate that *Tadarida* are competent transmission vectors of fungal spores including cold-tolerant spores similar to Pd. We will continue sampling in August to provide additional insight into whether *Tadarida* is a potential WNS vector.

**FRI-1095****DEVELOPING A NOVEL METHOD FOR GENERATING RECOMBINANT ADENOVIRUS**

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Genetic heart conditions, also known as cardiomyopathies, have been etiologically linked to mutations in sarcomeric proteins. There is a need to understand how these mutations affect functional aspects of the sarcomere and eventually lead to disease.  $\beta$ -myosin is an essential sarcomeric protein found in cardiac tissue, and 40% of heart disease-causing mutations occur in the  $\beta$ -myosin motor domain. The current system used to synthesize the  $\beta$ -myosin motor domain is long and cumbersome with a low yield. However, we have streamlined this process by exploiting site-specific recombinant processes to develop a faster and more efficient system for myosin production. By using FLP/FRT and multiple Cre/lox recombination mechanisms, a shuttle and recipient virus was engineered to produce high levels of adenovirus that synthesize the myosin motor protein much faster than the current system. We measured the efficiency of the recombination, using green fluorescent protein and luciferase reporters, by conducting transfection experiments and plaque assays. Our hope is that this process can also be used to synthesize other disease-related proteins so they may be studied more easily.

**FRI-1059****NOVEL BIOMARKERS FOR HIV-1 DISEASE PROGRESSION**

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Approximately forty million people worldwide live with the human immunodeficiency virus-1 (HIV-1), which can progress into HIV-1-associated neurocognitive disorder (HAND). Research suggests that pro-inflammatory proteins and other biomarkers may correlate with the level of neurological impairment in seropositive patients. The purpose of the study is to identify biomarkers that may correlate with neurocognitive decline in patients of varying gender, race, age, and disease progression. A study visit includes a review of HIV-1 relevant patient history, a socio-demographic survey, a neurocognitive assessment, and a donation of 30-40 milliliters (ml) of blood. Plasma samples isolated from patient blood were analyzed by ELISAs specific to human soluble CD40 ligand (sCD40L), interleukin (IL)-6, CCL2 or monocyte chemoattractant protein (MCP)-1, and tissue inhibitor of metalloproteinase (TIMP)-1. Biomarker levels were correlated to neurocognitive assessments, socio-demographic responses, and relevant measures of HIV-1 infection medical history. The inflammatory biomarkers CCL2 and TIMP-1 were elevated in the HIV-1 seropositive cohort as compared to non-infected controls. Further, as the neurocognitive abilities of the patient cohort declined, levels of CCL2, IL-6, and TIMP-1 were correspondingly elevated. While sCD40L demonstrated no significant correlations between infection status, longevity, or neurocognitive score, the inflammatory protein showed consistent, positive trends. Although patient T-cell counts did not correlate significantly with inflammatory biomarkers, trends were seen that may improve upon analyzing the entire

cohort. Our data shows that inflammatory biomarkers may play an important role in predicting HIV-1 disease progression through the comparison of plasma samples within the HIV-1 seropositive population.

#### **FRI-1078**

##### **ROLES OF *CCN1* AND *CCN2* IN REGULATING CHONDROCYTE PROLIFERATION AND APOPTOSIS DURING EMBRYONIC SKELETAL DEVELOPMENT**

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CCN proteins reside primarily in the extracellular matrix and serve regulatory rather than structural roles. They regulate various biological functions such as cell adhesion, migration, proliferation, senescence, apoptosis, and chondrogenesis. The absence of *CCN2* results in a range of skeletal defects; however, the role of *CCN1* has not been explored. We evaluated the roles of *CCN1* and *CCN2* during skeletal development and investigated their relationship in regulating the process of chondrogenic differentiation. Phenotypic and molecular changes that occur when either or both of these genes were knocked out in cartilage tissues were examined through histology and immunohistology. Proliferating and apoptotic cells were quantified to determine the role of *CCN1* and *CCN2* during skeletal development of the proximal tibia in the hind limbs. With *CCN1* and *CCN2* knocked out, skeletal dysmorphisms caused by impaired chondrocyte proliferation in the hypertrophic region of the growth plate was observed. *CCN1* and *CCN2* mutants displayed chondrodysplasia phenotypes, with *CCN2* playing a more dominant role in chondrogenesis than did *CCN1*. The double mutants exhibited an augmented effect on the proliferative defect seen in *CCN2* mutants, suggesting that *CCN1* and *CCN2* are involved in distinct pathways regulating chondrocyte proliferation. No additive effect of bone collar perichondrium chondrocyte apoptosis was seen in the double mutants compared to the individual mutants, which suggested that *CCN1* and *CCN2* had overlapping functions in endochondral bone formation. A better understanding of *CCN1*'s and *CCN2*'s functions in chondrocytes during development holds promise for preventive and therapeutic treatments of diseased conditions such as osteoarthritis.

#### **SAT-1065**

##### **DETERMINING METABOLIC ACTIVITY BY FLUORESCENCE-LIFETIME MEASUREMENTS USING FLOW CYTOMETRY**

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Measuring the dynamics of intracellular reduced nicotinamide adenine dinucleotide (NADH) is a novel way to determine the metabolic state of single cells. Previously, such measurements have been made using fluorescence microscopy in combination with fluorescence lifetime calculations of bound vs. unbound states. Intracellular NADH binds to various proteins, and the level of bound NADH can be altered by nutrient deprivation or exposure to toxins. The bound form of NADH has a shorter lifetime than the non-protein-bound NADH. Our work seeks to demonstrate that the dynamics of fluorescence lifetime for bound vs. unbound NADH can be

measured in a flow cytometry platform and be used as a parameter to metabolically map cells in a powerful, high-throughput screening assay. Additionally, we seek to demonstrate the ability to sort cells based on NADH fluorescence lifetime measurements. In this contribution, fluorescence lifetime changes of NADH in serum-starved or potassium cyanide (KCN) treated MCF-7 cells were measured and used as a parameter for cell sorting. Our results demonstrate a compelling change in the fluorescence intensity and a reduction in the fluorescence lifetime of NADH compared to untreated cells. Additionally, we demonstrate the ability to sort cells based on fluorescence lifetime changes of NADH. Our data demonstrate for the first time the ability to sort cells based on changes in fluorescence lifetime associated with the changes in cell metabolism. This technique could potentially be used as an initial diagnostic tool for certain disease states.

#### **SAT-1061**

##### **EXPRESSION OF SELF-REGULATED CHANNELRHODOPSIN BY TARGETING ENDOGENOUS PSD95**

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Channel rhodopsin is a light-activated calcium channel. When exposed to light, it triggers a current along a membrane. When expressed in neurons, channelrhodopsin can be used to trigger an action potential with light, allowing temporal control over activation of neuronal populations. The use of channelrhodopsins allows the opportunity to map the activity of neuron clusters, but this is hindered by the overexpression of the channelrhodopsins. We worked on creating a molecular construct that focuses on addressing these limitations. The construct localizes channelrhodopsin exclusively to excitatory synapses, thus allowing the initiation of channelrhodopsin propagated action potentials to occur at physiologically relevant sites. The channelrhodopsin construct contains 2 parts. The first is an intrabody against PSD95, a post-synaptic scaffold protein and excitatory synaptic marker bound directly to the channelrhodopsin. The purpose of fusing channelrhodopsin to the anti-PSD95 intrabody is to localize the channel specifically to the excitatory synapses in the dendrites of a neuron. The other part of the construct is a self-regulatory component that inhibits the expression of the entire construct when the binding of endogenous PSD95 by the intrabody is completely saturated; this occurs by the CCR5ZFL-KRAB domain binding to a CCR5ZFL binding site near the promoter of the plasmid, resulting in the recruitment of transcription. The targeted channelrhodopsin, excitatory-synapse-directed fibronectin intrabody, and the transcriptional control system were ideas proposed and developed in Don Arnold's lab, but this is one of the first attempts to fuse those concepts to limit the shortcomings of channelrhodopsins when used in neurons.

#### **SAT-1085**

##### **IN VITRO ANALYSIS OF EPICARDIAL CELL MINERALIZATION AND ITS IMPLICATIONS FOR CORONARY ARTERY CALCIFICATION**

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Coronary artery calcification is a disease affecting adult humans that involves the build-up of calcium deposits in coronary arteries affected by atherosclerosis. Over time, these deposits increase the risk of sudden heart attacks in adult humans. The epicardium is the non-

contractile, outer layer of the heart. Epicardial cells undergo the epithelial to mesenchymal transformation (EMT) to give rise to progenitor cells. Epicardium-derived cells are suspected to contribute to mineralization in the coronary vasculature. Previous studies have found that mineralization in vascular tissue is found to occur under 4 conditions: the secretion of extracellular matrix, the availability of an organic phosphate source, the presence of alkaline phosphatase to convert organic phosphate into inorganic phosphate, and the absence of inhibitors of mineralization. Our hypothesis is that mesenchymal cells derived from the epicardium have the ability to mineralize under these conditions. Our lab used stem cell lines generated from mouse embryonic ventricular epicardium called MEC1 to model epicardial cells. We found that epicardial cells mineralized *in vitro* in the presence of an organic phosphate source,  $\beta$ -glycerophosphate ( $\beta$ GP), and ascorbic acid. We also discovered that the secreted extracellular matrix from epicardial cells was necessary to support mineralization. Moreover, we found that live epicardial cells have the ability to incorporate organic phosphate into a secreted extracellular matrix and induce mineralization. Our findings will elucidate the biological basis of mineralization in epicardial cells and lead to better therapeutic methods to inhibit mineralization in adults with coronary artery calcification.

#### **FRI-1056**

#### **THE RED-, FAR RED- AND BLUE-LIGHT REGULATION OF THE PSBA RNA-BINDING PROTEIN GENES IN *CHLAMYDOMONAS REINHARDTII* SUGGESTS THE INVOLVEMENT OF A CRYPTOCHROME AND NOVEL PHYTOCHROME-LIKE PHOTORECEPTOR IN THE SIGNALING PATHWAYS**

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In the eukaryotic, unicellular, green alga *Chlamydomonas reinhardtii*, the photosynthetic D1 protein is translated from the chloroplast-encoded *psbA* mRNA. Translation of the mRNA is regulated by a set of nuclear-encoded RNA binding (RB) proteins (RB38, RB47, and RB60), which interact with a stem-loop structure in the 5'-untranslated region of the mRNA. Previous studies demonstrated that *rb38*, *rb60*, and *psbO* (encodes the photosystem II-associated oxygen evolving enhancer I protein) are induced by red light. To further characterize the light responses of these genes, dark grown *C. reinhardtii* cells were exposed to various combinations of light qualities and gene expression was measured by reverse transcription-polymerase chain reaction on the total extracted RNA. Preliminary data indicates that red and blue light induce the expression of the *rb38*, *rb60*, and *psbO* genes, and that far red light reverses the red light induction. These results suggest that a cryptochrome and yet to be identified phytochrome-like photoreceptor play a role in the signaling pathways of these genes. A bioinformatic analysis of the *rb60* promoter has revealed the presence of a g-box and GATA motif, two red light-responsive cis-elements that may play a role in the red-light induction of the *rb60* gene. To date, we have yet to identify prospective blue light cis-elements in the *rb60* promoter. Future studies aim to further describe the light responses of the *rb* genes and identify putative red and blue light cis-elements in each of the *rb* gene promoters.



**SAT-1081****GENETIC SCREEN FOR XENOBIOTIC DETOXIFICATION REGULATORY GENES IN *C. ELEGANS***

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Xenobiotics are chemical compounds produced by microorganisms (such as fungi and bacteria) that can attack essential cellular structures in hosts, such as in *C. elegans*. However, xenobiotic detoxification is conserved throughout many other higher eukaryotic organisms, including humans. When in contact with xenobiotics organisms activate detoxification responses to remove xenobiotics. However, little is known about how these detoxification responses are regulated. The proteasome is one such major cellular target of many xenobiotic-producing bacteria and fungi. Using an EMS genetic screen in *C. elegans*, we aim to discover new genes that are responsible for regulating the detoxification of xenobiotics that disrupt the proteasome. We are currently performing the EMS screen for new regulatory genes and will hopefully have a list of candidate genes in a few weeks from our screen. For future research, through the discovery of xenobiotic detoxification regulatory genes in other important cellular structures (such as the ribosome and the cytoskeleton) we will be able to see how xenobiotic detoxification is regulated in other core cellular structures. Learning more about the regulatory genes for xenobiotic detoxification may have future implications for designing better pharmaceuticals in response to negative detoxification responses (such as nausea and food suppression) that cancer patients face as a result of many current chemotherapeutic drugs. It is also possible that a misregulation in these regulatory genes may cause malaise in humans where no xenobiotics are present in the body.

**FRI-1064****INTRAUTERINE GROWTH RESTRICTION EFFECTS LUNG ESTRADIOL AND ER $\alpha$ ; OCCUPANCY OF THE PPAR $\gamma$ ; PROMOTER IN THE RAT**

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Intrauterine growth restriction (IUGR) refers to the failure to achieve normal growth *in utero*. IUGR increases morbidity and mortality from chronic lung disease and alters lung development, with males more severely affected than females. A key regulator of lung development is peroxisome proliferator-activated receptor gamma (PPAR $\gamma$ ). PPAR $\gamma$  expression is modulated by estrogen signaling. Estrogen binds to estrogen receptor alpha (ER $\alpha$ ), which causes translocation to the nucleus where ER $\alpha$  binds to an estrogen response element (ERE) on promoter 2 (P2) of PPAR $\gamma$ , inhibiting PPAR $\gamma$  expression. Our group previously showed that IUGR decreases PPAR $\gamma$  expression and increases circulating estradiol levels exclusively in male rats. We hypothesize that IUGR increases lung levels of estradiol, ER $\alpha$  and ER $\alpha$  occupancy of the PPAR $\gamma$  P2 in newborn male rat lung. IUGR was induced by bilateral uterine artery ligation on gestational day 19 in Sprague Dawley rats. Offspring were killed at birth and lung tissue samples were collected. ELISA, western blotting, and ChIP assay will be used to determine the lung estradiol levels, ER $\alpha$  protein abundance, and levels of ER associated with the PPAR $\gamma$  P2, respectively. We expect to see an increase of lung estradiol, ER $\alpha$  and ER $\alpha$  occupancy on PPAR $\gamma$  P2 in male, but not female

rat lung. We speculate that occupancy of the ER $\alpha$  on PPAR $\gamma$  P2 persistently inhibits transcription in male rats, while the PPAR $\gamma$  expression in female rats may result from a different mechanism.

#### **FRI-1087**

##### **CHARACTERIZING THE EFFECT OF NOVEL AGING GENES ON COMMON AGING PATHWAYS, REPRODUCTION, HEALTHSPAN, AND AGE-DEPENDENT NEURODEGENERATION IN *CAENORHABDITIS ELEGANS***

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Aging is characterized by the progressive degeneration of cellular components and deregulation of physiological processes resulting in mortality. Longevity is a complex genetic trait, influenced by numerous genetic loci acting in a variety of biological processes. Individual contributions from most genes to the overall aging process are relatively small and therefore challenging to pinpoint using classical forward genetic strategies. We have developed a multi-organism strategy to identify novel evolutionarily conserved genes involved in aging. Based on an initial list of candidate genes linked to mammalian aging through genome-wide association and age-associated gene expression studies, more than 50 novel genes have been identified for which reduced expression extends lifespan in the nematode *Caenorhabditis elegans*. The purpose of this study is to examine a range of worm reproductive and healthspan phenotypes in response to RNAi knockdown of 6 of these genes in order to define the range of age-associated processes and pathways each gene is capable of influencing. We will further assess the ability of each gene to alter activity through 2 commonly studied aging pathways: insulin signaling and target of rapamycin signaling. Three of our 6 genes have established links to neuronal function. We will therefore determine whether knock down of each gene is capable of delaying pathology in worm models of Alzheimer's and Huntington's disease. We anticipate that each gene will influence a distinct set of age-associated processes, suggesting classes of human disease that may benefit from interventions targeting each gene and informing targeted studies in mammalian systems.

#### **SAT-1056**

##### **DIRECT INTERACTION BETWEEN DISHEVELLED AND DISCS LARGE REGULATES SPINDLE ORIENTATION IN *DROSOPHILA* S2 CELLS**

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Asymmetric cell division, which generates cellular diversity, requires properly regulated cell polarity. Cell polarity is essential for proper development of adult tissues, and human diseases, like cancer, have been linked to defects in cell polarity. The mechanisms involved in cell polarity remain incompletely described. Two proteins that influence cell polarity in a range of cellular systems include dishevelled (Dsh) and discs large (Dlg), which are thought to induce cell polarity partly by regulating microtubule stability. Adenomatous polyposis coli (APC), a tumor suppressor protein, interacts with Dsh and Dlg enhancing microtubule stability. This suggests a

possible interaction between these three proteins. In our project, we have identified an interaction between the PDZ domain of dishevelled (Dsh<sup>PDZ</sup>) and an internal I3 region of the hook domain in discs large (Dlg<sup>Hook</sup>). By a series of truncations and point mutations to Dlg<sup>Hook</sup>, we were able to identify amino acid residues within the highly conserved I3 loop involved in binding. We hypothesize that the functional protein complex formed between Dsh-Dlg, accompanied by APC, is crucial for microtubule polarization. Lastly, we want to examine the function of the Dsh-Dlg complex in regulating spindle orientation in cultured *Drosophila* S2 cells. Overall, we want to see the function that is associated with this complex.

#### **SAT-1095**

##### **CELL MIGRATION INHIBITION INDUCED BY R-MOJ-DM**

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Disintegrins are non-enzymatic, small molecular weight peptides, which have the ability to bind to integrins. Integrins are transmembrane receptors composed of  $\alpha$  and  $\beta$  subunits that activate downstream signal transduction pathways. Previous studies have demonstrated that the recombinant disintegrin r-Moj-DM peptide inhibits migration of SK-Mel-28 cells, a cell line expressing  $\alpha v \beta 3$  integrins. Furthermore, SK-Mel-28 cells with a stable v knockdown failed to migrate. We hypothesized that r-Moj-DM peptide will inhibit migration of cell lines expressing the v3 integrin receptor (SK-Mel-2, HT-1080, BT-20). A wound-healing assay was performed to test for cell migration. Our hypothesis was not supported since preliminary results indicate that r-Moj-DM failed to inhibit the cell migration of HT-1080, a cell line that expresses  $\alpha v \beta 3$  integrin. We will be testing cell migration of SK-Mel-2, and BT20 next. Integrins activate migration through Rac-1, a G protein that induces the formation of lamellapodia and filopodia, which are necessary for cell spreading. RT-qPCR results indicate that Rac-1 expression is slightly downregulated after 6 hour of r-Moj-DM treatment of SK-Mel-28 cells. We will examine Rac-1 activity after r-Moj-DM treatment, using a pull-down approach in order to begin examining the signal transduction pathway initiated by r-Moj-DM treatment.

(This research was supported by National Science Foundation NSF-REU Grant# DBI 1004350.)

#### **FRI-1081**

##### **ANALYZING MITOCHONDRIAL AGE AND MOTILITY IN *DROSOPHILA* MOTOR NEURONS USING EOS2 AND MITO-TIMER PROTEIN**

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The vast size and asymmetry of neurons has raised questions about how their energy requirements are met by the ATP-producing mitochondria. The majority of mitochondria proteins are encoded by the genomic DNA, synthesized on cytoplasmic ribosomes, and later imported into mitochondria. The classical mitochondria biogenesis hypothesis proposes that new mitochondria are made in the neuron cell body and must be transported great distances to reach energy requiring destinations in the axon. We will use 2 different approaches to test the classical hypothesis. First, we will use mitochondria-targeted photoconvertible fluorescent

protein Eos2 that can be permanently converted with a 405 nm laser from green to red, which will help us uniquely mark and trace small groups of mitochondria in axons over prolonged time periods. Second, we will use a different fluorescent protein that spontaneously refolds and changes its emission spectrum from green to red over an ~12 h period and can serve as a mitochondrial fluorescent "timer" that allows us to distinguish the age of mitochondria. Both of these fluorescent proteins will be expressed in motor neurons and will be imaged in real time, using live *Drosophila*, to give us a better understanding of the behavior of mitochondria. Based on the classical hypothesis we predict that the converted mitochondria will move anterograde the closer they are to the cell body and retrograde/stationary further away. Alternatively, the timer mitochondria are red the older and further they are from the cell body, and green the younger and closer they are to the cell body.

### **FRI-1093**

#### **TRANSPOSABLE ELEMENT REPLICATION: STRUCTURE AND FUNCTION OF R2 RETROTRANSPOSON ENCODED DNA ENDONUCLEASE**

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Transposable elements (TEs) are genomic parasites with the ability to replicate within the host genome. Non-long terminal repeat retrotransposon (NLR), a major class of TEs, contribute to genome dynamics and content of many organisms (e.g., 33% of the human genome). NLRs transcribe an element RNA to cDNA directly at the site of insertion using an exposed free chromosomal 3'-OH, generated by an element encoded endonuclease. There are 2 major types of NLRs: those that encode an apurinic-apyrimidinic endonuclease (APE), and those that encode a novel endonuclease with putative structural homology to type IIs restriction-like endonuclease (RLE) and holliday junction resolvase. Little is known about the structure and function of the RLE or of its component amino acid motifs. Elements encoding an RLE are site specific, which facilitates biochemical dissection of NLR replication. R2 retrotransposons encode an RLE and target a specific sequence within the 28S rDNA. It is hypothesized that structure-function relationships of the RLE binding to and cleaving target DNA can be elucidated by mutating select conserved amino acid motifs within the RLE and assaying for DNA binding and cleavage activity. Site-directed mutagenesis was used to generate mutant R2 proteins. The mutants were expressed in *Escherichia coli*, affinity purified, and tested for loss of function in *in vitro* nucleic acid binding and cleavage reactions. Nucleic acid binding was assayed by electrophoretic mobility shift assays, and DNA cleavage by denaturing gel electrophoresis. The mutants facilitated defining of the endonuclease domain and generated a bioinformatic/biochemical structural model of the endonuclease.

**FRI-1072****EXPOSURE TO A CANNABINOID RECEPTOR 1 AGONIST DURING EARLY ADOLESCENCE IMPAIRS THE MATURATION OF GABAERGIC TRANSMISSION IN THE ADULT PREFRONTAL CORTEX**

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Converging epidemiological studies indicate that cannabis abuse during adolescence increases the risk of developing psychosis and prefrontal cortex (PFC)-dependent cognitive impairments later in life. However, the mechanisms underlying the adolescent susceptibility to chronic cannabis exposure are poorly understood. Given that the psychoactive constituent of cannabis binds to the cannabinoid receptor 1 (CB1), the present study was designed to determine the impact of a CB1 receptor agonist (WIN) during specific windows of adolescence on the functional maturation of the rat PFC. By means of local field potential recordings and ventral hippocampal stimulation *in vivo*, we found that a history of WIN exposure during early (postnatal days - P35-40) or mid-(P40-45) adolescence, but not in late adolescence (P50-55) or adulthood (P75-80), is sufficient to yield a state of frequency-dependent prefrontal disinhibition in adulthood comparable to that seen in the juvenile PFC. Remarkably, this prefrontal disinhibition could be normalized following a single acute local infusion of the GABA-A $\alpha$ 1 positive allosteric modulator indiplon, suggesting that adolescent exposure to WIN causes a functional downregulation of GABAergic transmission in the PFC. Accordingly, *in vitro* recordings from adult rats exposed to WIN during adolescence demonstrate that local prefrontal GABAergic transmission onto layer V pyramidal neurons is markedly reduced to the level seen in the P30-35 PFC. Together, these results indicate that early and mid-adolescence constitute a critical period during which repeated CB1 receptor stimulation is sufficient to elicit an enduring state of PFC network disinhibition resulting from a developmental impairment of local prefrontal GABAergic transmission.

**FRI-1068****THE ROLE OF MTORC1 SIGNALING IN SPERMATOGONIAL STEM CELL FATE**

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Continual sperm production in mammals is dependent on spermatogonial stem cells (SSCs). SSCs are unipotent stem cells with the ability to either undergo self-renewal or differentiate into all of the germ cells in the spermatogenic lineage, and eventually, sperm. Balanced self-renewal and differentiation of SSCs are essential for male fertility. Mammalian target of rapamycin complex 1 (mTORC1) is a multi-subunit protein complex that directs a cell's proliferation, growth, and protein synthesis. Recent evidence suggests that mTORC1 activity influences SSC differentiation. To confirm the role of mTORC1 in SSC fate, we are performing RNA interference (RNAi)-mediated gene knockdown of raptor, the component of mTORC1 that dictates substrate specificity, in cultured SSCs. This approach facilitates interrogation of mTORC1 without impacting the mTORC2 complex. Our hypothesis is that the decreased expression of raptor will result in less SSC differentiation. Raptor protein translation in mouse SSCs will be inhibited using RNAi through a short hairpin RNA (shRNA) delivered by lentiviral

vector. Currently, we are optimizing raptor knockdown using a co-transfection of a mouse raptor plasmid and our lentiviral shRNA plasmids. Ultimately, transient inhibition of mTORC1 signaling in SSCs *in vitro* using the shRNA lentiviruses will be followed by a biological assay for SSCs by transplantation. These studies will help determine whether mTORC1 is involved in control of SSC fate which has implications for understanding the molecular mechanisms controlling spermatogenesis.

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#### **FRI-1057**

##### **SUB-CELLULAR LOCALIZATION OF LORELEI PROTEIN IN *ARABIDOPSIS THALIANA* REPRODUCTION**

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In angiosperm reproduction, the pollen grain forms a pollen tube and extends through the transmitting tract to reach the female gametophyte where it releases two sperm cells; one fuses with the egg cell giving rise to the embryo, and the other fuses with the central cell giving rise to the endosperm. This completes double fertilization and marks the initiation of seed development. In *Arabidopsis thaliana* LORELEI (LRE) mutant, most female gametophytes fail to induce pollen growth arrest and remain unfertilized. LORELEI encodes a putative glycosylphosphatidylinositol (GPI)-anchored membrane protein and is hypothesized to localize in the plasma membrane of synergid cells of the female gametophyte. This class of protein is secreted into the endoplasmic reticulum (ER), where the GPI anchor is attached to the protein, and ultimately localizes to the plasma membrane. We showed that a wild-type LRE fused to YFP reporter gene (*LRE-cYFP*) is functional and localizes to the membrane-rich filiform apparatus (FA) of the synergid cells. We used this construct to investigate if predicted secretion signal, GPI attachment signal, and  $\omega$ -sites are required for localization in the FA of the synergid cells by deleting the conserved domains, transforming them into *lre/lre* null mutant, and determining subcellular localization of mutant proteins using confocal microscopy. Loss of signal sequence (*LRE<sub>(ΔSS)</sub>-cYFP*) resulted in no *cYFP* expression, indicating that secretion into ER is critical for *LRE* expression. Loss of GPI attachment signal and  $\omega$ -sites affected the localization of *LRE* in the FA, pointing the role of GPI anchor in subcellular localization of *LRE*.

#### **FRI-1098**

##### **DIVERSITY IN PLANARIAN STEM CELLS**

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Asexual planarians use binary fission as their primary means of reproduction resulting in clonal offspring. The lack of sexual reproduction raises questions of how these animals can achieve the phenotypic diversity necessary for species survival. Prior data from a large-scale, long-term experiment involving thousands of asexually reproducing specimens have revealed that these supposedly clonal planarians exhibit diverse reproduction and growth patterns, suggesting

some level of diversity within asexual offspring. Planarian asexual reproduction via binary fission is enabled by a population of stem cells called neoblasts. These cells are the only dividing cells in the animal and allow it to regenerate all missing body structures after fission within a week. While neoblasts were originally thought to be a homogenous cell population, recent studies suggest gene expression diversity among these cells. In our project, we are investigating whether this neoblast diversity could explain the observed population diversity. Using X-ray irradiation, we can remove all stem cells from an animal. Without stem cells, this animal would die within about a month because it cannot replace aging tissues; however, single cell injections using clonogenic neoblasts can rescue deadly irradiated animals and give rise to animals originating from a single stem cell. We will study whether worm families originating from these so-generated animals are exhibiting similar reproduction and growth pattern variability as observed in our other specimen.

#### **FRI-1097**

##### **HEDGEHOG SIGNALING IN POSTNATAL MOUSE NEURAL RETINA DEVELOPMENT**

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The vertebrate retina consists of seven specific neuronal cell types that are responsible for sensing and processing visual information. Elucidating the mechanisms underlying retinal development will provide insights into retinal degenerative disease processes and treatments. Previous studies have shown that Hedgehog (Hh) signaling profoundly influences progenitor cell proliferation and cell fate decision in the embryonic mouse retina. However, its role in postnatal stages remains uncharacterized. To study the requirement of Hh signaling in postnatal mouse retina, the cellular response to Hh signals was eliminated by conditionally ablating the *Smoothed* (*Smo*) gene, a critical component of the Hh signaling pathway, with the Cre-lox recombinase system. *Smo* was deleted in retinal progenitor cells at embryonic day 11.5, and retinas were analyzed at early postnatal stages and at maturation. At postnatal day 0 (P0), the mutant retina revealed an overproduction of retinal ganglion cells at the expense of progenitor cells. Surprisingly, mutant retina displayed phenotypes that were largely similar to wild-type retinas at P30. Here, we provide evidence suggesting that the *Smo*-deficient retina auto-corrected its excess of retinal ganglion cells and compensated for the reduced progenitor cells during early postnatal development. The adaptive changes observed in postnatal mouse retina offer broad implications for retinal plasticity and the capability in coordinating a balanced production of neuronal cell types.

#### **SAT-1090**

##### **MEASUREMENT OF CD8+ T CELL MEDIATED KILLING USING GAG CLONES FROM HIV-POSITIVE ELITE SUPPRESSORS**

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Elite suppressors (ES), also known as elite controllers, are HIV-1 positive individuals who maintain levels of viremia below the level of detection (< 50 copies of HIV-1 RNA/ml blood)

without clinical intervention. The cytotoxic T lymphocyte (CTL) response aids in the control of viremia in ES despite the ongoing replication and evolution of the virus. Recently our lab has shown that CD8+ T cells from ES have the ability to suppress viral replication even in the presence of escape mutations in Gag epitopes, and PBMC stimulation with gag peptides containing the escape mutations results in robust IFN- $\gamma$  and perforin expression. While previous work tested CTL response against Gag escape mutants that were generated by site-directed mutagenesis, our study is novel as it measures viral suppression using Gag clones amplified from replication-competent virus cultured from ES. In this study, pseudotyped virus containing the patients' gag clones were used to infect autologous CD4+ T cells to measure the inhibitory potential of ES CD8+ T cells. Through this data, we hope to better understand how CTL-mediated elite suppression is maintained in the presence of virologic escape. Understanding this mechanism of control will aid in the eventual development of a therapeutic HIV-1 vaccine.

#### **FRI-1089**

##### **AN APPROACH TO PREPARE 1-(10-AMINODECYL)-3-(BENZYLOXY)PYRIDIN-2(1H)-ONE**

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Chelators carrying the 3-hydroxypyridin-2-one (3,2-HOPO) ligand are of interest because of their ability to form strong complexes with hard metal ions such as iron. As part of a program for the synthesis of 3,2-HOPO chelators for potential therapeutic and diagnostic applications, a route to 1-(10-aminodecyl)-3-(benzyloxy)pyridin-2(1H)-one was required. The goal was to develop an approach that was both convenient and high yielding. Here we report an approach that uses a HOPO-tethered bromide as a key intermediate. Both the strategy and efforts to improve the efficiency of the route will be presented.

#### **SAT-1100**

##### **HOW THE ACCUMULATION OF PHOSPHATIDYLINOSITOL 4-PHOSPHATE IN THE YEAST *SACCHAROMYCES CEREVISIAE* AFFECTS CELL SIZE**

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The phosphoinositides (PIPs) are membrane-bound lipids that function as structural components of membranes as well as regulators of many cellular processes in eukaryotes, including vesicle-mediated membrane trafficking and actin cytoskeleton organization. In *Saccharomyces cerevisiae*, there are several proteins that play a role in the regulation of the levels of the different phosphoinositides through phosphorylation and dephosphorylation. The *Sac1* gene encodes for a phosphatase that is responsible for the dephosphorylation of the PI(4)P lipid to form PI, and the *Mss4* gene encodes for a kinase that phosphorylates PI(4)P to form PI(4,5)P<sub>2</sub>. It has been previously shown that PIPs affect cell size. The main goal of this project is to analyze how the lack of function of *Sac1* and/or *Mss4* affects cell size and if this is related to the accumulation of the PI(4)P lipid. A *Sac1* deletion in *S. cerevisiae* will be created by PCR mutagenesis. Four different strains of yeast will be analyzed: wild type, *Mss4-ts* (temperature sensitive), *Sac1* deletion, and *Sac1* deletion combined with *Mss4-ts*. These



experiments will test the hypothesis that accumulation of PI(4)P by either deletion of *Sac1*, mutation of *Mss4*, or both will make the cell smaller.

#### **SAT-1070**

##### **THE USE OF EPITHELIAL-TO-MESENCHYMAL TRANSITION SENSORS TO DETECT CANCER STEM CELLS**

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Metastasis is one of the deadliest and most difficult to treat aspects of cancer accounting for 90% of deaths. Metastatic carcinoma cells are proposed to have undergone an epithelial-to-mesenchymal transition (EMT). During EMT, epithelial cells lose their cell-to-cell adhesion capacity. Cells that have undergone EMT are also resistant to chemotherapy, and recent studies have found strong evidence that EMT equips carcinoma cells with properties similar to those of stem cells, thus leading them to behave as cancer stem cells (CSC). CSCs have been proposed to be the cells of metastatic origin and therapeutic resistance, suggesting a link between EMT and CSCs. Targeting EMT/CSCs could be of great clinical utility. The process of EMT is heavily governed by micro-RNAs (miRNA). These noncoding RNAs inhibit the production of proteins regulating many cellular processes. We have developed lentiviral-based fluorescent sensors of EMT to detect the induction/reversal of EMT. In this study, miR-200c, a member of the miR-200 miRNA family and potent inhibitor of EMT, was expressed using a tetracycline-inducible system to test our sensors and revert EMT in the human and mouse mesenchymal-like breast cancer cell lines MDA-MB-231 and T11, respectively. A series of doxycycline treatments at increasing concentrations was used to express miR-200c at different levels. Subsequently, different EMT reporters will be used to assess which best detects EMT reversion. Validation of these sensors will allow us to proceed to *in vivo* mouse models of breast tumorigenesis to detect and isolate EMT/CSCs.

(Supported by CPRIT grant RP130485.)

#### **SAT-1076**

##### **SPECTROSCOPIC INVESTIGATIONS OF TRANSITION METAL IONS IN REVERSE MICELLES**

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Although it is known that metal ions bind to membrane surfaces in biological systems, how this interaction affects the chemistry of the metal ions themselves is still not well understood. We have used well defined surfactant/water/oil microemulsions, known as reverse micelles (RMs), as a model for membrane surface studies. Our hypothesis is that the positively charged metal ions will associate differently with RMs that possess different charges (-, +, and neutral). We have examined pentaammine(N-heterocycle)ruthenium(II) complexes that have intense charge transfer bands in the visible region using a diode array spectrophotometer. The length and hydrophobicity of the N-heterocyclic ligand was varied, and spectra were recorded at different sized RMs. The observed changes in the spectra indicate different interaction which we have ascribed to potential insertion into the membrane (RM) interface.

**SAT-1051****INTERACTIONS BETWEEN A549 LUNG EPITHELIAL CELLS AND PNEUMOCOCCUS UNDER STRESSED CONDITIONS**

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*Streptococcus pneumonia* (the pneumococcus) is one of the primary causes of bacterial pneumonia. This is easily achieved through the bacteria's ability to easily access its host and adhere efficiently to epithelial cells followed by subsequent invasion. Systemic release of norepinephrine (NE) is a component of the acute host response to infection and studies in the area of microbial endocrinology indicate that NE increases bacterial growth rate and promotes invasive disease. Contrary to most bacterial responses to NE, pneumococcus demonstrates decreased invasion *in vitro* and dissemination *in vivo*. The  $\alpha$ -enolases have been implicated in pneumococcal dissemination. Pneumococcus takes advantage of  $\alpha$ -enolase localizing to the cell surface for capturing plasmin(ogen) and using its proteolytic activity to invade host lung epithelial tissue. We propose that NE mediates pneumococcal production and localization of  $\alpha$ -enolase thereby attenuating pathogenesis. In this study,  $\alpha$ -enolase activity of viable pneumococci are assessed using a coupled assay that measures the transformation of NADH·H<sup>+</sup> to NAD<sup>+</sup> and a direct assay at A<sub>240</sub>. Further, we used proteomic analysis through 2D and 1D gel electrophoresis along with antibodies raised toward Eno protein. Lastly, *in vitro* invasion assays with A549 lung epithelial cells and plasmin inhibitors with and without NE treatment are performed. Currently, 2D gel assessment suggest that NE decreases pneumococcal production of the Eno protein. Further, assessment of invasion assays will provide evidence toward acceptance or rejection of are proposed hypothesis. We conclude that pneumococcal Eno is regulated by NE.

**SAT-1059****PEROXYNITRITE-GENERATING PLATFORM**

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Peroxynitrite (PN) is a reactive nitrating and oxidative species that plays a key role in inflammation-mediated disease states, from neurodegenerative disorders to diabetes. PN is formed in the radical terminating reaction between nitric oxide (NO) and superoxide. It has been difficult to observe PN directly within cells due to its transient nature. With a photo-controlled peroxynitrite-generating platform, the Mascharak lab has developed a system that is able to release PN *in situ*, to better understand the dynamic chemistry of PN. Stable metal nitrosyl, [Mn(PaPy<sub>3</sub>)(NO)]ClO<sub>4</sub> (PaPy<sub>3</sub> = *N,N*-bis-(2-pyridylmethyl)amine-*N*-ethyl-2-pyridine-2-carboxamide), was used as the source of NO because it rapidly releases NO on illumination with visible light. To match the rapid release of NO from the nitrosyl, the xanthine oxidase/hypoxanthine (XO/HX) system was employed as the source of superoxide. Both sources were encapsulated in a sol-gel matrix to avoid contamination. A multi-well plate was used to study the chemistry of the precursors as well as PN. Construction of the PN-generating platform was completed by layering both NO and XO sol-gels at the bottom of individual wells. Release

of the precursor molecules is triggered with exposure to low powered visible light and the addition of HX. This light-activated platform allows the study of PN-mediated chemistry under varied flux ratios and pH conditions. We plan to use the multi-well platform to study the reactions of PN with various biomolecules such as amino acids, peptides, and lipids.

#### **FRI-1076**

##### **THE ROLE OF MINUS-END MOTOR PROTEINS, DYNEIN AND KINESIN-14 IN MITOTIC ENDOPLASMIC RETICULUM REORGANIZATION DURING MITOSIS**

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Mitosis is the process of cell division, which results in the production of 2 identical daughter cells with equal partitioning of chromosomes. However, there is limited information regarding the spatial rearrangement of organelles during mitosis. In our study, we focused on the movement of the endoplasmic reticulum (ER) organelle during mitosis. This organelle is responsible for various functions, including the post translational modifications of proteins, calcium ion regulation, and lipid synthesis. During mitosis, the ER experiences a dramatic rearrangement along the mitotic spindle and accumulates at the poles. It has been well established that the ER interacts with the microtubule network for its organization during interphase; however, the role of the microtubule network and associated proteins during mitosis is unknown. The microtubule motor proteins of interest in our study were dynein and kinesin-14, which facilitate the transport of cargo and organelles in the direction of the spindle poles during mitosis. We suggest that an active mechanism exists between these minus end motor proteins and microtubules, with respect to ER spatial rearrangement during mitosis. The goal of our research is to analyze how microtubules and these minus end motor proteins interact with the ER during mitosis. We will examine early embryos of *Drosophila melanogaster* in which expression of dynein and kinesin-14 are knocked down via dsRNA injection and genetic crosses. Using time-lapse microscopy we will analyze the movement of the ER during mitosis. We hypothesize that knock down of dynein and kinesin-14 will have a significant effect on ER re-location during mitosis.

#### **FRI-1099**

##### **UNDERSTANDING THE GLUCOSE TRANSPORTER AND PANCREATIC BETA CELL GLYCOSYLATION DURING STARVATION**

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As type 2 diabetes plagues our society, a better molecular understanding is required. A previous study has shown that a high-fat diet correlates with the reduction in the glucose transporter 2 (Glut2) on the surface of pancreatic *beta* cells diminishing the glucose-stimulated insulin secretion. This was due to a decrease of GnT-4a glycosyltransferase expression and thus N-linked glycosylation of Glut2 within the pancreatic *beta* cells. Starvation alters metabolic mechanisms, including the reduction of insulin and the ability of certain tissues to take in glucose in order to maintain stable glucose levels within the blood. By subjecting wild-type mice

to 72 h of starvation, we want to observe whether similar molecular events observed in the high fatty acid diet resurface. Collected data show there is a reduction in GnT-4a glycosyltransferase critical for the stability of Glut2 in the pancreatic *beta* cell membrane. However, further analysis of controls and additional trials still remain. Methods include histology to visually observe Glut2, and flow cytometry and ELISAs to quantify the Glut2 in 24 h intervals along with qPCR to quantify the expression of the GnT-4a glycosyltransferase gene. We expect data to show that there are similarities to the results from a high fatty acid diet, which include the decrease of GnT-4a glycosyltransferase leading to the reduction of Glut2 in the pancreatic beta cell membrane. This contributes to our hypothesis that this pathogenic mechanism is based on an advantageous response for energy conservation to prolong functional blood glucose levels during starvation.

#### **FRI-1054**

##### **EFFECTS OF THERMAL PROCESSING ON THE ANTIOXIDANT CAPACITY IN NUTS AND SEEDS**

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Epidemiological studies have suggested a positive association between the consumption of foods with antioxidant properties and their possible role in preventing chronic degenerative diseases. With antioxidants becoming more and more common within the food industry, this study evaluates how much antioxidant levels increase in nuts and seeds when they are processed with heat. The hypothesis for this experiment was that a nut in a raw natural state will have a higher antioxidant capacity compared to its roasted state. The TEAC (Trolox equivalent antioxidant capacity) method was incorporated to evaluate the antioxidant capacity of 5 different nuts and seed samples: pecan, walnut, sunflower seed, almond, and cashew. The TEAC method assesses the ability to scavenge stable radical cation, ABTS<sup>+</sup>, by comparing an ABTS and antioxidant nut solution against our Trolox standard, a water-soluble vitamin E analogue. Antioxidants in the nut milk sample, created by blending soaked nuts and seeds in water, were extracted using methanol as a solvent. The absorbance of the extract was then measured using a spectrophotometer set at a wavelength of 734 nm. The results were compared to a calibration curve that was constructed using Trolox as a standard. The percent change of antioxidant capacity was calculated from a raw state to a roasted state (230 °C at 15 min). The results indicated the following percent increase in antioxidant level: pecan-281.4%, almond-186.1%, cashew-159.6%, walnut-156.8%, and sunflower seed-118.7%. This study indicates that roasting nuts and seeds increases their antioxidant capacity.

#### **SAT-1074**

##### **DETERMINING IF TXNIP AND $\beta$ 1 INTEGRIN ARE INVOLVED IN THE APOPTOTIC PATHWAY INDUCED BY R-MOJ-DM PEPTIDE**

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Disintegrins are low molecular weight peptides that bind to integrins. Integrins are transmembrane receptors that are responsible for extracellular matrix interactions. The

recombinant disintegrin r-Moj-DM induces apoptosis of 27% of treated SK-Mel 28 cells. r-Moj-DM does not induce apoptosis by binding to the  $\alpha\beta 3$  integrin receptor. SK-Mel-28 cells with a stable  $\alpha v$  knockdown were not induced to initiate apoptosis after r-Moj-DM treatment. Several  $\beta 1$  integrin heterodimers are present on SK-Mel-28. We hypothesize that r-Moj-DM binds to a  $\beta 1$  integrin to activate apoptotic activity of SK-Mel-28. We predict that r-Moj-DM treatment will not induce apoptosis when  $\beta 1$  is knocked down. RNA sequencing of r-Moj-DM treated SK-Mel-28 indicated that *TXNIP* is upregulated 28 times. *TXNIP* is downstream to the  $\beta 1$  receptor. Therefore, we also knocked down *TXNIP* to determine if this factor is involved in the r-Moj-DM apoptotic-inducing pathway. We will use cell viability assays and confocal microscopy to determine if  $\beta 1$  and *TXNIP* are involved in the apoptotic pathway induced by r-Moj-DM. We predict that  $\beta 1$  knocked down cells will have no integrin clustering or apoptotic activity after treatment with r-Moj-DM peptide. We also predict that *TXNIP* knocked-down cells will have integrin clustering and no apoptotic activity after treatment with r-Moj-DM. (This research was supported by National Science Foundation NSF-REU Grant# DBI 1004350.)

#### **FRI-1049**

#### **IDENTIFYING NOVEL PROTEIN INTERACTORS FOR SGTA IN THE ANDROGEN RECEPTOR SIGNALING PATHWAY**

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Molecular chaperones facilitate proper folding and regulation of steroid hormone receptors (SHRs). Upon proper folding, SHRs bind ligand with high affinity, translocate to the nucleus, and initiate gene expression. A novel cochaperone, human small glutamine rich TPR (tetratricopeptide repeat) containing protein *alpha* (SGTA), is a downregulator of androgen (AR), glucocorticoid (GR), and progesterone (PR) receptors. It binds to heat shock protein (Hsp) 70 and 90 kDa. Additionally, SGTA plays a role in cellular processes such as cell cycle progression and apoptosis. Therefore, a top-down proteomic approach was used to determine novel interactors in LNCaP human prostate cancer cells. Recombinant FLAG-tagged SGTA was purified using a FLAG peptide and further analyzed for unknown interacting proteins with liquid chromatography mass spectrometry (LC-MS/MS). A comparison of normal (150 mM) versus high (300 mM) salt concentration was used to determine strong interactors. Preliminary studies have identified RanBP2 E3 SUMO-Ligase and microtubule to be present along with SGTA in both concentrations. Thus, future studies aim to validate these interactions with SGTA using nickel purification and assess their functional relevance, which will contribute to the understanding of the role SGTA plays within the chaperoning pathway.

**FRI-1096****INHIBITION OF THE MITOGEN ACTIVATING PATHWAY KINASE REDUCES CELL GROWTH IN ZEBRAFISH: AN ATTRACTIVE THERAPEUTIC TARGET FOR HYPERTROPHIC CARDIOMYOPATHY**

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Hypertrophic cardiomyopathy (HCM) is a genetic disorder characterized by excessive growth of myocardium, leading to an increased risk of arrhythmias and sudden cardiac death. The mitogen activated protein kinase (MAPK) plays an important role in regulating cardiomyocyte growth and differentiation. Inhibiting MEK, a key kinase in the MAPK, could attenuate abnormal cellular growth in HCM. Eight MEK inhibitors (ranging from 10  $\mu$ M-10 pM) were screened in zebrafish embryos at 2, 24 and 48 h post-fertilization (hpf) and assessed at 12, 24 and 48 h following drug administration. PD0325901 or ARRY424704 (10  $\mu$ M) administered at 2 hpf were toxic to all embryos, whereas at 1  $\mu$ M all embryos survived until 48 hpf displaying body axis defects and pericardial edema. Both drugs (10  $\mu$ M) when administered at 48 hpf lead to moderate cardiac edema in all embryos when assessed at 96 hpf. Cardiac contractility was assessed at 48 hpf following 2 h drug addition or at 96 hpf following administration at 48 hpf. The cardiac output, stroke volume, and heart rate did not differ significantly between the experimental and control groups in the former, but in the latter there was evidence of significant effects on myocardial function. Down regulation of cell growth by MEK inhibitors could attenuate adverse growth of myocardium in HCM, but will require careful personalization to achieve optimal results.

**FRI-1083****COMPARISON OF ZINC FINGER NUCLEASES, TALE NUCLEASES, AND CRISPR/CAS9 NUCLEASE SYSTEM TO CORRECT THE SICKLE MUTATION**

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Sickle cell disease (SCD) is the result of a substitution of the amino acid valine for glutamic acid in the beta-subunit of hemoglobin due to a point mutation in the *beta*-globin gene. The mutation leads to changes in the protein properties of hemoglobin which results in the formation of sickle-shaped red blood cells under low oxygen conditions. Site-specific genome editing technology can correct the sickle mutation of the *beta*-globin gene in hematopoietic stem cells to produce red blood cells that permanently make normal adult hemoglobin. Zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9 nuclease system can target and correct the sickle mutation when delivered alongside a corrective donor template. K562 cells were electroporated with ZFN, TALEN and CRISPR/Cas9 plasmids with a corrected wild-type donor designed to bind near the sickle mutation in *beta*-globin. Using the surveyor nuclease assay, cleavage rates were quantified and compared between the ZFNs, TALENs and CRISPR/Cas9. Nuclease off-target activity at other globin genes was also evaluated for each technology. Restriction fragment length polymorphism (RFLP) analysis using quantitative PCR

was used to quantify site-specific gene modification at *beta*-globin. The preliminary results suggest that the CRISPR/Cas9 nuclease system has higher on target cleavage and gene modification at the beta-globin gene as well as lowest off-target globin cleavage in comparison to ZFNs and TALENs. Further research must be conducted to confirm these results and determine the most suitable targeted nuclease to pursue for gene therapy for sickle cell disease.

#### **FRI-1055**

##### **ACID SENSING ION CHANNELS CONTRIBUTE TO HYPOXIA-INDUCED MIGRATION IN HUMAN PULMONARY ARTERIAL SMOOTH MUSCLE CELLS**

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Our laboratory has recently shown that acid sensing ion channel 1 (ASIC1) contributes to the arterial remodeling associated with chronic hypoxia-induced pulmonary hypertension. This is consistent with the reported involvement of ASIC in migration, proliferation, and apoptosis in a variety of cells types. However, the contribution of ASIC to hypoxia-induced migration, proliferation, and apoptosis has not been examined. Therefore, we hypothesize that ASIC1 and ASIC3 contribute to hypoxia-induced migration in human pulmonary arterial smooth muscle cells (hPASMC). To test this hypothesis, hPASMC were grown to confluence and placed into basal media 24 h prior to executing an *in vitro* scratch assay. Following the scratch, hPASMC were treated with the non-selective ASIC inhibitor amiloride, the specific ASIC1 inhibitor psalmotoxin 1, the specific ASIC3 inhibitor APETx2, or vehicle and were then exposed to normoxia (21% oxygen, 5% CO<sub>2</sub>) or hypoxia (2% oxygen, 5% CO<sub>2</sub>) for 12 h. Inhibition of ASIC1 and ASIC3 did not alter migration of hPASMC exposed to normoxia, but prevented the hypoxia-induced migration. This data demonstrates that ASIC1 and ASIC3 contribute to hypoxia-induced migration in hPASMCs and describes a potential mechanism in which ASIC contributes to pulmonary arterial remodeling. We will further examine the specific role of ASIC1 and ASIC3 in hypoxia-induced proliferation and apoptosis.

#### **FRI-1080**

##### **AN INVESTIGATION INTO THE FUNCTIONAL ROLE(S) OF THE LNC-RNA XIST REPEAT DOMAINS DURING INITIATION OF X-CHROMOSOME INACTIVATION**

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One function of the rapidly growing class of non-coding RNAs (lncRNAs) is to effect changes in chromatin state. However, the mechanism by which these lncRNAs exert their function remains unclear. Here we use X-chromosome inactivation (XCI) in mouse embryonic stem cells (ESCs) to study how the lncRNA X-inactive specific transcript (Xist) regulates chromosome-wide gene silencing. In mammalian female cells, one of the two X-chromosomes (Xi) is transcriptionally silenced during development to compensate for the dosage imbalance of X-linked genes between XY-males and XX-females. The crucial RNA molecule required for initiation of XCI is Xist. On differentiation of female ESCs, Xist is rapidly upregulated and coats the Xi in cis, leading

to a transcriptionally silenced state of the chromosome that is maintained throughout all subsequent somatic cell divisions. Recent work has revealed that during the initiation of XCI, Xist exploits the three-dimensional architecture of the chromosome to spread in a sequence-independent manner across the X chromosome. This finding has prompted us to define the function of 6 repeat-regions of Xist in mediating Xist-RNA function. To this end, we are engineering 6 targeting vectors that, on homologous recombination on the X-chromosome in mouse ESCs, will each generate a version of the Xist transcript that has a single repeat deleted. We will test the ability of each Xist mutant to induce XCI. By elucidating the function(s) of the repeat-regions of Xist in initiation of XCI, we hope to gain critical insights into the mechanisms of lncRNA domain function in epigenetic remodeling and determination of cellular identity.

#### **SAT-1089**

#### **TRANSFORMATION OF TOBACCO (*NICOTIANA TABACUM*) WITH ESPS (5-ENOLPYRUVYLSHIKIMATE 3-PHOSPHATE SYNTHASE)-A KEY ENZYME IN THE SHIKIMATE PATHWAY**

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The shikimate pathway was discovered to be the biosynthetic route to the aromatic amino acids phenylalanine, tyrosine, and tryptophan. EPSP (5-enolpyruvylshikimate 3-phosphate synthase) synthase catalyzes a key step leading to the synthesis of aromatic amino acids serving as precursors for a wide range of secondary metabolites with multiple biological functions, including protection against various abiotic and biotic stresses like pathogens. EPSP synthase (EPSPS) is a plastid-localized enzyme required for the production of aromatic amino acids. Inhibition of EPSPS results in cell death in plants. The role of EPSPS is to catalyze the synthesis of 5-enolpyruvylshikimate-3-phosphate and inorganic phosphate by transferring the enolpyruvyl moiety from phosphoenol pyruvate (PEP) to shikimate-3-phosphate (S3P). We isolated a full-length cDNA clone for the EPSPS gene from chile and made a construct for constitutive expression. We have introduced this gene construct into tobacco (*Nicotiana tabacum*) by *Agrobacterium tumefaciens*-mediated whole plant transformation method. Putative transgenic tobacco plants have been regenerated from the leaf discs on selection media. The transformants have been checked for the integration of the transgene by PCR using gene specific primers for the selectable marker NPTII. Accumulation of the EPSPS protein has been shown by western blot analysis using antibodies for EPSPS protein. Thus, one of our postulates is that increased expression of EPSPS could lead to the synthesis of many of these defense molecules. The transformants along with control plants will be subjected to metabolite analysis to check for any changes in key metabolites related to metabolism of aromatic amino acids like the phytoalexins.



**FRI-1077****IDENTIFICATION AND CHARACTERIZATION OF THREE UNIQUE CELL CYCLE CONTROL GENES IN *C. CRESCENTUS***

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The bacterium *Caulobacter crescentus* undergoes asymmetric cell division whereby it differentiates between a reproductive stalked cell and a motile swarmer cell. Orchestrating this advanced reproductive cycle are 4 master transcription regulators whose combined functioning affects over 150 other genes within the cell. Many of these genes encode for proteins that play essential roles in *Caulobacter's* cell cycle. Although much work has been done to understand how these essential proteins coordinate the cell cycle, the function of several genes regulated by one or multiple master regulators remains unknown. The unique dimorphism of *C. crescentus* presents an extraordinary opportunity to identify the function of these genes and examine their role in the cell cycle of *C. crescentus*. Using multiple genetic tools including electroporative transformation and spectroscopy, we constructed several *Caulobacter* strains that modify the expression of 3 genes with unknown function thought to be regulated by 1 or 2 master regulators with the goal of characterizing the effect of either depleting (underexpressing) or overexpressing these genes. We hypothesize that under or over expression of these highly regulated genes will affect the proper progression of the cell cycle. We will test our hypothesis by determining growth rate, swarmer-cell motility, reproductive viability, and difficulty in cell division when compared to wild-type *Caulobacter* cells. Ultimately, unmasking novel protein functions will potentially change the way we approach the control and manipulation of bacterial growth in pathogenic and nonpathogenic species alike.

**SAT-1066****THE SIGNIFICANCE OF MIRNAS FOR INDUCED NEURONAL CONVERSION**

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The miRNAs are non-coding RNA molecules that are involved in post-transcriptional gene regulation. Changes in expression levels of miRNAs during reprogramming suggest that they have a key role in the conversion of fibroblasts to induced neuronal cells (iN). To study the role of miRNAs, we took advantage of DGCR8 conditional knockout (KO) mouse embryonic fibroblasts (MEFs). DGCR8 is a critical component of the miRNA biogenesis machinery, and cells missing this gene are void of miRNAs. Using MEF DGCR8 conditional KO cells, we show that the reprogramming efficiency of fibroblasts to iN cells decreases dramatically in the absence of miRNAs, which further illustrates the importance of miRNA regulation during iN reprogramming. To better understand the role of miRNAs and to identify the pathways they regulate during iN reprogramming, we are taking a two-tier approach. We use both bioinformatic and experimental approaches to pinpoint potential miRNA target genes. These target genes could be potential roadblocks to iN reprogramming and thus, interesting candidates for enhancing iN reprogramming. We are currently building a luciferase reporter system for the validation of these prospective miRNA targets.

**SAT-1052****RAB11A AND RAB11B DISTINCTLY REGULATE PROTEASE-ACTIVATED RECEPTOR-1 RECYCLING AND CONSTITUTIVE DEGRADATION**

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Protease-activated receptor-1 (PAR1) is a G protein-coupled receptor (GPCR) expressed throughout the vasculature. Thrombin irreversibly activates PAR1, therefore receptor signaling and expression is tightly regulated. Upon activation, PAR1 is rapidly internalized and sorted directly to lysosomes for degradation, a process critical for signal termination. Naïve PAR1 is constitutively internalized, generating an intracellular pool of PAR1 that recycles and repopulates the cell surface with uncleaved PAR1 after thrombin stimulation, a process critical for rapid recovery of thrombin signaling. The mechanisms that mediate recycling of naïve PAR1 are not known. Using an siRNA library screen of 140 membrane trafficking proteins, we identified Rab11B as a key regulator of PAR1 trafficking to the cell surface. We confirmed that siRNA depletion of Rab11B, and not Rab11A, reduced PAR1 surface expression, but did not affect expression of the thromboxane GPCRs, TP $\alpha$  and TP $\beta$ . Rab11B knockdown had no effect on PAR1 constitutive internalization but blocked PAR1 recycling, resulting in loss of surface expression and enhanced receptor degradation that was blocked by lysosomal protease inhibitors. In contrast to Rab11B, knockdown of Rab11A by siRNA disrupted PAR1 sorting from endosomes to lysosomes leading to accumulation without affecting surface expression, suggesting that Rab11A and Rab11B distinctly regulate PAR1 trafficking. The mechanisms by which Rab11A and Rab11B distinctly regulate intracellular trafficking of PAR1 are not known and are currently being investigated. Given that elevated PAR1 expression contributes to malignancy of certain cancers, understanding the mechanisms that control PAR1 surface expression could aid in the development of therapeutic approaches.

**SAT-1080****A NOVEL RTS1-DEPENDENT CHECKPOINT CONTROLS CELL SIZE AT COMPLETION OF MITOSIS**

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Cells divide only when they have undergone sufficient growth, which ensures they maintain a specific size. The mechanisms that link cell division to cell growth are called cell-size checkpoints. In addition to maintaining size, cell-size checkpoints are capable of modulating cell size. Thus, the critical size for cell division is reduced in poor nutrients which allows cells to divide more frequently under starvation conditions. The molecular mechanisms by which cell-size checkpoints maintain and modulate cell size are poorly understood. The most important cell-size checkpoint is thought to link cell cycle entry in G1 phase to attainment of a critical size. However, our recent work suggests there is an equally important checkpoint that works at the end of mitosis to determine the size at which yeast cells are born. We discovered that cells grow throughout mitosis, and the duration of mitosis is increased in poor nutrients because cells grow more slowly. Moreover, cells in poor nutrients exit mitosis and enter the following

G1 at a smaller size. We have identified key players in the checkpoint and are testing hypotheses for how they function. Our working hypothesis is that a conserved phosphatase called PP2A<sup>Rts1</sup> controls the duration of mitosis via the Wee1 kinase which inhibits progression through mitosis. Discovering the molecular mechanisms that link cell division to cell growth could shed light on diseases such as cancer.

#### **SAT-1073**

##### **IDENTIFYING THE MOLECULAR FUNCTION OF ORF73 IN ONCOGENIC MURINE HERPESVIRUS 68**

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Two human gamma-herpesviruses, Epstein-Barr virus (EBV) and Kaposi's sarcoma-associated herpesvirus (KSHV), are known to establish life-long infections in lymphocytes and are associated with several malignancies. Their life cycles are composed of 2 distinct phases, lytic replication and latency. The latent phase of EBV and KSHV has been directly linked to tumorigenesis. During latency, gamma-herpesviruses are relatively dormant within host cells, progressively shutting down viral gene expression. The only viral protein expressed during latency is latency-associated nuclear antigen (LANA). LANA is essential for latency establishment and maintenance. While there are many molecular functions proposed for LANA, the precise *in vivo* function is unclear. A closely related rodent gamma-herpesvirus, murine gammaherpesvirus-68 (MHV-68), has a LANA homologue, ORF73. To elucidate the mechanism of ORF73, we propose to investigate the molecular interactions of ORF73 in the context of viral infection. Since there is no available antibody for immunoprecipitation of MHV-68 ORF73, we will introduce a FLAG tag at the C-terminus of ORF73 within the viral genome to create a recombinant virus, 73F. We will infect a variety of cells, including fibroblasts, macrophages, and B-cells, with the 73F and perform co-immunoprecipitation followed by mass spectrometry to identify the associated cellular and viral proteins. Subsequently, we will determine whether these interactions play significant roles in ORF73's function of establishing and maintaining latency. By identifying the specific role of ORF73, we may be able to develop novel strategies to counter viral persistence using chemotherapy or vaccination. Synthesis of the recombinant virus is in progress.

#### **SAT-1057**

##### **COMPARING METHYLATION PREFERENCE OF WILD TYPE AND MUTANT DNA ADENINE METHYLTRANSFERASE**

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Our lab studies a methyltransferase found in *Escherichia coli* called DNA adenine methyltransferase (Dam). Dam methylates the adenine in GATC sites, which is important for bacterial processes such as mismatch repair and gene expression. The sequence surrounding a GATC site influences Dam's likelihood of methylating the site; generally, G/C rich flanking sequences are preferred to A/T rich sequences. The objective of our study was to compare the preference of wild type and 2 Dam mutants (R116A and N126A) for different GATC flanking sequences. Arginine 116 and asparagine 126 both

interact with DNA surrounding the GATC sites, so substitution of these residues was predicted to affect Dam's preference for specific flanking sequences. Our methods involved purifying a plasmid from *E. coli* expressing wild type or mutant Dam and isolating a region of the plasmid containing a preferred and non-preferred GATC site. The DNA was digested by DpnII, which cuts non-methylated GATC sites, and the fragments were separated by electrophoresis. After measuring the intensity of the bands, a plot was created to compare the percentage of methylation at both sites. Our primary results demonstrate that although R116A and N126A do not methylate as efficiently as wild type, they are able to methylate the GATC sequences with dependence on the flanking sequences. This demonstrates that mutants show methylation preference in a similar manner to the wild type. Our next step will be to determine whether the decrease in efficiency of the mutants is due to their structure or stability within the cell.

#### **SAT-1099**

##### **IMD PATHWAY ACTIVATION UPON INJURY IN *DROSOPHILA MELANOGASTER***

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The Toll signaling pathway as well as the immune deficiency (Imd) pathway are 2 of the most important mechanisms known to be responsible for the regulation of immune response in *Drosophila melanogaster*. The discovery and following analysis of these pathways have helped us understand more in depth the relationship between the insect and mammalian immune systems and how these work. Shortly after the identification of the *Drosophila* Toll pathway, pattern recognition receptors known as Toll-like receptors (TLRs) were identified in humans, leaving no doubt that the Toll pathway is an evolutionary conserved signaling cascade. However, although these pathways are known to be activated in response to infection, little is known about their activation upon injury. Preliminary results from our laboratory show that the Toll regulated NF- $\kappa$ B factors Dorsal and Dif are activated in the hematopoietic organ (the lymph gland) and in circulating blood cells of third instar larvae after injury. Although Toll does not cause activation of the Imd pathway based on data from our lab, we propose that the alternative NF- $\kappa$ B protein Relish is involved in the process. To test the involvement of the Imd, we injured third instar larvae then dissected and immunostained the lymph gland with anti-Relish antibody. The lymph glands were imaged using confocal microscopy. Nuclear translocation of Relish would suggest the involvement of either canonical Imd signaling or a novel regulatory mechanism in the context of sterile injury.

#### **SAT-1091**

##### **IDENTIFYING ALTERED MICROBIAL COMMUNITY PROFILES IN IMMUNODEFICIENT MICE**

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The microbiomes of the human body act as an interface mediating human response to surrounding microbial environments, daily life cycles, and metabolism. Additionally, bacterial strains within the body can directly interact with the mechanisms of disease through the production of natural antibiotics and performing preliminary immune signaling. The recently

discovered microbiome of the lungs has been observed to play a fundamental role in the pathology of chronic obstructive pulmonary disease (COPD), asthma, and cystic fibrosis, all diseases heavily influenced by the body's own immune response. However, gaps in knowledge exist on the microbial inhabitants themselves and the mechanisms forming these relationships. To identify factors contributing to the lung microbiome, this study aims to characterize the essential microbial inhabitants of the lung microbiome and ascertain those linked to healthy immunological response. The lungs from a series of immunocompromised mice were extracted and their microbial communities determined through 16S metagenomic analysis. This data was used to map a microbial profile for the diseased lung by physical region that was then compared to the standard communities observed in a set of normal mice lungs. It is expected this will identify key strains and mechanisms responsible for mediating immune response in the lungs. Thus, this would offer a platform for further metagenomic exploration of the pulmonary microbiome to ascertain biochemical factors that could assist in the formation of therapeutic treatments for immune dependent pulmonary conditions.

#### **FRI-1074**

##### **LIPID-PROTEIN INTERACTION DURING PKC ACTIVATION IN PLATELETS**

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Determining mechanisms of platelet activation is key for new potential therapeutic interventions of thrombotic diseases. Currently, some modern therapeutics inhibit platelet function by antagonizing the  $\alpha\text{IIb}\beta\text{3}$  integrin, but these drugs can cause major bleeding in some patients. Therefore, it is necessary to study signaling pathways leading to the activation of  $\alpha\text{IIb}\beta\text{3}$  to characterize key protein interactions that could potentially be exploited for decreased platelet aggregation. Previously, an enzyme expressed in human platelets called arylacetamide deacetylase-like 1 (AADACL1) was discovered. AADACL1 is known to deacetylate ether lipid substrates including 2-acetyl MAGE. Since others have shown that AADACL1 lipid substrates like 2-acetyl MAGE directly inhibit protein kinase C (PKC), we hypothesize that AADACL1 affects platelet signaling by inhibiting PKC through ether lipid metabolism. We plan to determine if lipids that act as AADACL1 substrates also directly bind and affect PKC activity by utilizing cosedimentation assays and protein kinase assays. We predict that certain isoforms of PKC will bind to 2-acetyl MAGE which will inhibit PKC kinase activity and reduce activation of  $\alpha\text{IIb}\beta\text{3}$ . Data from these experiments will further our understanding of lipid-protein interactions in platelets and may uncover novel pathways of platelet activation.

#### **FRI-1069**

##### **EXAMINING THE TEMPORAL LOCALIZATION OF *C. ELEGANS* PUTATIVE PROTAMINES SPCH-1/2/3**

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The integrity and proper compaction of sperm DNA is crucial for fertility and the accurate transmission of genetic information from one generation to the next. During meiosis, histones,

the main DNA packaging proteins, are replaced with small, highly basic proteins called protamines. These proteins contribute to both the protection and further compaction of sperm DNA. While differences in protamine expression are associated with male infertility in humans, the exact timing of expression during meiosis remains unclear. *Caenorhabditis elegans* provides a useful model for examining male fertility *in vivo*. The stages of sperm development can be easily identified within the gonad, and both males and hermaphrodites produce sperm. While the identity of *C. elegans* protamines has remained elusive, proteomic analysis has identified three nearly identical proteins, SPCH-1/2/3, as possible protamines. Since they are small, basic proteins abundant in sperm chromatin and the loss of function of spch-2 has a negative effect on fertility, we hypothesize that SPCH-1/2/3 function as protamines in *C. elegans*. We are monitoring the expression *in vivo* with GFP-tagged versions of the SPCH proteins using gateway cloning to construct expression vectors containing SPCH::GFP that will be inserted into the worms via microinjections. If the SPCH proteins are functioning as protamines, we expect SPCH::GFP to localize to spermatogenic chromatin during meiosis and be removed after fertilization. Examining the localization of SPCH proteins and determining the role of SPCH-1/2/3 in *C. elegans* will yield new insight into the function and expression patterns of protamines.

#### **SAT-1077**

##### **TITIN, LAMINS, AND METABOLIC SYNDROME**

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Titin, the ~3,000 kD bungee cord protein in muscle sarcomeres, is essential for mitotic chromatin condensation. Nuclear titin binds A-type and B-type nuclear intermediate filament proteins known as lamins. Mutations in A-type lamins, encoded by LMNA, cause over 15 tissue-specific diseases (laminopathies) including Hutchinson-Gilford progeria syndrome, Dunnigan type familial partial lipodystrophy (FPLD), diabetes, and metabolic syndrome (MetSyn). MetSyn affects about 30% of adults worldwide and is defined as a collection of risk factors (e.g., abdominal obesity, high triglycerides, and high blood pressure) that leads to cardiovascular disease, stroke, and type-2 diabetes. About 11% of MetSyn patients have misshapen nuclei, characteristic of laminopathy. MetSyn has been genetically linked to 8 different missense mutations in the lamin A tail domain, which binds many partners, including a C-terminal region of titin. Our collaborator identified a MetSyn patient with a missense mutation (M419T) in the lamin-binding domain of titin (*Mis7*). We proposed this mutation affects titin-lamin association, thereby disrupting nuclear architecture and lamin function. To test this hypothesis, immunofluorescence microscopy was used to examine nuclear shape and other phenotypes in human cells that transiently overexpressed either GFP, GFP-*Mis7* (wildtype (WT) or M419T mutant), or a control titin fragment (GFP-*Mis6*) that does not bind lamins. Current results from HeLa and HEK293 cells suggest the M419T mutation reduces titin binding to lamins. This possibility will be tested by immunoprecipitation with GFP antibodies and western blot quantification of lamin association with WT vs. M419T-mutated titin.

**SAT-1078****EFFECTS OF BISPHENOL-A ON MCF-10A G-COUPLED ESTROGEN RECEPTORS**

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Bisphenol-A (BPA) is a known estrogen receptor agonist toward the G-coupled protein estrogen receptor (GPER/GPR30) that is found within many plastics, epoxy resins, and non-polymer additives. BPA alters the development of the mammary gland during puberty when female rodents are exposed prenatally and increases risk of breast cancer later in life. Little is known about the immediate effects of BPA on the developed mammary gland. We have investigated BPA-dependent direct physiological changes in the non-tumorigenic human breast epithelial cell line MCF10A grown in 3-dimensional culture. Cells were grown on recombinant basal lamina matrix to induce 3D spheroid growth and then treated for 4 days with BPA (1 – 100 nM), or with BPA plus GPER antagonist G36 (5-fold molar excess). Estrogen and vehicle alone served as positive and negative controls. After paraformaldehyde fixation, proliferation and apoptosis levels were determined by immunofluorescence assays using anti-Ki-67 and anti-cleaved caspase 3 respectively. Cell number, spheroid size, and lumen size were also quantified to determine if changes in proliferation/apoptosis also influence spheroid size and shape. The results are expected to show increases in cell proliferation, decreased apoptosis, increased cell number, spheroid size and luminal filling, which would be consistent with *in vivo* studies demonstrating that BPA increases risk of carcinogenesis. These results will support the hypothesis that BPA exerts direct physiological changes in breast epithelia through GPER, and extending these studies could provide further insight into the molecular actions of BPA and the signaling pathways it modulates through GPER.

**SAT-1049****CELLULAR ZINC LEVELS ARE INFLUENCED BY THE INTERACTION BETWEEN THE MUCOLIPIDOSIS IV-ASSOCIATED TRPML1 PROTEIN AND TMEM163 PROTEIN**

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Loss of function mutation in the mucolipin-1 (TRPML1) ion channel protein causes the human lysosomal storage disorder mucopolipidosis type IV (MLIV). Cells affected by MLIV have significantly higher intracellular zinc levels when exposed to exogenous zinc compared to normal cells; however, the mechanism of zinc elevation remains unknown. Using a membrane-based yeast two-hybrid technique, we identified a putative zinc-binding protein called transmembrane-163 protein (TMEM163) as an interacting partner for TRPML1. We confirmed the interaction between the two proteins by co-immunoprecipitation and mass spectrometry. Confocal microscopy of TMEM163 and TRPML1 each tagged with a unique fluorescent protein showed co-localization and a punctate distribution pattern inside the cells. We hypothesized that the interaction between TMEM163 and TRPML1 plays a role in regulating TMEM163, and thus intracellular zinc. RNA interference targeting TMEM163 alone or TMEM163 and TRPML1 in HEK-293 cells resulted in significant increase of intracellular zinc. Meanwhile, deletion of the N-terminus of TMEM163 protein disrupts its binding to TRPML1. We also found that disruption of

the interaction resulted in changes in intracellular zinc levels that were only apparent when TRPML1 is co-expressed with the deletion mutant versions of TMEM163. Overall, our data suggest that both TRPML1 and TMEM163 proteins play a role in regulating intracellular zinc. Thus, the loss of TRPML1 protein interaction with TMEM163 and/or the reduction of TMEM163 protein could result in zinc dyshomeostasis in MLIV.

#### **FRI-1091**

##### **SLIT/ROBO1 SIGNALING REGULATES THE SELF-RENEWAL OF MAMMARY STEM CELLS BY CONTROLLING THE LEVELS OF INSCUTEABLE THROUGH SNAIL**

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Mammary gland regeneration following each estrus cycle and pregnancy relies on the self-renewal of a population of mammary stem cells (MaSCs). Stem cells self-renew either through an asymmetric cell division (ACD), which also generates a progenitor cell, or through a symmetric cell division (SCD) that expands the stem cell population. Disruption of the balance between ACD and SCD can lead to tissue dysfunction. Therefore, understanding how these divisions are regulated is critical, but the mechanisms involved remain poorly understood. Research from the Hinck laboratory has shown that Inscuteable (mINSC), a regulator of mitotic spindle orientation, is critical in determining whether a cell divides asymmetrically or symmetrically. Furthermore, the lab has discovered that the extracellular cue SLIT, signaling through its ROBO1 receptor, regulates mINSC expression. Assessing the levels of mINSC in mammary epithelial cells by immunoblotting, we have found that loss of Robo1 leads to increased SNAIL expression. We further determined that cells over-expressing the transcription factor SNAIL express higher mINSC levels. Thus, given these collective data, we hypothesize that SLIT signaling regulates the asymmetric self-renewal of MaSCs by controlling the levels of mINSC through the transcription factor SNAIL. Future research will include identifying if SNAIL regulates mINSC expression directly, by binding to the mINSC promoter region, or indirectly, by interacting with secondary factors. The balance between ACD and SCD of MaSCs is often disrupted in cancer. Thus, understanding the mechanisms that regulate this delicate balance is crucial for identifying new targets for anti-cancer therapeutics.

#### **SAT-1097**

##### **MICROFLUIDICS CULTURE OF HUMAN NEPHRON SEGMENTS FOR THE ANALYSIS OF NATRIURESIS AS REGULATED BY DOPAMINE: A PILOT STUDY FOR THE TREATMENT OF HYPERTENSION**

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In the United States, the leading cause of death is cardiovascular disease. Hypertension is the most expensive disease in the United States, generating over \$69 million in treatment costs in 2008. Worldwide from 2000 to 2025, it is predicted that 500 million people from low-income areas will become hypertensive. Patients without hypertension have a 98% probability to reach the age of 70, while patients with hypertension only have a 50% chance to reach the same age.



Hypertension is associated with the decrease in the regulation of sodium balance by the kidneys. In an attempt to find a novel method for the analysis of natriuresis, recent studies have been using the fabrication of enzymatically crosslinked microchannels made of gelatin for microfluidic cell culture. This gelatin structure mimics the physiological environment of a proximal tubule inside a nephron for growing proximal tubule cells in the right geometry. This culturing process allows the measurement of sodium in each segment that is needed for the cells to develop the primary cilia to absorb sodium from the bloodstream by modeling the natriuresis process using microfluidics. For the development of these channels, we used an inexpensive child shrink disk to make microchannels of the appropriate dimension in which to grow human kidney cells. With this study, we can define how much sodium is needed for the cells to absorb in the proximal tubule and establish a range of minimum quantity of sodium needed to start increasing the blood pressure.

#### **FRI-1065**

#### **RELAXIN-H2 LIMITS TGF- $\beta$ 1-MEDIATED UPREGULATION OF MATRIX METABOLISM GENES AND MESENCHYMAL MARKERS IN NORMAL AND CYSTIC RENAL EPITHELIAL CELLS**

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Autosomal dominant polycystic kidney disease (ADPKD) is an inherited, progressive disorder characterized by the formation and growth of hundreds of cysts in both kidneys. In addition, irreversible events, including renal inflammation, abnormal matrix metabolism, and fibrosis, destroy renal architecture. Collectively, cyst growth and fibrotic progression causes renal failure in the fifth to sixth decade of life. The anti-fibrotic hormone relaxin-H2 acts directly on fibroblasts to limit fibrosis, but little is known about relaxin-mediated signaling in kidney epithelia. Therefore, we tested the hypothesis that renal epithelial cells express the relaxin receptor RXFP1, and relaxin treatment will inhibit changes in expression of matrix proteins and mesenchymal markers under simulated fibrotic conditions. We used immunoblotting and real-time PCR techniques to evaluate the effects of TGF- $\beta$ 1 (a master regulator of fibrosis) and relaxin-H2 on normal and ADPKD, cyst-derived renal epithelial cells. TGF- $\beta$ 1 induced expression of aberrant genes linked to ADPKD pathogenesis. Our data demonstrate that relaxin-H2 inhibited expression of genes linked to abnormal matrix synthesis, including collagens I and III, and matrix degradation, including matrix metalloproteinases and their associated inhibitors. Cystic kidney epithelia partially de-differentiate and express mesenchymal proteins such as vimentin, and vimentin over expression was limited in the presence of relaxin-H2. Our studies show that relaxin-H2 directly targets kidney epithelia and, thus, relaxin-H2 could serve as a potential therapeutic to minimize de-differentiation of human ADPKD renal epithelial cells and limit fibrotic progression in ADPKD.

**SAT-1096****OPTIMIZING URANIUM ABATEMENT FOR POTABLE WATER ON THE NAVAJO NATION**

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According to a study by the United States Environmental Protection Agency (EPA) Region 9 which included 36 unregulated water samples, 5 water sources (14%) in 5 chapters exceeded the maximum contaminant levels (MCLs) for uranium. EPA and World Health Organization MCLs are 30 ppb and 15 ppb, respectively. Fortunately, clay is a natural and local solution to problem of uranium contamination in water. Clay materials are known for their cation exchange capacity for heavy metal abatement; therefore, we are investigating the use of clay pellets for uranium abatement. Our preliminary sorption studies verify S-curve isotherm abatement, indicating uranium sorption. The objective is to maximize uranium abatement with clay pellets by introducing porosity and, thus, overall surface area yet maintaining robustness of the fabricated pellets. Recycled coffee grounds, which are universal and readily available, will be added to the clay pellets in increments of 5%, 10%, 15%, and 20%. The optimal percentage of coffee grounds will be established by analyzing pellet robustness. We hypothesize that creating macroporosity will affect adsorption isotherms: H-curve sorption characteristics will be indicative of large, initial abatement. For this characterization, fluorometry will model the kinetics and thermodynamics of uranium abatement. A pocket penetrometer will determine robustness and pellet strength, reported in tons/ft<sup>2</sup>.

**FRI-1052****LOCALIZATION SHIFT OF SPERM-SPECIFIC PHOSPHATASES THROUGHOUT SPERM DEVELOPMENT**

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Assisted reproductive technologies are advancing to aid infertile couples; however, the cause of infertility remains unclear at the molecular level. Male infertility studies have shown that mice lacking PP1 $\gamma$ 2, a sperm-specific isoform of protein phosphatase one (PP1), experience impaired sperm meiosis and deformed sperm tails. In *Caenorhabditis elegans*, we identified 2 sperm-specific PP1s, GSP-3 and GSP-4 (GSP-3/4), which are functional homologues of PP1 $\gamma$ 2. RNA interference (RNAi) against gsp-3/4 causes improper chromosome segregation during spermatogenesis and sperm immobility. Previous studies have shown that GSP-3/4 co-localizes to DNA during early spermatogenesis. Yet, between early and late spermatid development, GSP-3/4 shifts to co-localize to a major sperm protein that regulates the extending pseudopod, which provides the sperm's crawling motility. In fully developed sperm, the phosphatases reside in the pseudopod. Thus, it is hypothesized that the localization shift from DNA to the pseudopod occurs when spermatids bud off from the residual body after meiosis II in spermatogenesis. To address our hypothesis, we are generating separate GSP-3 and GSP-4 tagged with green fluorescent protein (GSP-3/4::GFP) stains by using gateway cloning and Mos1 single copy insertion in order to conduct live imaging. These constructs are vital, as the 2 phosphatases cannot currently be differentiated with antibodies due to their extensive

similarity. In future studies, the fluorescent strains will enable us to individually follow our phosphatases throughout sperm development and, thus, elucidate their respective roles *in vivo*.

#### **SAT-1072**

##### **NOVEL METHODOLOGY TO IDENTIFY HOST AND PATHOGEN DETERMINANTS OF *CANDIDA ALBICANS* INFECTION**

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*Candida albicans* comprises a significant portion of the human microbiome, and when invasive, can cause high rates of mortality and morbidity. The first lines of defense in the immune response to invasive *C. albicans* are macrophages. *C. albicans* invasion is associated with a phenotypic “switch” from a commensal yeast form to a virulent filamentous form, making it difficult for macrophages to phagocytose them. Little is known about the host-pathogen interaction between *C. albicans* and the human immune system, and in particular, the transcriptional networks underlying these interactions. This paucity of knowledge, in part, because it is difficult to study this interaction through conventional genetic and immunological approaches. Therefore, we have developed an imaging and RNA-Seq pipeline. Using live-cell microscopy, we discovered significant heterogeneity in the outcome of infection of single macrophages. In some cases, macrophages successfully phagocytized and neutralized the *C. albicans*, yet in others, *C. albicans* would filament and burst the macrophages. We explored novel microscopy, fixation, and RNA isolation methods culminating in a pipeline to isolate macrophages infected with *C. albicans*, separate host-pathogen pairs based on the outcome of infection into distinct subpopulations, and extract RNA from each subpopulation for downstream RNA sequencing. This work will help to better understand the mechanistic and transcriptional basis of infection outcome, ultimately aiding in the identification of targets for therapeutic intervention.

#### **FRI-1053**

##### **ELUCIDATING A MITOCHONDRIAL PROTECTIVE TRANSCRIPTIONAL NETWORK**

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The mitochondrial unfolded protein response (UPR<sup>mt</sup>) is a pathway that is activated during times of mitochondrial dysfunction and is regulated by the transcription factor ATFS-1. During periods of mitochondrial dysfunction, mitochondrial import efficiency is decreased allowing ATFS-1 to traffic to the nucleus via its nuclear localization signal (NLS). Nuclear ATFS-1 then activates a cytoprotective transcriptional response that alleviates the mitochondrial dysfunction. Our objective was to identify other candidate transcription factors that act as regulators of *UPR<sup>mt</sup>* gene expression. Previous work identified seven transcription factors that are either induced during mitochondrial dysfunction or have been found to physically interact

with ATFS-1 *in vitro*. An initial RNA interference (RNAi) screening was performed against these transcription factors in the clk-1(qm150) background, a mitochondrial stress mutant background that results in activation of the *UPRmt*. From these candidates, ZIP-5 was identified as a transcription factor required for *UPRmt* activation. RNAi against ZIP-5 resulted in reduced levels of the *UPRmt* reporter transgene hsp-60::GFP in the clk-1(qm150) mutant background. Interestingly, loss of function of ZIP-5 also suppresses the slowed growth phenotype, which is characteristic of mitochondrial stress animals. We hypothesize that ZIP-5 may act as a negative regulator of electron transport chain gene expression (*ETC* genes), which would allow ZIP-5 loss of function mitochondrial stressed animals to grow at a faster rate due to increased respiration rates. Our observations provide preliminary evidence that ZIP-5 is a component of a mitochondrial protective transcriptional network, acting as a negative regulator of mitochondrial biogenesis.

#### **FRI-1051**

##### **INHIBITION OF CELL MIGRATION USING R-MOJ PEPTIDES**

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Cancer is a term used for diseases in which abnormal cells divide without control and are able to invade other tissues. Cancer cells can spread to other parts of the body through the blood and lymph systems in a process known as metastasis. Cancer is one of the leading causes of death in the United States. We are investigating anti-cancer effects of recombinant disintegrins r-Moj-DV, r-Moj-DG, r-Moj-DN, and r-Moj-DA on several human cancer cell lines. Recombinant mojastin (r-Moj-) peptides were cloned from a Mojave rattlesnake venom gland, and mutated using site-directed mutagenesis. We hypothesized that r-Moj-D\_ peptides will inhibit migration of T24 cancer cell lines. We tested the ability of the peptides to inhibit the migration of treated T24 cells, by performing a wound-healing assay. We seeded the T24 cell line in a 24-well microplate with a plug insert, to produce a “wound” in the middle of the well. After 24 h of incubation the cells formed a monolayer, and the treatment was added. Experiments were done in triplicate. The cells were monitored after another 24 h of incubation. The area of “wound” closure was measured and the percent of closure of each disintegrin was calculated. All of the disintegrins tested inhibited cell migration. The least potent was r-Moj-DA (51% inhibition), whereas r-Moj-DG was the most potent (100% inhibition). Understanding the effect of r-Mojastin disintegrins on cell migration may allow us to develop effective treatments against metastasis.

#### **FRI-1067**

##### **ANALYZING EXPRESSION PATTERNS OF CCN1 AND CCN2 IN ARTICULAR CARTILAGE**

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Osteoarthritis is a common and progressive degenerative joint disorder characterized by loss of articular cartilage. The matricellular CCN family of proteins mediates chondrogenesis, angiogenesis, wound repair, and injury response by activating receptors in the extracellular

matrix (ECM). Cyr61 (CCN1) and connective tissue growth factor (CTGF, CCN2), part of the CCN family, induce proliferation and ECM responses in inflammatory and otherwise damaged environments and in development of the skeletal growth plate. Due to these roles, we hypothesized that CCN1 and CCN2 may provide similar support in articular cartilage maintenance. To assess the hypothesis, the spatial and temporal expression of CCN1 and CCN2 were examined from embryonic development to aging in mice models using immunohistochemistry and immunofluorescence. Our preliminary data showed that CCN1 expression was localized to the surface layer (superficial zone) of cartilage in adult mice where more proliferation may be present. CCN2 expression was localized to the deep layer (deep zone) that is adjacent to the subchondral bone in adult animals, which may imply a greater role in maintenance than in maturation. Future directions are to investigate *CCN1* and *CCN2* gene expression in diseased conditions. It is crucial to characterize their expressions in both healthy and damaged cartilage tissues to understand their roles in mediating cellular responses at the molecular level. A better understanding of these proteins could in turn be applied to diagnostics and therapeutics for inflammatory conditions like osteoarthritis.

#### **FRI-1060**

#### **CHMP4, VPS4, AND ALIX REGULATE THE UBIQUITIN-INDEPENDENT LYSOSOMAL SORTING PATHWAY OF P2Y<sub>1</sub>**

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As part of the G-Protein coupled receptor (GPCR) family, the purinergic P2Y<sub>1</sub> receptor transmits signals from extracellular stimuli when it is activated by nucleotide adenosine diphosphate (ADP), activating signal transduction inside the cell. Degradation of GPCRs by sorting to lysosomes following agonist stimulation is important for regulation of proper receptor signaling and cellular responses. Most GPCRs are modified with ubiquitin, a protein that acts as a targeting signal for the lysosome. Here, we show that P2Y<sub>1</sub> is degraded via a ubiquitin-independent pathway. P2Y<sub>1</sub> contains a novel YPX<sub>n</sub>L (where x is any amino acid) lysosomal sorting motif within the second intracellular loop of P2Y<sub>1</sub>. A mutant of P2Y<sub>1</sub>, P2Y<sub>1</sub> Y155A, created using site-directed mutagenesis, has been discovered to produce a blockage in P2Y<sub>1</sub> degradation. The P2Y<sub>1</sub> Y155A mutant does not affect internalization, suggesting that the mutation of P2Y<sub>1</sub> within the YPX<sub>n</sub>L motif inhibits trafficking within the endosomal system. YPX<sub>n</sub>L motifs are binding sites for the endocytic adaptor protein ALIX, which is known to mediate ubiquitin-independent lysosomal sorting of another GPCR, protease-activated receptor 1. Interestingly, P2Y<sub>1</sub> lysosome sorting is also regulated by ALIX. In addition, we discovered that the ESCRT-III complex protein CHMP4 regulates the lysosomal sorting of P2Y<sub>1</sub>. CHMP4 sorts proteins into intraluminal vesicles, forming multivesicular bodies from the late endosome. Finally, we discovered that VPS4 also regulates the lysosomal sorting of P2Y<sub>1</sub> by regulating CHMP4. Experimentation on the proteins CHMP4 and VPS4 has extended our knowledge about the lysosomal sorting pathway of P2Y<sub>1</sub> and its regulation in mammalian cells.

**FRI-1073****INVESTIGATION OF TNF-5Z-7 INDUCED CELL DEATH**

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Regulated cell death plays a large role in development, maintaining homeostasis, and in a wide range of diseases. Various forms of programmed cell death, such as apoptosis and necroptosis, have been extensively studied and characterized. Tumor necrosis factor (TNF)-induced cell death observed during inhibition of the transforming growth factor-beta-activated kinase 1 (TAK1) has characteristics of both apoptosis and necroptosis. TNF-induced cell death after inhibition of TAK1 has been shown to induce caspase activation, similar to apoptosis. However, it also requires RIP1 kinase activity and can be inhibited by Necrostatin-1, similar to necroptosis. In order to determine the characteristics of this induced cell death, a cell death model was first determined. Various *in vitro* models were explored by culturing cells with 5Z-7-oxzeaenol, an inhibitor of TAK1. Based on CellTiter-Glo and Toxlight assays, mouse embryonic fibroblasts (MEFs) appeared the most promising cell model. To phenotypically characterize this cell death, we focused on the nuclear changes occurring during cell death. Specifically, to investigate the extent of DNA laddering, a hallmark of apoptosis, MEFs were cultured with 5Z-7 and mTNF and were harvested at different time points. Future experiments will determine the changes that occur in proteins involved in nuclear fragmentation and proteins involved in this cell death signaling pathway.

**FRI-1063****REGULATED PROTEOLYSIS OF THE CYCLIN DEPENDENT KINASE INHIBITOR DACAPO CONTROLS THE *DROSOPHILA* ENDOREPLICATION CYCLE**

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Developing tissues require precise regulation of the cell cycle to differentiate and mature. Differentiation sometimes requires remodeling of the canonical cell cycle. Some cells become polyploid by endoreplication, a modified cell cycle with alternating rounds of G and S phase (DNA synthesis) without mitotic divisions. Endoreplication is controlled by oscillations of cyclin dependent kinase (Cdk) activity. CDK inhibitors (CKIs) act as important regulators of CDK activity during both canonical and endoreplication cycles. Previous studies have identified the CKI Dacapo (Dap) as a key regulator of the endoreplication cycle in multiple tissues during *Drosophila* development. Dap is known to be targeted for destruction by the E3 ubiquitin ligase CRL4<sup>Cdt2</sup>, but our data suggest that another ligase may act in concert with CRL4<sup>Cdt2</sup> to control Dap accumulation and endocycle frequency. We hypothesized that the CRL1<sup>Skp2</sup> E3 ubiquitin ligase regulates Dacapo in coordination with CRL4<sup>Cdt2</sup>. We tested this hypothesis by generating transgenic flies that express RNA interference (RNAi) against Skp2 to reduce CRL1<sup>Skp2</sup> activity in endocycling salivary glands. We then dissected third instar larvae salivary glands and monitored DNA replication using EdU labeling and confocal microscopy. Our results show that salivary glands expressing RNAi against Skp2 have decreased S phase frequency, suggesting partial

inhibition of the endoreplication cycle in the absence of CRL1<sup>Skp2</sup> function. Future studies will determine whether Dap stability is altered in the presence of Skp2 RNAi. Our results indicate that E3 ubiquitin ligase CRL1<sup>Skp2</sup> regulates DNA replication in endocycling cells of the salivary gland, potentially through regulation of Dap stability.

#### **SAT-1054**

##### **MOLECULAR CHARACTERIZATION OF IRON STRESS RESPONSES IN SOYBEAN**

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Iron deficiency chlorosis (IDC) is a crop disease resulting from lack of useable iron and eventually results in yield loss at the end of the season. This is particularly important in the Midwestern part of the United States because soil conditions favor the development of IDC. Therefore, we are interested in characterizing soybean's short- and long-term response to iron stress. Our research takes advantage of 2 near isogenic lines that are 98% genetically identical but differ in their iron response. Clark plants are iron efficient, while IsoClark plants are iron inefficient and develop symptoms of IDC under iron-stress conditions. We have conducted an experiment comparing short-term and long-term iron stress by using a shocking method. Both Clark and IsoClark plants were grown in hydroponics in a greenhouse for a total of 10 days. A subset of plants were iron stressed for the entire 10 days whereas another set were iron stressed for the final 2 days of the experiment. We looked at transcriptional responses by QPCR and tested candidate genes by viral-induced gene silencing. Further, we used bioinformatic methods to compare RNA-seq data from the 48 generated samples. This approach allowed us to identify genes differentially expressed in response to short- and long-term iron deficiency and genes expressed in a genotype-dependent matter. Further, we documented the bioinformatic methods that allowed us to accurately store, retrieve, organize, analyze, and visualize biological data that could be a resource for other scientists.

#### **FRI-1048**

##### **GILZ REGULATES HEMATOPOIETIC STEM CELL SELF-RENEWAL**

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Hematopoietic stem cells (HSCs) establish, maintain, and on transplantation, can reconstitute the entire blood system. Attempts to generate functional HSCs from pluripotent cells have yielded cells of limited self-renewal ability which are of no therapeutic use. Increasing our understanding of the basic biology of HSCs will bring us closer to generating functional HSCs *in vitro*. To identify potential regulators of HSC function, we used microarray analysis to compare the transcriptomes of CD34+, CD38-, CD90+, and GPI80+ human fetal liver hematopoietic cells, a population highly enriched for self-renewing HSCs, to CD34+, CD38-, CD90+, and GPI80- cells, composed of closely related, but non-self-renewing progenitors. The gene Glucocorticoid-

induced leucine zipper (*GILZ*) was among the most differentially expressed genes uncovered by this analysis. As *GILZ* has been shown to regulate apoptosis in other stem cell systems and since effective regulation of apoptosis is vital for self-renewal, we hypothesized a role for *GILZ* in maintaining self-renewal by regulating HSC stress. We tested this hypothesis by infecting hematopoietic cells with lentiviral overexpression vectors for *GILZ*. After culture, *GILZ*-overexpressing cells showed a higher proportion of CD34+, CD38-, and CD90+ cells, a population enriched for HSCs, whereas control GFP-infected cells had lost this population, suggesting that *GILZ* can enhance self-renewal. Furthermore, lentiviral shRNA knockdown of *GILZ* in hematopoietic cells resulted in complete loss of the stem cell-enriched CD34+, CD38-, CD90+, and GPI80+ cell population, as compared to control-infected cells, revealing an essential role for *GILZ* in self-renewal. These findings call for further investigation into the mechanism by which *GILZ* regulates HSC function and will enable us to improve strategies to generate functional HSCs.

#### **FRI-1058**

##### **OVEREXPRESSION OF *C-JUN* LEADS TO *OCT-4* EXPRESSION AND ALTERNATIVE SPLICING**

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*OCT-4* regulates pluripotency and self-renewal in embryonic stem cells. It can encode three spliced variants known as *OCT-4A*, *OCT-4B*, and *OCT-4B1*. Unpublished data in our laboratory suggests the *c-Jun* transcription factor may regulate *Oct 4* gene expression. Data from the cell culture system suggests *cJun* binds to the *Oct4* promoter. We are using RT-PCR, western blot analysis, and reporter gene assays to test the function of this interaction.

#### **FRI-1061**

##### **UNDERSTANDING THE FUNCTIONAL ROLE OF LIPID DROPLET-MITOCHONDRIA CONTACTS**

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Lipid droplets are organelles important for the storage of neutral lipids in the cell. Their phospholipid monolayer membrane contains proteins crucial for the regulation of cellular lipid homeostasis. The increasing prevalence of lipid related diseases (e.g., obesity) emphasizes the significance of understanding the biological mechanisms by which lipid droplets carry out their functions. For over 50 years, extensive contacts between lipid droplets and mitochondria have been observed via electron microscopy. However, the function of these contacts remains poorly understood. We hypothesize that these contacts exist to increase energy production by directly channeling lipolytically released fatty acids into the mitochondria for  $\beta$ -oxidation. To determine whether the induction of lipid droplet-mitochondria contacts is sufficient to increase  $\beta$ -oxidation, we developed an FKBP-FRB inducible heterodimerization system that provides temporal control of lipid droplet-mitochondrial tethering. Fluorescence microscopic analyses indicate that our FKBP-FRB heterodimerization system rapidly induces lipid droplet-mitochondrial tethering without causing detrimental effects on organelle function that would lead to cell death. We will exploit this novel experimental system to measure and compare cell



survival, fatty acid transport, and  $\beta$ -oxidation levels in the presence or absence of induced lipid droplet-mitochondrial tethering. The results of these experiments will further our understanding of the underlying molecular mechanisms by which cells control lipid homeostasis and energy production.

#### **SAT-1064**

##### **IDENTIFYING FACTOR C, AN IMMUNE COMPONENT OF INVERTEBRATES, IN THE SQUIDS *EUPRYMNA SCOLOPES* AND *EUPRYMNA TASMANICA***

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The bobtail squid *Euprymna scolopes* and the southern dumpling squid *Euprymna tasmanica* are marine invertebrates that form symbiotic associations with the luminescent bacteria, *Vibrio fischeri*. Our laboratory is interested in understanding the effects on the immune system of animal interactions with beneficial microbes. One of the most ancient immune mechanisms in the animal kingdom is the complement pathway. The complement system consists of plasma- and cell-associated proteins that, after recognition of a foreign cell, interact with each other and activate the protein C3. C3 is the main component of this immune cascade, leading to opsonization and destruction of pathogens. Activation of C3 is usually accomplished by a protease that varies among organisms. C3 was already identified in the light organ (LO) from *E. scolopes*, the tissue that harbors *V. fischeri*, but until now, no protease has been identified to be responsible for its activation. In a recent transcriptome analysis, a sequence similar to factor C, a known C3-activator in the horseshoe crab *Tachypleus tridentatus*, was found to be expressed in the LO of *E. tasmanica*. The purpose of this study is to verify the presence of this protease in *Euprymna* sp. and characterize its expression profile in different tissues of the squid. Identification of factor C in *Euprymna* will provide a better understanding of how the immune system of molluscs functions and the type of molecular communication present between *Euprymna* squid and its bacterial symbiont, *V. fischeri*.

#### **SAT-1060**

##### **INVESTIGATING DEFENSE RESPONSES OF *NICOTIANA BENTHAMIANA* INVOLVING THE 14-3-3 GENE FAMILY IN VIRUS-INDUCED EFFECTOR-TRIGGERED IMMUNITY**

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Plants possess multiple tiers of immunity, the most specific of which involves resistance proteins that provide effector-triggered immunity (ETI). ETI is often associated with hypersensitive response (HR), a type of programmed cell death. The 14-3-3 gene family is conserved across eukaryotes and acts in myriad cellular processes, including plant immunity involving resistance (R) proteins mediating ETI. Using co-immunoprecipitation and mass spectrometry, we identified a 14-3-3 isoform from *Nicotiana benthamiana* interacting with the R protein Tm2-2 from *Solanum lycopersicum* (tomato), conferring resistance against tobacco mosaic virus (TMV) through recognition of the virus 30K movement protein (MP). By silencing *N. benthamiana* 14-3-3 homologs using virus-induced gene silencing (VIGS), roles in plant

defenses and the HR-like response are being investigated. The *14-3-3* homologs identified from the *N. benthamiana* genome database were cloned into the tobacco rattle virus vector pTV:00, transformed into *Agrobacterium tumefaciens* and agroinfiltrated into *N. benthamiana* leaves to induce *14-3-3* gene silencing. To detect roles for *14-3-3* proteins in plant resistance responses, *N. benthamiana* silenced for different *14-3-3* genes were examined for loss of HR-like responses when challenged with the MP in the presence of Tm2-2; the degree of silencing was assessed by RT-PCR. Additionally, interactions between the ten *14-3-3* genes described from tomato (TFTs) and Tm2-2 or the MP were examined by co-immunoprecipitation, as well as the effect of TFT overexpression on R protein-mediated HR. Data from these studies will be presented and the potential of a biological role for *14-3-3* proteins in TMV MP-induced immune responses will be discussed.

#### **FRI-1079**

##### **VANGL2 INFLUENCES PRIMARY CILIA IN THE MURINE MAMMARY GLAND**

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The mammary gland (MG), or breast, is a branched epithelial ductal structure that originates at the nipple and grows to fill the mammary fat pad. Each duct is composed of an outer layer of myoepithelial cells (MECs) encircling an inner layer of luminal epithelial cells (LECs). MG growth involves many factors coupled with signaling events including *WNT* and *Hedgehog* (Hh) signaling. The planar cell polarity (PCP) pathway, incorporating non-canonical *WNT* signaling, controls *VANGL2* function along with cilia orientation. *VANGL2* is required for normal development of branched organs such as the kidney and lung, but its function has not yet been identified in the MG. To investigate, we examined primary cilia in loss-of-function *Vangl2*<sup>lp/lp</sup> (LP) mammary outgrowths, comparing them to wild type (WT) by immunostaining with anti-acetylated tubulin to stain cilia structure and anti-gamma tubulin to stain the centrosome. We found that *Vangl2*<sup>lp/lp</sup> mammary outgrowth shows more than one cilium per cell in the LEC compartment and fewer cells containing cilia in the MEC compartment, suggesting that *VANGL2* regulates cilia numbers. In addition, we observe that *Vangl2*<sup>lp/lp</sup> mammary outgrowths have stunted growth and exhibit ductal size differences. Current studies focus on understanding how *VANGL2* regulates primary cilia, and if *VANGL2* signals through the *WNT/PCP* pathway or by novel mechanisms. Our studies provide new insight into mammary gland development.

#### **SAT-1084**

##### **EFFECTS OF PATERNAL HIGH-FAT DIET ON OBESITY IN OFFSPRING**

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Obesity and associated diseases such as cardiovascular disease (CVD) and diabetes and the corresponding rise in the incidences of obese infants have reached epidemic proportions. This rise in obese children under 12 months old would imply there is likely a genetic basis for the disease. A growing body of evidence has shown that a parent's diet can predispose offspring to

obesity. Recent studies have focused on the maternal effects of diet, but the extent by which paternal diet influences cardiovascular pathologies has yet to be elucidated. Compared to the complex mammalian model, *Drosophila* is a simplified, highly conserved metabolic system that has been established as an important model for studying the genetic mechanisms of heart function and obesity. Using *Drosophila*, we determined the paternal and maternal effect of high-fat diet (HFD) in the first (F1) generation and their correlation to the parental (P) generation. F1s generated were tested using triglyceride (TG) assays and motion-capture microscopy to monitor heartbeats to analyze systolic/diastolic diameters, heart period, and fractional shortening. F1 TG levels increased compared to controls, with PHFD males generating higher TG levels than HFD females. Progeny of HFD males experienced fractional shortening, and reduced heart period and diastolic diameter, with systolic diameter remaining unchanged, suggesting a paternal effect similar to that of the maternal. Future experimentation will determine whether this condition persists through the second generation, which could help elucidate each parent's effect, through diet, on their offspring's metabolism and susceptibility to developing diseases like CVD and type-II diabetes.

#### **FRI-1084**

##### **PROMOTER ANALYSIS OF THE *GRICH70* GENE: DELETION OF SP1, A PHYLOGENETICALLY CONSERVED ELEMENT**

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Once damaged, nerve fibers of the adult mammalian central nervous system (CNS) are unable to repair themselves; in contrast, the CNS of cold-blooded vertebrates has the inherent ability to regenerate damaged axons and thrive. To understand this capacity, studies on the nerve regeneration capabilities of these lower vertebrates have been carried out, particularly, studies on the optic nerve regeneration of goldfish. In this study, one aspect of the regulation of the *gRICH70* gene, a gene overexpressed during optic nerve regeneration in goldfish, was explored in a laboratory setting. After analyzing the genetic sequence of *gRICH70*, a few sequences within the promoter region containing several putative promoter elements were found to be phylogenetically conserved between the promoter regions of the homologous genes in goldfish and zebrafish. To determine the significance of one of these elements (Sp1) with regard to its role in transcriptional regulation, the element will be deleted and observations will be made on the effects of the deletion on the transcriptional activity of a promoter construct. The significance of the results is that achieving a better understanding of the regulation of genes required for nerve regeneration will offer insight into methods of increasing neuronal plasticity and promoting CNS nerve regeneration in humans.

**SAT-1075****EPITHELIAL *RXFP1* EXPRESSION IN MODELS OF INHERITED CYSTIC KIDNEY DISEASE**

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Autosomal dominant polycystic kidney disease (ADPKD) has no cure and affects approximately 600,000 Americans, with therapy costing more than \$2 billion per year. Mutant proteins linked to ADPKD cause up-regulated cellular proliferation, which contributes to renal cyst growth, fibrosis, and, ultimately, end-stage kidney failure. The relaxin-H2 hormone decreases proliferation in non-epithelial cell types indicating possible mitigation of ADPKD pathogenesis. Therefore, we treated cystic Cy/+ male rats with relaxin-H2 for two weeks and found that renal function was improved and cellular proliferation and cyst area were decreased in relaxin-treated animals compared to vehicle controls. Thus, we hypothesized that the relaxin-H2 receptor, *RXFP1*, is expressed on cystic renal epithelia and is therapeutically activated by relaxin-H2 ligand. To test our hypothesis, we used immunohistochemical, immunofluorescent, and spectral imaging techniques to evaluate *RXFP1* expression in multiple cystic kidney disease models. We identified *RXFP1* on the apical surface of renal cysts in all tested models. Furthermore, we determined *RXFP1* expression was not limited to specific tubule segments. Considering relaxin-mediated activation of *RXFP1* inhibits TGF- $\beta$  receptor signaling, we predicted that activation of downstream transcription factor, SMAD2, would be decreased in cystic rats treated with relaxin-H2. Thus, we developed a spectral imaging protocol to quantify nuclear expression of active, phosphorylated SMAD2. Our protocol will allow us to detect changes in cellular signaling within tissue sections. Conclusively, our findings regarding *RXFP1* expression on cystic kidney epithelia indicate that *RXFP1* is a potential therapeutic target for reducing pathogenic cellular proliferation in ADPKD.

**FRI-1075****URANIUM SORPTION UTILIZING CLAY PELLETS TO PRODUCE POTABLE WATER ON THE NAVAJO NATION: PURSUING A SURROGATE CATION TO MODEL URANIUM ABATEMENT**

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Many water sources on the Navajo Nation which straddles Arizona, Utah, New Mexico, and Colorado are contaminated with high concentrations of uranium. Some uranium concentrations exceed the safe drinking water level established by the United States Environmental Protection Agency (EPA) and the World Health Organization, 30 ppb and 15 ppb respectively. A study by the EPA Region 9 included 36 unregulated water samples; 5 water sources (14%) in 5 chapters exceeded the maximum concentration levels (MCL) for uranium. Clay pellets are an appropriate solution to remove uranium from polluted water sources to provide potable water. Our research objectives are two-fold: 1) that the final uranium concentrations are acceptable and at safe drinking water limits; and 2) find a surrogate for uranium because direct uranium studies are potentially dangerous and expensive. Therefore, we will investigate iron (II) bromide, iron (III) bromide, cobalt chloride, copper (II) acetate and cupric sulfate to find the best metal cation that mimics uranium abatement, and we propose an S-curve adsorption isotherm. Handheld colorimeters and fluorometry will be used to probe kinetics and thermodynamics for surrogate and uranium adsorption. We anticipate that uranium and surrogate adsorption will be optimal in a pH range of 1 to 6 and a redox potential range of 0.2 to 1.4.

**FRI-1092****RHO GTPASES AS THERAPEUTIC TARGETS IN OVARIAN CANCER**

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Rac1 and Cdc42 GTPases regulate proliferation, adhesion between cells, migration of cells, and invasion of cells, which are important for tumor expansion and malignant progression. Cdc42 and Rac1 were identified as targets that can be used with FDA-approved NSAID drugs and used as therapeutic cancer treatments. The data collected from the flow cytometry effector binding assay will play an important role in determining if chemically related but distinct drugs tested have different activities when tested on Cdc42 and Rac 1 activity. Our hypothesis is that repurposed R-Ketorolac will inhibit the activity against GTPases Rac 1 and Cdc42 in ovarian cancer cells. The results from the flow cytometer will quantitatively distinguish differences in activities and time course for the drug to have an inhibitory effect on cells. Ketorolac is used to help with inflammation and pain, and reports have also said that it has been seen to control the growth of tumors. The histogram that represents the addition of ketorolac will have a decrease in the height of the peaks. The decrease is important to see because the use of ketorolac should inhibit Rac1 and Cdc42. R-ketorolac is expected to inhibit the GTPase while S-ketorolac is not. With these comparisons, the data will show whether the FDA approved R-ketorolac is better in inhibiting these Rho GTPases and a candidate for drug repurposing.

**SAT-1087****CHARACTERIZING THE ROLE OF IFI16 IN HEPATITIS C INFECTION**

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Viral hepatitis is a widespread global problem with roughly 500 million people presently infected with hepatitis C virus (HCV) and hepatitis B virus (HBV). Hepatitis is characterized by chronic inflammation of the liver, which results in reduced liver function that can progress to liver failure and even hepatocellular carcinoma. Even with treatment, many patients progress to end-stage liver disease. Interestingly, humans and chimpanzees infected with HCV demonstrate a strong innate immune response to HCV infection. This is evidenced by detectable secretion of interferon proteins (IFNs) and upregulation of IFN-stimulated genes (ISGs) in the liver. IFNs are cytokines that recruit immune cells to sites of infection and help trigger the production of an anti-viral state within host cells. Most ISGs are involved in helping cells clear and fight viral infection. Particularly interesting is a relatively new ISG called interferon gamma-inducible protein 16 (IFI16). The IFI16 protein has known functions in the immune response to viral infections including binding viral DNA, promoting secretion of various cytokines (including IFNs), activation of anti-viral pathways, and inflammatory functions. We used primary human hepatocytes (PHH) and several hepatoma-derived cells as a model system to characterize the expression and function of IFI16 in the innate immune response of liver cells. Following treatment of cells with IFN and viral mimetics, we used Q-PCR and western blot

to characterize the expression of IFI16. We also knocked down and upregulated IFI16 and observed changes in the expression patterns of other ISGs through Q-PCR and western blot.

### **SAT-1093**

#### **CANCER-ASSOCIATED HEPARANASE DETECTION VIA GLYCO-NANOPROBE**

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Cancer is a non-communicable disease which causes nearly 8 million deaths worldwide each year. There is an urgent need to design and develop a robust, reliable and sensitive diagnostic tool to detect heparanase, a biomarker for metastatic cancer. Detection of this disease increases the survivability of certain cancer types. To detect breast cancer in mice, we have developed a nanometal surface energy transfer (NSET)-based gold, heparan sulfate dye (Au-HS-dye) nanoprobe which can detect increased heparanase activity. Metastatic cancer cells upregulate the expression of heparanase, an endoglycosidase which depolymerizes heparan sulfate (HS) expressed on both the cell membrane and extracellular matrix (ECM); this modification alters the ECM and results in pathogenesis. Our Au-HS-dye nanoprobe detects the upregulation of active heparanase in mouse plasma. The active heparanase digests the nanoprobe releasing the oligosaccharide-dye fragments resulting in an increase in fluorescence. This enhancement is recorded through an *in vivo* imaging system (IVIS) and charged coupled device (CCD) camera. In summary, we have developed a glyco-nanoprobe that diagnoses an active heparanase enzyme, a pathophysiological biomarker of cancer.

### **SAT-1098**

#### **EXPLORING HOW THE ENVIRONMENT AFFECTS MITOCHONDRIAL FUNCTION**

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Understanding cross talk between the environment and mitochondria will unravel the importance of environmental agents in regulating cell proliferation and tissue development. Defects in mitochondrial function are associated with numerous neurodegenerative diseases (Alzheimer's and Parkinson's) and in particular with metabolic syndromes. Data regarding cross talk between the mitochondrion and the environment led to the investigation of environmental agents such as micro biome, infection, and diet and their influences on mitochondrial function. Using genetically mutant fly lines that are incapable of producing viable forms of the terminal oxidase cytochrome c oxidase subunit Va (CoVa) in mitochondrial electron transport, we generate a sensitized background in which we can investigate the interactions between environmental agents and the mitochondrion. The genetic combination *eyeless-Gal4, UAS-CoVa<sup>RNAi</sup>*, partially impairs mitochondrial function in the developing eye. By itself, it does not cause significant developmental eye phenotypes. By looking for phenotypic enhancements, we are investigating whether the environment could influence mitochondrial structure, organization, and function using this sensitized background *in vivo*. The agent causing such enhancement is currently unknown. We have found that a compromised environment in which multiple generations of flies are raised in crowded conditions will lead to an enhanced

phenotype approximately 71% of the time. This preliminary result supports the hypothesis that an environmental agent can enhance the phenotype expressed in the compound eye, thus suggesting cross talk between the mitochondrion and the environment.

#### **FRI-1094**

##### **DEPLETION OF SEROTONIN, BUT NOT DOPAMINE, REDUCES REGENERATION OF LOST BODY PARTS IN *LUMBRICULUS VARIEGATUS***

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The freshwater oligochaete *Lumbriculus variegatus* possesses extraordinary powers of regeneration. A fragment only a few segments long can regenerate to produce a full-sized worm. In this study, we investigate the role of serotonin in regulating segment regeneration following complete transection of the body. Following transection into three equal pieces, worms (n = 10/drug) were allowed to regenerate for 10 days in pond water containing the drugs mentioned below. The regenerating regions were photographed, and the lengths of the regenerating regions were quantified using ImageJ. Depletion of all amine neurotransmitters (serotonin, dopamine, octopamine, and histamine) by 1 mM reserpine treatment greatly reduced regeneration of all body parts. Depletion of serotonin by treatment with the tryptophan hydroxylase inhibitor 10 mM 4-Chloro-DL-phenylalanine (PCPA) reduced regeneration to a degree similar to reserpine treatment. However, depletion of dopamine by treatment with the tyrosine hydroxylase inhibitor 2.5 mM  $\alpha$ -methyl-DL-tyrosine did not alter regeneration from control levels. Regeneration was unaffected by treatment with the serotonin 5-HT<sub>2/1C</sub>, histamine H<sub>1</sub> antagonist cyproheptadine (10 mM). Attempts to rescue regeneration ability in PCPA-treated worms are under current study.

#### **SAT-1071**

##### **DEEP SEQUENCING OF HIV-1 GAG REVEALS SEQUENCE DIVERSITY OF PROVIRAL RESERVOIR CELLS**

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HIV-1 infection is incurable due to the establishment and persistence of reservoir cells containing a provirus that is integrated into the cell host genome. Latent reservoir cells with proviral DNA will be able to escape the host immune response with no production of viral proteins. Additionally, due to their inactive replicative state, they remain unaffected by combined-antiretroviral therapy (cART). Therefore, the persistence of latent reservoir cells represents a major barrier to cure HIV. It is not clear how soon after acute infection the reservoir is established. We sought to determine whether the proviral reservoir is established during acute infection or after initiating cART. Sequences from 2 subjects from the Acute Infection Early Disease Research Program (AIEDRP) in California who started cART during the acute infection period were sampled at different time points: 1) from plasma collected at peak viremia during acute infection, 2) from plasma collected at the last viremic sample after initiating cART, and 3) from proviral DNA from PBMCs at several time points after complete

suppression of viremia on cART. Gag amplification products from these time points were subjected to tag linkage sequencing, aligned with reference sequences, and then used to build phylogenetic trees. Clonal sequencing results with limited sensitivity suggested that proviral reservoir sequences were established during the acute phase. This study will potentially determine whether virus during the acute phase establish latent HIV reservoir cells before initiating cART.

#### **FRI-1050**

##### **KLOTHO OVEREXPRESSION IN HUMAN LUNG EPITHELIAL CELLS DECREASE SENSITIVITY TO CIGARETTE SMOKE-INDUCED CELL DEATH**

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Chronic obstructive pulmonary disease (COPD) is the third leading cause of death in the United States. COPD is characterized by progressive airflow limitation. Cigarette smoke (CS) is the primary cause of COPD although exposure to air pollution, respiratory infections, and genetic factors also contribute to the disease progression. Exposure to CS induces oxidative stress in the lung which results in aging of the lung, leading to decreased proliferation of epithelial cells and the destruction of alveolar structure resulting in pulmonary emphysema. Although aging is a natural process, in the presence of CS, cellular senescence increases dramatically. Given that CS accelerates lung aging, therapies that significantly reduce or delay cellular senescence may be important in the overall management of this disease. The anti-aging gene, *klotho*, encodes a membrane bound protein, which has been shown to be a key regulator of oxidative stress, cellular senescence and inflammation. Mice with a defect in the *klotho* gene have a short life span and develop a syndrome resembling emphysema. In this study, the role of Klotho was investigated in human epithelial cells. Individual clones that stably overexpress *klotho* were generated through retroviral transfection and geneticin selection. Compared to control cells which were stably transfected with the retroviral control vector only, constitutive *klotho* overexpression resulted in decreased sensitivity to cigarette smoke-induced cell death *in vitro*. Therefore, our results suggest that enhancing *klotho* activity in pulmonary epithelial cells, particularly those exposed to CS, may be a promising strategy to alleviate the development of COPD.

#### **SAT-1058**

##### **CONSTRUCTION OF AN ADENOVIRUS VECTOR EXPRESSING THE LATENT LOCUS OF KAPOSI'S SARCOMA-ASSOCIATED HERPESVIRUS**

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Kaposi's sarcoma-associated herpesvirus (KSHV) is a human pathogenic  $\gamma$ -herpes virus and is the infectious cause of Kaposi's sarcoma (KS). The KS tumor is highly vascularized and is characterized by latently infected spindle cells of endothelial origin. While in the KS tumor 1 to 5% of the cells are lytic and producing new virions, greater than 90% are latently infected and not producing virus. Our lab and others have previously shown that KSHV induces angiogenic



phenotypes, altered cell metabolism, and oncogenic signal transduction. The current goal is to investigate if the major latent locus genes expressed by KSHV are sufficient to alter endothelial cells to induce the described phenotypes or if the small percentage of lytic genes play a paracrine role. We have cloned the entire 12 kbp KSHV latent locus into a gutted adenovirus expression vector that eliminates the contamination from expression of adenovirus genes. The latent locus includes the 4 genes expressed during latency and the 12 virally encoded microRNA loci. The adenovirus vector expressing the latent locus will be used to infect endothelial cells, and we will examine the cells expressing the KSHV latent locus for changes in factors involved in angiogenesis, metabolic pathways, and oncogenic cell signaling. If the latent genes recapitulate the pathways of a KS infection, this will indicate that latent gene expression alone, without the low percentage of lytic genes in the culture, is sufficient to induce many cellular pathways activated by KSHV that are relevant for the pathogenesis of KS tumors.

#### **FRI-1090**

##### **UNCOVERING THE STAGES OF REPROGRAMMING USING LINEAGE-SPECIFIC TRANSCRIPTION FACTORS**

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Induced pluripotent stem cells (iPSCs) can be obtained by overexpressing transcription factors such as Oct4, Sox2, Klf4, and c-Myc (OSKM). However, the molecular mechanisms and chromatin dynamics, especially in iPSC generation techniques that do not utilize the OSKM combination, are widely unknown. Here, we address the sequence of epigenetic events that occur during X chromosome reactivation in lineage specific transcription factor reprogramming to iPSCs. Reprogramming using retroviral infection of Klf4, c-Myc, Sox2, and Gata6 (SKMG6) coupled with epigenetic profiling of reprogramming intermediates revealed that SKMG6 ectopic expression may induce similar epigenetic changes as seen in OSKM induced reprogramming intermediates. Additional culturing conditions need to be applied in order to increase reprogramming efficiencies before thorough epigenetic profiling of SKMG6 reprogramming intermediates. Successful generation of iPSC with SKMG6 ectopic expression will allow us to understand mechanistically how transcription factors interact with chromatin to activate the pluripotency network.

#### **SAT-1068**

##### **A *DROSOPHILA* MODEL OF LAMIN-ASSOCIATED CARDIOMYOPATHY REVEALS ALTERED REDOX HOMEOSTASIS AND SHORTENED LIFE SPAN**

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Laminopathies are a group of genetic disorders caused by mutations in the LMNA gene encoding A-type lamins, intermediate filaments that line the inside of the nuclear envelope. Patients with laminopathies exhibit a spectrum of phenotypes including cardiac and skeletal muscle dysfunction, dysplasia, diabetes, and progeria. Among these, dilated cardiomyopathy

(DCM) is a major cause of death, yet the underlying mechanisms of pathology remain unknown. We have developed a *Drosophila* model to functionally dissect the roles of lamins in the heart. We investigated laminopathy-associated cardiac dysfunction by expressing *Drosophila* lamin (LamC), possessing mutations analogous to those that cause human disease, in the heart. Heart-specific expression of wild-type LamC caused no observable phenotypes. In contrast, heart-specific expression of mutant LamC caused conduction defects accompanied by either restricted or dilated cardiomyopathy, depending on the specific mutation. Expression of mutant LamC in the heart also caused nuclear envelope deformation, cytoplasmic aggregation of lamins, age-dependent altered redox homeostasis, and a shortened life span. Currently, we are investigating candidate genes and pathways that are able to modulate these pathological phenotypes, which will provide potential avenues for therapeutic intervention.

#### **SAT-1088**

##### **THE ROLE OF GRB7-RA DOMAIN OLIGOMERIZATION IN GRB7 PROTEIN SELF-ASSOCIATION**

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What causes 2 proteins to associate, or bind, to each other? We have discovered a characteristic of a model protein, the Grb7 protein, which allows us to address the issue of how proteins recognize each other. Grb7 is a 5-domain modular protein that dimerizes (and potentially trimerizes) through 2 distinct mechanisms. The larger contribution to dimerization takes place through the C-terminal SH2 domain. However, it has been recently recognized that Grb7 dimerization is also mediated to an appreciable extent by the tandem RA-PH domains. We modeled the Grb7 RA-PH domains based upon the available sister protein Grb10 domain structure. The Grb10-RA-PH domain structure indicates the PH domain could be primarily responsible for RA-PH domain dimerization. Yet, physical characterization of the Grb7-RA domain by our laboratory shows the RA domain alone is capable of multiply-associated forms. Based upon our modeled Grb7-RA-PH domains we will test the effect of mutations within the RA domain on oligomerization state. In contrast to the mutations suggested by the above modeling approach, we report the protein docking program Hex-8.0.0 predicts the C-terminal region of the Grb7-RA domain is most likely responsible for higher multimeric states. In the future, mutations in this region will also be explored to measure their effect on Grb7-RA domain oligomerization. Access to freeware protein modeling and docking programs provides valuable tools to test oligomerization interface prediction against actual laboratory measurements.

#### **FRI-1086**

##### **THE EFFECT OF THE OVEREXPRESSION OF THE CZF TRANSGENE ON SPERMATOGENESIS IN MICE**

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A sequential process of mitosis, meiosis and cellular differentiation takes place within the seminiferous epithelium, beginning with the spermatogonia and ending with spermatozoa.

Success of this life long process in men is essential for the production of sperm and more importantly the preservation of a species. This research seeks to understand consequences of the overexpression of CZF (CTCF zinc finger protein) in mice testis. It is hypothesized that overexpression of CZF will disrupt differentiation of spermatids. We found that average weight of testis in adult mice bearing the CZF transgene was 0.0657g, approximately half of the control, weighing 0.1025g. Consistent with this decrease in testis weight, CZF caudal sperm number was  $3 \times 10^6$  sperm, while the control contained a substantial  $21 \times 10^6$  sperm. This data confirmed a defect in spermatogenesis. We directed our focus to post-meiotic germ cells, and analyzed testes at postnatal day 24, a time when round spermatid differentiation begins. Average weight of day 24 testis showed a decrease from 0.0486g in control to 0.0256g in CZF mice (p-value = 0.0067). Using immunohistochemistry with an antibody specific to the acrosomal protein sp-10, we observed that germ cell production progressed normally in CZF mice up to round spermatid formation. We conclude that overexpression of the CZF transgene has a direct effect on the ability of round spermatids to differentiate into spermatozoa. Through further research on the specific pathway of spermatogenesis that this overexpression affects, we hope to be able to aid in discovery of novel treatments for men diagnosed with oligospermia.

#### **FRI-1085**

#### **BUILDING A PROMOTER SYSTEM FOR IDENTIFICATION OF GENE REGULATION INVOLVED IN AMYLOIDOGENIC LIGHT CHAIN PROTEO-TOXICITY**

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Amyloidoses are a family of diseases in which proteins mis-fold and aggregate as amyloid fibers in various organs. AL amyloidosis is the most common systemic amyloidosis in the United States and more than half of AL amyloidosis patients experience cardiac dysfunction with very poor survival rate. Recently, our laboratory found that amyloidogenic light chain proteins (AL-LC) elicit a cardiac proteo-toxicity via activation of STC1. Using gain and loss function assays our results showed that STC1 is critical for AL-LC induced redox stress, cellular dysfunction, and cell death *in vitro* and *in vivo*. Herein, we propose to use STC1 activation as a readout of AL-LC induced toxicity and screen for drug or small molecules that can prevent AL-LC mediated STC1 activation. Therefore, we aim to establish an STC1 reporter assay system to monitor the activation of STC1 using luciferase fluorescence. Using cloning techniques, we have transformed plasmids containing the human stc-1 promoter region into *E. coli* to amplify the quantity of the plasmid. We will transfect cardiomyocytes with STC1 to examine the luciferase activities in response to AL-LC. We will also screen for molecules that are able to prevent the activation of STC1 in the presence of AL-LC, with an established p38MAPK inhibitor as a positive control. Coupling with the administration of various membrane receptor inhibitors, this reporter system will allow us to reveal the interactome of AL-LC and the molecular mechanism by which AL-LC activates STC1 expression and results in the cellular pathology.

**SAT-1082****MER1, A SPLICING FACTOR, MAY HAVE OTHER IMPORTANT ROLES IN THE REGULATION OF RNA METABOLISM**

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Splicing is an essential step in gene expression that removes introns from pre-mRNA to make messenger RNA (mRNA). Pre-mRNA can sometimes be spliced in different ways to produce different mRNAs, a process known as alternative splicing. Mer1 is a yeast RNA binding protein that controls whether an alternative splicing event (intron retention) will occur or not in 4 different yeast pre-mRNAs expressed during meiosis. Many splicing factors in mammalian cells also function to regulate RNA stability and translation in the same cells where they regulate splicing. To identify other yeast transcripts possibly regulated by *Mer1* we added the HB tag to the N-terminus of *Mer1*. The HB tag is composed of a 6 histidine tag and a biotinylation tag. We will use the HB-Mer1 construct to identify RNAs bound to *Mer1* by using a cross linking-purification method (CLIP). After UV crosslinking in yeast, tagged *Mer1* and its covalently cross-linked RNA binding partners will be purified. The RNA will be recovered and sequenced and the sequences will be mapped to the genome. We expect the 4 known pre-mRNAs that *Mer1* binds to be present as well as other RNA that can help us learn whether *Mer1* has other roles in the regulation of RNA metabolism besides splicing.

**SAT-1050****DETERMINING THE FUNCTION OF THE *OCULOCUTANEOUS ALBINISM 2* GENE IN PIGMENTATION**

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Mutations in the *oculocutaneous albinism 2 (OCA2)* gene lead to the most prevalent form of the pigmentation disorder oculocutaneous albinism, characterized by the absence of pigment in the skin and eyes. This disorder results in increased skin cancer risk and pronounced visual defects. Despite the immense importance of the *OCA2* gene in pigmentation, the molecular function of *OCA2* remains unknown. Data from our laboratory suggests that *OCA2* might function as an ion channel residing in the membrane of melanosomes, organelles responsible for the production and storage of the pigment melanin. Consistent with the disease phenotype, we hypothesize that reduced *OCA2* expression in pigmented tissues will affect melanosome ion channel activity and subsequent pigmentation. Furthermore, we hypothesize that albinism-associated mutations in *OCA2* will affect channel activity required for melanosome function and pigment production. To test these hypotheses, we are using *OCA2*-targeted siRNA to reduce endogenous *OCA2* expression in pigment cells and site-directed mutagenesis to make specific *OCA2* mutations found in patients with oculocutaneous albinism disorder. We will then examine ion channel activity and melanin production in cells with decreased or mutated *OCA2*. Correlating the different *OCA2* variants' genetic identity, channel activity, and contribution to melanin production will allow us to determine *OCA2*'s significance in pigmentation. We

anticipate our results will help discern the molecular function of *OCA2* and directly assess its dysfunction in oculocutaneous albinism disorder.

#### **SAT-1092**

##### **DETERMINATION OF THE TOPOLOGY OF PORCUPINE**

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Wnt signalling is critical for proper embryonic development and adult tissue homeostasis. Wnt proteins require palmitoylation for optimal secretion and receptor binding. Porcupine (Porcn), a membrane bound O-acyl transferase (MBOAT) family member is thought to be the protein that palmitoylates Wnt. Porcn is localized to the endoplasmic reticulum (ER), Golgi apparatus, and plasma membrane. Porcn is known to mediate proper tissue patterning in developing embryos; however its topology is poorly understood. Determining the topology of Porcn may have useful applications in areas of embryonic development and targeted cancer therapies. Although numerous bioinformatic algorithms that predict membrane topology are available, no clear picture for Porcn has emerged. Therefore, our goal is to experimentally determine the membrane topology of Porcn. Our data using Myc tags orient the N- and C- termini toward the luminal and cytosolic regions of the ER, respectively. To further determine topology, we are using recombinant DNA technology, cellular transfection, and selective permeabilization immunofluorescence to visualize orientation of FLAG tagged motifs either within the cytosolic or luminal region of the ER. FLAG tags were inserted at amino acid sequences 118 and 145 to determine orientation of these protein motifs in the ER. Our preliminary results suggest the 118 and 145 amino acid positions are oriented toward the cytosolic region of the ER.

#### **FRI-1066**

##### **LOWER ABUNDANCE OF EUCHROMATIC POST-TRANSLATIONAL MODIFICATIONS ON ACTIVE GENES IS ASSOCIATED WITH RESISTANCE TO HEART FAILURE PHENOTYPES**

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Heart failure, a condition in which cardiac output is insufficient to meet the oxygen needs of the body, affects about 5 million Americans. During disease, there is a global shift in gene expression toward a more primitive phenotype, although the chromatin regulatory mechanisms responsible for this change are unknown. We hypothesize that heterochromatin formation in development is a mechanism by which this gene expression program is normally silenced in the adult heart and that differences in chromatin structure, resulting from underlying genetic/epigenetic differences, regulate heart failure susceptibility. Cardiac chromatin was measured following acid extraction of histone proteins in 2 strains of mice: BALB/cJ, which is susceptible, and BUB/BnJ, which is resistant, to isoproterenol-induced heart failure. The abundance of heterochromatic proteins (Linker Histone H1, Histone H3 Lysine-9 trimethylation (H3K9me3), H3K27me3), euchromatic post-translational modifications (PTM) (H3K4me3), and

other chromatin proteins (high mobility group B2/3 [HMGB2/3], active RNA polymerase II) were measured by immunoblotting. Linker Histone H1, H3K9me3, H3K27me3, HMGB2, and HMGB3 showed no difference between the strains, whereas the PTM H3K4me3 was found to be less abundant in BUB/BnJ. Lower levels of H3K4me3 imply fewer active genes and possibly less active transcription in BUB/BnJ. To confirm whether these findings hold true for susceptibility to heart failure, these experiments will be repeated in other heart failure susceptible or resistant mouse strains. Proteomic mass spectrometry is being used to measure the stoichiometry of chromatin structural proteins and to determine the role of genetic variation in the accessibility of chromatin.

#### **SAT-1048**

##### **THE ENDOCYTIC PROTEINS EPSIN AND THE HUNTINGTIN-INTERACTING PROTEIN 1-HOMOLOG (SLA2) COOPERATE FOR THE REGULATION OF CELL DIVISION IN YEAST**

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Huntington's disease is one of the several neurodegenerative disorders caused by expansion of the number of glutamines (Q) present in the protein huntingtin. Research has extensively focused on the toxic gain-of-function phenotypes acquired by the Q-expanded huntingtin. However, loss-of-function effects (inability to fulfill biological functions) that also result from Q expansion lead to neurodegeneration. The purpose of this project is to address the question of how the polyQ in huntingtin function to mediate protein-protein interactions. Although yeast does not have a huntingtin homolog, Q-rich regions are present in the endocytic protein epsin, and the Ent2 paralog is crucial for the regulation of cell division. Importantly, the yeast homolog of the huntingtin binding partner HIP1 (huntingtin interacting protein 1), known as Sla2, binds epsin. This further supports the idea that epsin's Q-rich regions may functionally replace huntingtin Q stretches in yeast. Using microscopy and extensive image analysis, we show that Ent2 dominant negative (E2DN) constructs (lacking C-terminal determinants) induce cell division defects in a Sla2-dependent manner. Conversely, truncations of the C-terminus of Sla2 suppress the E2DN-dependent phenotype. Further, our data suggest that Q-rich regions of Ent2 and the second coiled coil domain (CC2) of Sla2 is necessary for this regulation of cell division. To summarize, we have discovered the first physiological function of Q regions in endocytic proteins. We believe that this research will provide important insights into the function of Q that are disrupted upon expansion.

#### **FRI-1071**

##### **LOCALIZATION OF A DIVERGENT FILAMIN PROTEIN, FLN-2, IN *C.ELEGANS* LARVAL HYPODERMAL P-CELLS**

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During development of *C. elegans*, P-cells and their nuclei migrate from the lateral side into the ventral cord and give rise to the hypodermis, vulva, and motor neurons. Mutations in UNC-83 and UNC-84 proteins, which reside at the nuclear envelope, disrupt nuclear migration by

removing interactions between the nucleoskeleton and cytoskeleton. Genetic screens for enhancers of the nuclear migration defect of *unc-83/84* mutants have identified two genes, *toca-1* and *fln-2*; here we will focus on the large divergent filamin gene *fln-2* which may be involved in actin organization in the cytoskeleton. The morphology of cytoplasmic actin in P-cells appears normal prior to nuclear migration in *unc-84/fln2* mutants; however, the actin cytoskeleton is disorganized during nuclear migration. This suggests that FLN-2 may be involved in actin regulation during P-cell nuclear migration, and we hypothesize that FLN-2 is involved in organizing actin in these cells. To localize FLN-2, we are performing a CRISPR-Cas9 technique to insert a GFP tag at the C-terminus and a P-cell specific promoter of the *fln-2* gene for live imaging to determine where FLN-2 localizes. We have been able to PCR stitch together the GFP and 3' UTR and isolated the reporter gene *unc-119* in order to perform a Gibson assembly to create the construct for microinjection to create our transgenic worms. This will allow us to observe where FLN-2 localizes in P-cells during nuclear and cellular migration.

### **SAT-1083**

#### **THE ESTABLISHMENT AND CHARACTERIZATION OF PRIMARY CELL CULTURES DERIVED FROM THE CTENOPHORE *MNEMIOPSIS LEIDYI***

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Primary cell cultures are derived from tissue explants removed from an organism and maintained in an artificial environment. These *in vitro* cell cultures can be used to approximate the *in vivo* cellular environment, facilitate the isolation of specific cell types, and often provide a better representation of normal cell biology than immortalized cell lines. We have developed a primary cell culture system from the marine invertebrate *Mnemiopsis leidyi*, a lobate ctenophore that can serve as a proxy for adult somatic cells. Tissue isolated from ctenophore lobes is used to generate both a solid matrix for cell adhesion and support as well as a liquid overlay. This complex media provides essential nutrients to the cells. Approximately 72 h after explant incubation, several different cell morphologies are consistently observed. Many have active processes and are highly motile. Extended cell processes often connect cells. An additional distinct class of round proliferative cells that lack processes are reliably isolated. Experiments to further characterize these primary cell cultures will facilitate our ongoing molecular genetic analysis of unique aspects of cell differentiation associated with ctenophore development and evolutionary history from a cell biological perspective. We are currently employing several methods to characterize these cells that can be loosely classified by morphology as round cells, bipolar cells, multipolar cells, and elongated cells. We are performing experiments to monitor the functional response of calcium channels to small molecules as well as the use of rt-PCR to develop gene expression profiles associated with distinct cell morphologies.

## ECOLOGY/EVOLUTION

FRI-702

### PARASITE AND HOST COEVOLUTION: COMPARATIVE PHYLOGENETICS OF CHIPMUNKS (RODENTIA) AND PINWORMS (OXYURATA)

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Climate change may influence the evolution of pathogens such as parasites. However, the degree to which codivergence between host and parasite and environmental factors, such as climate, controls pathogen evolution remains unclear. The effects of geographic variation on divergence and the possibility of cryptic diversity have not been explored for many parasite species. Western chipmunks (Sciuridae *Tamias*) are distributed across western North America and inhabit a wide range of habitats. High geographic and species diversity of these hosts provides an opportunity to explore the relationship between host diversity and the diversity and evolution of their parasites. We examined one endoparasite of chipmunks, a pinworm (*Syphacia eutamii*), collected from ten species of chipmunks. DNA was extracted and a portion of a mitochondrial gene (cytochrome c oxidase subunit I) was sequenced to create a phylogenetic tree for comparison with host phylogenetic relationships. This comparison showed some congruent branching, which suggests partial codivergence of the parasite and host, with additional genetic structure partitioned by geography. Branching that does not match the host tree could be caused by other factors such as environment or host-switching. Although studies such as this often find evidence of cryptic diversity within parasite species, our preliminary results revealed no such diversity within this pinworm. Our results provide the background for further investigation of the complex mechanisms of host-parasite coevolution. Determining the mechanisms of host-parasite coevolution will lead to a better understanding of host-switching in parasites and potential implications of climate change on pathogen emergence.

SAT-626

### A META-ANALYSIS OF THE INFLUENCE OF TIMBER HARVEST ON NORTHERN GOSHAWK REPRODUCTIVE OUTPUT

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The northern goshawk (*Accipiter gentilis*) is a species of conservation concern, but despite decades of research, the sensitivity of reproduction to habitat quality remains uncertain. These relationships had yet to be systemically reviewed; therefore, we studied the effects of timber harvest on goshawk reproduction. To answer our question, we used a meta-analytic test which combines published statistical results into a single, stronger statistical value bounded by confidence intervals. We assembled all published studies that compared reproductive output in harvested and unharvested areas and compared reproductive success in relation to tree size near nests. A negative value for our standard effect size and an associated confidence interval that broadly encompassed zero ( $Z_r = -0.0634$  ; 95% CI = -0.3037 to 0.1769,  $N = 8$  studies) indicated that goshawk reproductive output was not negatively affected by harvest or absence



of older trees. While goshawks occupying territories near timber harvest do not suffer reduced reproduction, many goshawks may respond to timber harvest by abandoning nests, so we plan to conduct another meta-analysis determining the effects of harvest on site occupancy by goshawks.

#### **SAT-632**

##### **MYCORRHIZAL FUNGI TARGETED BY TWO CLOSELY RELATED MYCOHETEROTROPHIC ORCHIDS**

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Non-green, mycoheterotrophic plants have lost the capacity to fix carbon through photosynthesis, becoming specialized in obtaining carbon and energy through symbiotic relationships formed with particular species of fungi which link them to green photosynthetic plants. Roots of surrounding trees are colonized by ectomycorrhizal fungi that are parasitized by the mycoheterotrophic orchid *Corallorhiza*. We investigated the mycorrhizal community growing near three species of non-photosynthetic orchids, *Corallorhiza maculata*, *Corallorhiza wisteriana*, and *Corallorhiza striata* to better understand the community context in which mycoheterotrophy occurs. We hypothesized that *Corallorhiza* would be found in microsites where its preferred fungus is a dominant member of the fungal community. Twenty-two samples of *Corallorhiza* were collected in the Magdalena, Sacramento, Sandia, Sangre de Cristo, and San Pedro mountain ranges of New Mexico. Ectomycorrhizal (ECM) tree roots from soil samples were morphotyped and counted. Fungi from tree roots and orchid rhizomes were identified using PCR and DNA sequencing. ECM were ranked by relative abundance in the soil adjacent to the orchid rhizome. Fungi within the rhizomes of 12 orchids match ECM fungi found in the soil. *Russula* species, match 11 *C. maculata* samples and rank third in abundance within a sample, on average. Thelephoraceae matched one *C. wisteriana*, ranking second in abundance. Molecular analysis to identify host trees is still under way. Current results suggest, in small areas of soil where nearly 20 different species of ECM fungi occur, these two orchids target mycorrhizae that are relatively abundant compared with other fungi, though not always the dominant taxon in the community.

#### **SAT-628**

##### **RECENT GENETIC DIVERGENCE IN CORAL REEF FISH WITHIN A MARINE BIODIVERSITY HOTSPOT**

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Previous research has shown that speciation has occurred throughout the Coral Triangle, a biodiversity hotspot located in the tropical western Pacific Ocean, within different groups such as starfish, giant clams, and snapping shrimp, but this phenomenon is less understood in fishes. This area is the focal point of this research project. Pygmy gobies of the genus *Eviota* are excellent candidates for studying fine-scale speciation because of their high site fidelity, rapid turnover, and low dispersal capabilities. We used PCR amplification of 2 different genetic markers, a mitochondrial gene and a nuclear gene, to determine the relatedness of 128

samples from 23 putative species. The mitochondrial marker was able to tell us about any recent mutations that occurred between species, while the nuclear marker was able to show any slow evolving mutations that occurred between species. Preliminary results from analysis showed us that speciation is occurring all throughout the Coral Triangle, and that this phenomenon now includes fishes. We have data spanning at least 4 independently evolving species complexes that show similar genetic breaks or speciation boundaries within the Coral Triangle. These results suggest that recent speciation is occurring at fine geographic scales within the Coral Triangle and thus actively contributes toward the maintenance of the biodiversity hotspot.

#### **FRI-720**

##### **GEOGRAPHIC VARIATION WITHIN AND BETWEEN *CLARKIA* SISTER TAXA**

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We are investigating the evolutionary significance of geographic variation in seed mass and other reproductive traits among wild populations of 2 California native wildflower species, *Clarkia unguiculata* and *Clarkia exilis*. A large greenhouse experiment has been conducted to investigate genetically-based variation and covariation among flowering time, floral, and life history traits within and between both taxa. We are using the seeds produced by > 950 plants in this experiment to test whether seed mass and flowering time are genetically correlated under greenhouse conditions. Specifically, we will test whether correlations observed among maternal families within each species and among population mean are consistent with the differences between species. We will evaluate whether these traits may evolve independently in these species or whether a genetic correlation between them strongly constrains their independent evolution. Differences in seed mass between these species are also associated with differences in the elevation of wild populations; *C. exilis* is restricted to lower elevations than *C. unguiculata*. We will also test whether the association between seed mass and elevation observed in the field persists in a common environment. Statistical analyses will be conducted using the software program JMP. Seed mass has previously been found to be an indicator, or predictor, for a variety of species attributes, including the habitat types that a species may occupy. Revealing correlations between seed mass and other traits important to the survival of plant populations can contribute to our understanding of how wild species may evolve in response to environmental alteration and climate change.

#### **SAT-635**

##### **INTERACTIONS BETWEEN MANZANITAS AND COAST LIVE OAK AND THEIR EFFECT ON HERBIVORY BY DEER AND WOODRATS IN MARITIME CHAPARRAL**

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Work in maritime chaparral at Fort Ord in coastal California shows that biotic interactions including herbivory, competition, and facilitation affect the community. We investigated how interactions between manzanita shrubs and coast live oak affected browsing by black-tailed and

Monterey dusky-footed woodrats. We hypothesized that 1) oak saplings are less browsed by deer when they grow inside dense manzanita mounds compared to growing on their own; 2) oak saplings are negatively affected by competition from the manzanitas; and 3) young oaks may eventually outcompete the manzanitas when they become taller than the manzanitas. To assess these interactions, we measured the structure of manzanita clumps (e.g., height, intactness, distance from oak to manzanitas, and age of manzanita stems growing next to the oaks) and assessed browsing damage and the age of oaks from wood samples. Deer browsing is much higher in oaks growing outside compared to inside manzanita clumps, but woodrat damage did not change at all. Also, the average height with respect to age was higher in oaks growing inside a clump, showing that dense clumps of manzanita can benefit oak growth by making a natural fence that shelters young oaks from browsing, despite likely strong competition from the manzanitas. Furthermore, browsing on oaks increases as clumps become less intact. Finally, oaks within a clump are in average 7 years younger than nearby manzanitas, but manzanita growing immediately beneath taller, older oaks eventually die. These interactions potentially determine community composition of marine chaparral where oak trees might eventually become the dominant species.

#### **SAT-636**

#### **AN INVESTIGATIVE ANALYSIS OF COASTAL UPWELLING DYNAMICS ON ROCKFISH RECRUITMENT IN CENTRAL CALIFORNIA**

Serena Thurston, Mark Carr.

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Regional climate models suggest that global climate change will alter sea surface temperature, the intensity and direction of winds and ocean currents, and the frequency, intensity, and location of coastal upwelling along the west coast of North America. Past studies have suggested that all of these processes influence the transport and delivery of juvenile rockfish (*Sebastes* spp.) to adult populations associated with kelp forests along the coast of California. As prevalent components of both recreational and commercial fisheries along the west coast of North America, rockfishes are both economically and culturally important. Together, these predicted changes in ocean processes and observed effects on rockfish recruitment suggest that climate change may have profound effects on the size and dynamics of rockfish populations. The goal of this study is to better understand how changes in coastal winds and upwelling influence rates of larval recruitment to adult populations of rockfishes in central California. Our approach to better understand the relative importance of these processes in explaining variation in rockfish recruitment was to apply multiple regression analysis to a multiyear time series of annual rates of rockfish recruitment and annual variation in winds, water temperature, chlorophyll (as a proxy of ocean production), and coastal upwelling indices. SMURFs (standard monitoring unit for the recruitment of fishes) were deployed just offshore of coastal kelp forests to estimate annual variation in the level of recruitment of three species of rockfishes: *S. atrovirens*, *S. carnatus*, and *S. chrysomelas*. We are currently collecting and analyzing these data.

**FRI-637****THE COORDINATION OF LEAF STOMATAL AND VEIN TRAITS AND THEIR INFLUENCE ON WATER USE AND DROUGHT TOLERANCE IN LOS ANGELES URBAN TREE SPECIES**

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Physiological processes and anatomical adaptations including leaf vein and stomatal traits differ widely across different plant species. These traits are major determinants of plant performance, especially water use and response to drought. This study tested the hypothesis that leaf anatomy is a predictor of leaf physiology in urban tree species from the Los Angeles area. The goal was to determine if there was a correlation between leaf vein traits and stomatal traits with plant water use and growth, and measures of drought tolerance such as turgor loss point. Three leaf samples from at least 14 urban tree species were chemically treated so veins could be visualized under a light microscope and measured using imaging software. Stomatal traits were visualized and calculated from epidermal peels. We expected a positive correlation between vein density and stomatal density and a positive correlation of stomatal area with leaf hydraulic conductance and plant growth rate. We expected more drought tolerant species to have higher vein and stomatal densities. In addition, we expected sun leaves to have higher vein and stomatal densities than shade leaves. These results will further enhance the understanding of plant adaptation and plant diversity. Furthermore, the relationships between leaf anatomy and physiology can be critical in agricultural developments and engineering.

**SAT-634****TEST OF THE AMPLIFICATION MODEL FOR THE EVOLUTION OF LACTASE ACTIVITY IN *EBG***

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How genes evolve novel functions is a fundamental question in evolutionary genetics. Most inferences about molecular evolution are based on retrospective analyses of gene sequences and their functions. In contrast, experimental evolution can be used to test evolutionary hypotheses in real time. It has previously been shown that the *ebg* (evolved beta-galactosidase) locus in *Escherichia coli* can evolve a lactase activity in strains where the native lactase gene, *lacZ*, has been deleted. The natural substrate of the EBG protein is still unknown. We will test to determine if gene amplification plays a role in the evolution of lactase activity of the *ebg* gene. Specifically, we will test whether selection for multiple copies of *ebg* on lactose medium facilitates the evolution of the lactase activity of the gene. Duplications of the *ebg* gene will be constructed in *lacZ* deletion strains. Both deletions and duplications will be performed using  $\lambda$  Red technology. The rate of lactase evolution will be compared in strains that have 1 or 2 copies of *ebg*. If there is no selection for multiple copies of *ebg* during adaptation on lactose, strains with 2 copies should evolve lactase activity at a two-fold rate compared to strains bearing a single copy. In the event of natural selection for increased gene copy-number of the wild-type *ebg* gene because of a preexisting insignificant lactase activity, strains with 2 copies of *ebg* are expected to evolve lactase activity at greater than 2 times the rate relative to strains with a single copy.

**SAT-701****DEMOGRAPHICS AND MOVEMENT OF A SKY-ISLAND POPULATION OF *SCELOPORUS OCCIDENTALIS* (WESTERN FENCE LIZARD)**

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Populations isolated on mountain peaks, or sky islands, often have lower genetic diversity and are subject to increasing periods of drought due to climate change, both of which increase the risk of local extinction. Therefore, sky-island populations could make good indicators of the effects of climate change. We studied the sky-island population of *Sceloporus occidentalis* (western fence lizard) on Ord Mountain, California, in the Mojave Desert, to examine population demographics and measure individual movement. Based on the demographics of non-isolated populations of *Sceloporus occidentalis*, we hypothesized we would find 3 distinct age classes on Ord Mountain and that individuals would disperse throughout the habitat. We established 4 half-hectare plots (50 × 100 m), 2 north and 2 south of a long-term monitoring site on Ord Mountain. We captured *S. occidentalis* over 2 days in June, marked each individual, and measured mass, snout-vent length (SVL), substrate temperature, and GPS coordinates. Individuals fell into 3 age classes based on SVL: juveniles, sub-adults, and adults. Based on recapture data, we estimated the population density to be 35 individuals/hectare, similar to other populations. Movement among individual lizards varied greatly. Individual movement ranged from 1 to 68 meters (mean: 12.76 m ± 17.19, SD). Movement was generally on the east-west axis and may have followed rock formations. Our findings suggest that some individuals dispersed rather than moved within their home range. Population density and the presence of multiple age classes indicate that the Ord Mountain population is robust.

**FRI-638****TRACING THE PAST: INVESTIGATING CURRENT AND ANCESTRAL BODY SHAPE EVOLUTION IN DEEP-SEA DRAGONFISHES (STOMIIFORMES)**

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The deep sea is a cold and dark area of the ocean (below 200 meters) that is among the least explored habitats on Earth. While much remains to be discovered about the deep sea, there are some groups of fishes that are well known from this habitat, such as the order Stomiiformes (dragonfishes). Dragonfishes are among the most abundant vertebrates on earth, and their body shapes show considerable variation from the spade-like marine hatchetfishes (Family Sternoptychidae) to the elongated eel-like dragonfishes (Family Stomiidae). For this study, we are interested in investigating how different body shapes have evolved in fishes that are adapted to living in the deep sea and open ocean. Dragonfishes (Stomiiformes) are located almost exclusively in deep-sea environments, and they will be used in this study because of the variation of short and elongated bodies across different species. Dragonfishes are typically brown, black, or in some cases silver, and they possess bioluminescent organs on their bodies

that are used for camouflage, to hunt for food, to attract a mate, or as a defense mechanism. We collected over 250 photos of specimens, representing taxa from all five families that spanned the body shape diversity of dragonfishes. Photos of the specimens were analyzed with geometric morphometric approaches to quantitatively assess changes in body shape. We then compared body shape evolution within the group to hypotheses of evolutionary relationships of dragonfishes to infer patterns of body shape evolution over time in this highly diverse group of deep-sea fishes.

#### **SAT-630**

##### **EVALUATING HABITAT PREFERENCES OF MIGRANT AND RESIDENT BIRD COMMUNITIES IN A SUBTROPICAL DRY FOREST IN PUERTO RICO**

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Food and shelter are limiting factors for optimal development of migratory birds for which habitat selection is crucial for survival and successful migrations. Habitat characteristics such as forest degradation and human impact can affect available resources, deterring avian development. We seek to test the hypothesis that bird presence will be greater in sites with greater habitat diversity and forest maturity. The abundance, species richness, and diversity of avian communities were evaluated in relation to general characteristics of three sites with distinct degrees of disturbance and successional stages: S1—mature, S2—early monoculture, and S3—early mixed. Using fixed-radius point counts and mist netting, bird presence and fitness (body condition index, BCI) was quantified for three seasons: migratory dry (M2, January-April), non-migratory (NM, May-August), and migratory wet (M1, September-December). To assess body condition and possible interactions within habitat, special focus was placed on resident bananaquit (*Coereba flaveola*), a sedentary species known to roost in their foraging habitat. Preliminary results show higher diversity and number of species present for S3, a mixed early-successional secondary forest. BCI for bananaquits varied within sites, and results were inconclusive; further examination is required. To better understand the interactions, vegetation and arthropod profiles need to be included in the analysis. Contrary to previous evidence, even degraded habitats can prove to be beneficiary to avian communities and need to be considered. This information can help establish better conservation plans for migratory and resident birds, aiding in the restoration and conservation of favorable spaces.

#### **SAT-637**

##### **EVALUATING HABITAT USE OF YEARLING CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) IN THE COLUMBIA RIVER ESTUARY USING TROPICALLY TRANSMITTED PARASITES**

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The spring-run Chinook salmon (*Oncorhynchus tshawytscha*) of the mid/upper Columbia River genetic group are listed as endangered under the Endangered Species Act, and the Columbia

River estuary, on the border of Oregon and Washington, serves as an important habitat for subyearling Chinook salmon. However, the extent to which yearlings use and benefit from the estuarine habitats is unclear as they are believed to move rapidly through the estuary. This study examined trophically transmitted parasite assemblages in yearling Chinook salmon to evaluate their use of the estuary for foraging. Salmon were collected with a purse seine from 2 locations in the lower estuary between the years 2007 and 2012. They were examined for tags and clipped adipose fins, measured, and identified to a genetic stock group. Stomach contents were examined by National Oceanic and Atmospheric Administration and Oregon State University researchers for diet. Stomachs and intestines were also examined for trophically transmitted parasites. Preliminary results from 34 mid/upper Columbia River chinook salmon collected in 2007-2009 show these yearling salmon harbor a trophically transmitted parasite community that consists of freshwater and estuarine parasite taxa including trematodes, nematodes, and acanthocephalans. Results suggest interannual variation with higher prevalence of trematodes in 2009 (83%) (n = 12) followed by 2008 (81.8%) (n = 10) and 2007 (25%) (n = 12), and higher prevalence of nematodes in 2007 (58.3%) compared to 2008 (36.4%) and 2009 (8.3%). The overall prevalence of the marine-estuarine parasite species *Hysterothylacium aduncum* (25%) suggests that yearling chinook salmon are feeding in the Columbia River estuary.

### SAT-733

#### FUNCTIONAL TRAIT COMPARISON OF POTENTIALLY INVASIVE EXOTIC PLANTS AND CO-OCCURRING NATIVE ANALOGUES IN A SOUTHERN CALIFORNIA RIPARIAN HABITAT

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Restoration efforts typically focus on the problem of invaders displacing native species. Investigating functional traits of exotic species can help evaluate the potential for their spread. Functional traits are morpho-physio-phenological traits that impact fitness via growth, reproduction, and survival. Similar traits between natives and exotics may indicate that a native can compete with an exotic and provide biotic resistance to invasion. We compared the functional traits of three pairs of co-occurring native and exotic species with similar life forms (herbaceous forbs, vines, and trees) and hypothesized that each exotic species would be functionally equivalent to its native counterpart. The herbaceous pair consisted of native mugwort (*Artemisia douglasiana*) and exotic mint (*Mentha spicata*). The vines were native wild grape (*Vitis girdiana*) and exotic periwinkle (*Vinca major*), and the trees were native coast live oak (*Quercus agrifolia*) and exotic olive (*Olea europaea*). We sampled 6-8 individuals from each species at 3 sites along the ephemeral Bell Creek, Trabuco Canyon, California, and measured specific leaf area (SLA), leaf dry-matter content (LDMC), chlorophyll content indexed by mass (CCI), and leaf water potentials. The trees were similar for all traits except water potential. Periwinkle had similar traits to grape but had a lower LDMC. The mint had a lower LDMC than mugwort and higher SLA and CCI. The trait similarity of the oak and grape to their paired exotics indicates they may provide some invasion resistance; however, management efforts may need to focus on other strategies to prevent the spread of mint.

**FRI-721****LITTERFALL DYNAMICS AT DIFFERENT DISTANCES INTO THE FOREST FROM PRIMARY TO SECONDARY FOREST ECOTONE IN LAS CRUCES, COSTA RICA**

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Edge effects can alter forested ecosystems due to changes in light, wind, and soil moisture that occur when forests become fragmented. Litterfall dynamics are affected by edge effects due to phenological responses of plants and animals to the altered abiotic factors. We predict that there will be a difference in litterfall biomass from the edge to the interior of a primary forest. In this study we placed ten 50 x 50 cm baskets on a 100 meter transect at the ecotone of a secondary and primary forest. We placed litterfall baskets at 0 meters, 30 meters, and 100 meters into primary forest. Litterfall was collected once a week over a 3 week sampling period, sorted into 5 categories to get individual biomass of leaves, reproductive parts, woody parts, mosses, and miscellaneous. There was no difference in litterfall biomass from the ecotone into the primary forest. However, litterfall complexity was greater 100 m into primary forest compared to either 0 or 30 m into primary forest. Greater litterfall complexity could provide more niches to support greater arthropod diversity, and this may affect decomposition and nutrient cycling.

**FRI-701****GENETIC MAPPING OF DEVELOPMENTAL DELAY PHENOTYPE IN *CAENORHABDITIS BRIGGSÆ* TROPICAL X TEMPERATE HYBRIDS**

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Populations of the nematode *Caenorhabditis briggsæ* show great genetic variation between geographical locations, making them well suited for speciation studies. Biological species are defined as populations whose hybrids have zero fitness. Previous experiments have shown a reduction in fitness exhibited by a developmental delay in F2 hybrids of tropical (AF16) and temperate (HK104) strains. The developmental delay phenotype present in *C. briggsæ* F2 hybrids signals the onset of speciation between temperate and tropical strains. AF16 homozygosity at an unknown locus in the middle of chromosome III has been associated with this developmental delay phenotype. We hypothesize that the developmental delay phenotype in F2 hybrids is caused by a locus on chromosome III that is homozygous for the AF16 allele. To begin the identification of the genetic variant on chromosome III that produces hybrid developmental delay, we are performing genetic mapping of the delay phenotype using polymerase chain reaction genotyping. Preliminary results show 15% occurrence of F2 hybrid delay and a perfect association between locus cb-m205 and the developmental delay phenotype. These results suggest that the frequency of developmental delay in F2 hybrids is not a simple Mendelian trait and that the developmental delay locus is near cb-m205. Future efforts will involve genotyping loci across chromosome III to identify recombination breakpoints in F2 hybrids and narrow down the locus where genes implicated with developmental delay are found. By finding the genes significant to the onset of speciation, a better understanding of the process of allopatric speciation and evolution can be obtained.



**FRI-632****HYBRIDIZATION RATES OF *TYPHA LATIFOLIA* AND *TYPHA ANGUSTIFOLIA* IN THE MIDWEST UNITED STATES**

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Two plant species- native *Typha latifolia* and exotic *T. angustifolia*, hybridize to form *T. x glauca* (F1 hybrid). Fertile F1 hybrids backcross to either parental species creating advanced-generation hybrids. These hybrid swarms threaten wetlands by forming dense monocultures that out-compete native species and thus lower plant biodiversity. Our goal is to use previously-identified microsatellite markers from *T. latifolia*, *T. angustifolia*, and a related species, *T. minima*, to quantify hybridization rates in cattail populations across the Midwest. We have sampled plants from 32 populations in 7 Midwestern states and have identified 6 previously described microsatellite loci that discriminate between the parent taxa and hybrids. We are currently screening 7 additional loci. Contrary to a smaller study in the same region that found *T. latifolia* stands to be rare, we found that approximately 30% of the populations sampled contained pure *T. latifolia*. However, none of the populations contained pure *T. angustifolia*. Similar to another study of comparable size, we found regional differences in the relative abundances of each species. In comparing our 2 most sampled states, Illinois and Minnesota, we found a significantly greater abundance of *T. x glauca* in Minnesota than in Illinois ( $P = 0.034$ ). Furthermore, we found that the abundance of hybrids is negatively correlated with the abundance of the native *T. latifolia*. Our preliminary data suggest that the hybrid is replacing both parental species within the Midwestern region, which could have implications in the management of *Typha* stands as well as conservation of the native parental species.

**SAT-719****INTRA-SEXUAL SELECTION IN *HABRONATTUS CLYPEATUS* JUMPING SPIDERS**

Harleen Athwal, Damian Elias.

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Natural selection is the process that allows the spread of heritable traits through a population. If individuals with specific traits are favored over others, this leads to changes in allele frequency within the species. Sexual selection is a similar process, but, in this case, traits directly influence reproductive fitness and may drive changes in the frequency of traits such as color, size, and ornamentation. Sexual selection research on the jumping spider genus *Habronattus* has shown that males use combinations of vibratory songs, colorful ornaments, and motions to entice females to mate. This type of inter-sexual selection is hypothesized to be driving the evolution of elaborate behavior and ornamentation. While many studies have explored inter-sexual selection, the role of intra-sexual competition has yet to be explored in this group. For this study, we will examine competitive interactions between male jumping spiders in *Habronattus* by staging contests and analyzing the factors that predict contest success as well as decision-making strategies. We will test the hypothesis that heavier and larger males are more likely to win contests. Using evolutionary game theory, we will also test

competing hypotheses on decision-making. This study will be the first to explore the intra-sexual competition in the emerging model taxon *Habronattus* and set the stage for future sexual selection work in jumping spiders.

#### **FRI-635**

##### **POPULATION ECOLOGY OF SPOT (*LEIOSTOMUS XANTHURUS*) IN THE MARYLAND COASTAL BAYS**

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Spot (*Leiostomus xanthurus*), a saltwater fish belonging to the family Sciaenidae, is found in estuaries and coastal waters along the eastern coast of United States, Gulf of Mexico, and the Caribbean. Spot support significant commercial harvests concentrated along the Atlantic coast of the United States from the Chesapeake Bay through the Carolinas. Because of their abundance, spot are considered to be ecologically important, influencing the structure and function of estuarine systems. The Maryland Coastal Bays Trawl and Seine Survey (MCBTSS) collected data from 1990 to 2012 to monitor the spot population. The MCBTSS sampled with a bottom trawl in 20 different sites across the five coastal bays once a month. Because the weight of each fish was not previously collected, we are using a length-weight relationship to convert the length of each fish into weight so we can calculate the biomass of each bay. This study aims to understand ecological dynamics of spot in Maryland's coastal bays and to determine recruitment and biomass patterns as a response to seasonal environmental conditions. The results from this research will be used as resource for commercial and recreational fisheries as well as being a useful tool for conservation efforts because it can give an overall view of the survival ability of populations.

#### **SAT-702**

##### **DISTRIBUTION AND SPECIES RICHNESS MODELING OF THE WATER SCAVENGER BEETLE GENUS *TROPISTERNUS* IN NORTHEASTERN SOUTH AMERICA (COLEOPTERA: HYDROPHILIDAE)**

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The biodiversity of the world's vast tropical regions is poorly understood. To increase our knowledge of what lives in these difficult-to-access areas, known occurrence records may be used to create species distribution models for taxa and areas of interest. Here, we focus on the distribution of aquatic beetles of the genus *Tropisternus* (Hydrophilidae), which along with other macroinvertebrate groups, are used in the bioassessment of freshwaters. The study area is centered on northeastern South America (Venezuela, Guyana, Suriname, and French Guiana). Published literature was reviewed to extract previously reported distribution records for *Tropisternus*. This data was combined with unpublished occurrence records from several museum collections. Additionally, recent collections of *Tropisternus* obtained from the study area were identified to species and georeferenced. A total of 14 species were found in the region, including eighteen new country records (Venezuela: 3, Guyana: 5, Suriname: 8, French

Guiana: 2). From this combined dataset of occurrence records, species distribution models for each species were made using the program Maxent. These maps show possible invadeable habitats as well as potential current distributions. Conclusively, species of the genus *Tropisternus* inhabit a larger range of northeast South America than was previously known.

#### **FRI-636**

##### **COMPARISON OF RECAPTURE RATES BETWEEN PARTHENOGENETIC *ASPIDOSCELIS TESSELATA* AND GONOCHORISTIC *ASPIDOSCELIS MARMORATA* (SQUAMATA: TEIIDAE) AT THE INDIO MOUNTAINS RESEARCH STATION, HUDSPETH COUNTY, TEXAS, UNITED STATES**

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Recapture studies provide general information on a species' biology, such as home range, growth, reproduction, and longevity. This study was conducted to determine if there is a significant variance in recapture rates between syntopic parthenogenetic and gonochoristic whiptail lizards *Aspidoscelis tessellata* and *A. marmorata*, respectively. Because of potential distinctions between the two species, such as size, reproductive potential, foraging behavior, and wariness, it was hypothesized that their recapture rates will be significantly different. Lizards were captured at the University of Texas at El Paso's Indio Mountains Research Station, Hudspeth County, Texas. Prospect Pits and Ranch House arrays were surveyed from 2011 through 2013, using 81 pitfall traps. For future identification, lizards were given unique toe clip numbers involving one or two digits. In 2011, 156 lizards were sampled, with 38 recaptures; 30 of 84 were *A. marmorata* and 8 of 72 were *A. tessellata*. In 2012, 127 lizards were captured, with 42 recaptures; 37 of 58 were *A. marmorata* and 5 of 69 were *A. tessellata*. In 2013, 99 lizards were sampled, with 27 recaptures; 24 of 58 were *A. marmorata* and three of 41 were *A. tessellata*. Results indicate that *A. marmorata* had a significantly higher recapture rate ( $200/91 = 46\%$ ) than *A. tessellata* ( $182/16 = 9\%$ ), which validates the hypothesis that there are differences between the 2 species. The implications of these results provide useful facts for other researchers to pursue projects on the ecological and physiological causes for the differences in recapture rates between these 2 whiptail species.

#### **SAT-638**

##### **THE EFFECTS OF HERBICIDES ON ARBUSCULAR MYCORRHIZAL FUNGAL ASSOCIATIONS IN ROOTS**

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Arbuscular mycorrhizal fungi (AMF) are fungi that are essential in ecosystem restoration as they allow native plants to establish mycorrhizal associations that improve nutrient acquisition in plants. Southern California landscapes have greatly been invaded by *Brassica nigra*, or black mustard, a non-mycorrhizal plant that has been known to exhibit allelopathic effects that suppress the growth of beneficial fungi in native soils, causing a strain to the native environment. In landscapes impacted with mustard, herbicide application is a common practice for removing the invasive species. Some fungal species are known to metabolize certain toxic

components found in herbicides, but we expect that prolonged exposure may inhibit the AMF. Two different types of herbicides, wick and selective, are utilized to remove *Brassica nigra*. Wick sprays seed banks and weeded areas with broad spectrum glyphosate, while selective herbicide selectively marks for the invasive plant, desiccating the mustard root. We hypothesized that AMF root colonization will be higher in soils treated with the selective herbicide, because the specificity of the application will not permit prolonged exposure of the herbicidal toxins to the native plants. To compare herbicide effect, soils were collected from both plots sprayed with wick and selective treated plots. To assay for the AMF community in these soils, the growth of the native grass, *Stipa pulchra*, was used to “bait” the fungi. *Stipa pulchra* growth was monitored weekly, and after 90 days, bioassays were harvested and plant roots were stained to compare AMF colonization in roots from the 2 different herbicides.

**FRI-633**

### **CONSEQUENCES OF DROUGHT ON AQUATIC INVERTEBRATES IN INTERMITTENT STREAMS**

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Intermittent streams are seasonal streams, which only flow during certain parts of the year. Seasonal drought affects intermittent streams by decreasing streamflow and water levels. When intermittent streams stop flowing, some individual pools dry completely (temporary pools) whereas others remain wetted across the dry season (perennial pools). Our objective is to understand how seasonal drought affects the abundance and species richness of aquatic invertebrates in both perennial and temporary stream pools in John West Fork, an intermittent stream in northern California. We monitored invertebrate populations monthly from June to October 2012, using a standardized timed-sweep method with a D-net, in 3 perennial pools as well as three temporary pools. The temporary pools dried completely during early September, while water depth in the perennial pools declined by an average of 27% by the end of the study. We analyzed the samples by sorting the invertebrates to order first, and then identifying them to the finest taxonomic level practical (usually genus). We will use these data to compare species richness as well as total invertebrate abundance at different stages of the summer in individual pools. As water levels in the pools decrease, we expect species richness and abundance to decrease as total habitat available contracts and water quality conditions deteriorate (e.g., lower dissolved oxygen). Because aquatic invertebrates are an essential food source for many species, such as fish, understanding how seasonal drought affects aquatic invertebrates will provide insight into the effect of drought on the ecosystem as a whole.

**SAT-627**

### **MOLECULAR EVOLUTION OF THE *CYTOCHROME-B* GENE IN MOLES (LIPOTHYPHLA: TALPIDAE) WITH VARYING LEVELS OF FOSSORIALITY**

Brian Rodriguez, Jorge Salazar-Bravo.

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Members of the family Talpidae are broadly distributed in Asia, Europe, and North America and present a rich variety of anatomical and physiological specializations that have enabled them to exploit a diverse range of habitats: terrestrial, semi-aquatic, aquatic/fossorial, semi-fossorial,

and fossorial. It is known that the energetically demanding lifestyle, coupled with the hypoxic atmosphere characteristic of the subterranean and aquatic environment may change the selective regime of genes that encode proteins involved in cellular respiration. The molecular evolution of the *cytochrome-b* gene, a mitochondrially-encoded gene participating in oxidative phosphorylation in talpids is the model of interest. It is hypothesized that the colonization of the subterranean and aquatic niches created regimes of positive, directional selection in the *cytochrome-b* gene. Methods such as GTR Gamma+I, HyPhy, Maximum likelihood estimates using RAxML GUI with 1,000 bootstrap replications, and TreSAAP were used to detect the presence and directions of selection at the molecular level require a phylogenetic tree for the group of interest. The results concluded that the rates of synonymous (dS) and nonsynonymous (dN) substitutions and  $\omega$  along different branches, across codons, and simultaneously across codons and along lineages in the family, and, preliminarily concluded that this gene appears to be evolving under purifying selection as only 2 codon positions demonstrated the effect of diversifying selection. Despite numerous studies to that effect the phylogeny of this group remains controversial. In order to combat this, future projects will be aimed at reconstructing a well-resolved phylogenetic tree for the family.

#### **SAT-631**

#### **PHOTOSYNTHETIC CHARACTERISTICS OF INVASIVE *DELAIREA ODORATA* AND NATIVE COASTAL SAGE SCRUB PLANTS**

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Cape ivy (*Delairea odorata*) is an invasive plant from South Africa, introduced to the United States in the mid-1800s. This herbaceous, evergreen vine out-competes native species and has created large monocultures along California's central coast, replacing native coastal sage scrub. To date, studies on cape ivy have focused on the result of its growth. Few studies have investigated the attributes that allow its successful invasion. We tested the hypotheses that leaf-level photosynthetic capacity and water-use efficiency were greater in *D. odorata* as compared with 8 native coastal sage scrub plants in the same area. We compared the physiology of cape ivy with that of eight native perennial plants. Live leaves were measured and their stomatal conductance, photosynthesis, transpiration, and water use efficiency were determined using the LI-6400 Portable Photosynthesis System. Preliminary results show that the rate of stomatal conductance in cape ivy is half that of native plants on hot, sunny days, and its water use efficiency is more than 10% better than *Baccharis pilularis*, which suggests that cape ivy is better at closing its stomates and preventing water loss. We are continuing field measurements to compare all 9 plants in fog and full sun. A better understanding of the attributes of invasiveness may be useful for predicting invasiveness.

**FRI-627****IMPACTS OF INVASIVE *TAMARIX* AND ITS HYBRIDS ON INFAUNA AT SAN DIEGUITO LAGOON**

Anita Arenas, Christine Whitcraft, Tania Asef.

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*Tamarix* spp., introduced from Eurasia and Africa to North America in the 1800s, is one of the most invasive species in the United States. Its impacts are well-known in riparian and desert ecosystems. Yet, little is known about how *Tamarix* affect salt marshes. We hypothesized that the impact of *Tamarix* on the infaunal macroinvertebrate community in a Southern California salt marsh would vary with the genetic type of *Tamarix* (1 of 2 hybrids). This study was conducted in San Dieguito Lagoon, a salt marsh located in north San Diego County, California. Infaunal invertebrate samples were collected in a paired design under *Tamarix* canopies (both pure and hybrid species) and under non-*tamarisk* canopies. This study found higher infauna diversity under non-*tamarisk* than under *Tamarix* ssp. and higher infauna diversity under hybrid *Tamarix* than pure *Tamarix chinensis*. The presence of *Tamarix* spp. altered invertebrate community composition in the marsh microhabitat, increasing the abundance of an isopod *Littorophiloscia richardsonae* (90% of total composition) relative to non-*tamarisk* canopies (39% of total composition). These discoveries suggest that removal of pure *Tamarix* should be prioritized over removal of hybrid *Tamarix* in salt marshes for restoration strategies. Further studies still need to be conducted on the driving mechanisms behind the observed differences in the infaunal community.

**FRI-634****ANALYSIS OF INTERSPECIES ATTRACTION USING EXTRACTED PHEROMONES FROM ITHOMIINE BUTTERFLIES**

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Ithomiine butterfly males consume pyrrolizidine alkaloids of the dead shoots of *Heliotropium indicum* L. and other species for mating, defense, and chemical communication purposes. Pheromones, derived from pyrrolizidine alkaloids, are released through androconial hairs. Ithomiine butterflies have many mimetic color patterns that warn predators they are toxic. During a lek, or at a multi-species aggregation, males display these hair pencils to attract a mate. Females must be able to locate and distinguish their own species from mimics and similar species to reproduce. The purpose of this study was to determine if different species of the Ithomiine butterfly tribe differentiate each other by scent. Ithomiine butterflies were caught at the Las Cruces Biological Research Station in Costa Rica. Male Ithomiine butterfly pheromones of conspecifics and heterospecifics were extracted from androconial hairs with the use of hexane. With butterflies of both genders, a choice test was conducted with pheromones from conspecifics, and then a second choice test was conducted with pheromones from heterospecifics. Preliminary results reveal that butterflies were more likely to be in the area of the enclosure where pheromones from the same species were released. Interactions with distant and closely related species' pheromones were not as common as conspecifics

interactions. This research will increase the overall scientific knowledge of the Ithomiine butterfly tribe, contribute to the total awareness of the use of pheromones within the Ithomiine tribe and mimics, and provide information about behaviors exhibited by Ithomiine butterflies toward their species and other species.

#### **FRI-629**

##### **IS IT POSSIBLE TO ACCURATELY ESTIMATE CARCASS DECOMPOSITION**

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One of the most challenging components of a death investigation is estimating the postmortem interval (PMI). This is most likely due to corpse decomposition being poorly understood. Recently, a decomposition scoring system (Total Body Score, TBS) was established to visually describe and document the progress of decomposition. However, it remains to be determined if TBS, an indirect measure of decomposition, is correlated to actual mass loss, a direct measure of decomposition. This is important to determine because a newly established method to estimate PMI requires an estimate of soft tissue mass loss. If it can be determined that mass loss and TBS are correlated, then it would be possible to estimate soft tissue mass loss more effectively. This, in turn, will allow us to estimate PMI more effectively. To address this gap in knowledge, a 15-day experiment was conducted to measure mass loss and its relationship to TBS. Three swine carcasses were placed in a field setting in Palolo Valley, Oahu, Hawaii. Carcasses were weighed (kg) and TBS was measured twice a day for 13 days, and once a day for the remainder of the experiment. A significant ( $P < 0.0001$ ,  $R^2 = 0.956$ ) positive relationship between mass loss and TBS was observed. This relationship was described with a quadratic equation ( $y = 0.0021x^2 - 0.021x + 0.052$ ) where  $y$  = soft tissue mass loss (%) and  $x$  = TBS. It is expected that this approach will aid criminal investigators in estimating postmortem interval more effectively.

#### **FRI-719**

##### **CHARACTERISTICS OF REPRODUCTIVE HABITAT FOR HARPY EAGLES IN DARIEN PROVINCE, PANAMA**

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Harpy Eagle (*Harpia harpyja*), largest raptor of the Americas, is globally near threatened and regionally critically endangered. Their reproductive cycle is distinctive among all raptors and can take up to 3 years to successfully rear juveniles. Therefore, obtaining detailed knowledge of their reproductive habitat would assist in creating new management policies and conservation guidelines. We measured variables describing forest characteristics within five 0.5 ha plots around each of 10 nesting and control trees in the Pacific region of Darién Province, Panamá. Variables measured were tree family richness; tree density, height, and diameter; shrub density; and coverage of understory and canopy foliage. We used Akaike's information criterion to compare a series of models specified *a priori* to assess the importance of forest characteristics. Results indicated that Harpy Eagles nested in forests having high heterogeneity

represented by high tree richness, variability in tree height and forest openings. Findings improve our understanding of suitable reproductive habitat and provide greater ability to conserve their environment to ensure the population growth.

#### **FRI-626**

##### **MORPHOLOGICAL AND GENETIC CHARACTERIZATION OF CALIFORNIA PIPEFISHES (SYNGNATHIDAE)**

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California pipefishes are highly diverse and particularly difficult to identify consistently. The widely used Miller and Lea *Guide to the Coastal Fishes of California* does not include all of the recognized Californian province species. We reexamined the key morphological traits emphasized in pipefish keys, seeking to improve the diagnostic separation of pipefish species. Our data indicate that certain features, such as barred markings or a truncated snout, are reliable in separating 3 recognized species in California: kelp pipefish (*Syngnathus californiensis*), barred pipefish (*S. auliscus*), and snubnose pipefish (*Cosmocampus arctus*). In contrast, a combination of morphological and molecular analyses (mitochondrial 16S and COI) have so far not supported 3 currently recognized species as distinct from *S. californiensis*: the bay pipefish (*S. leptorhynchus*), chocolate pipefish (*S. euchrous*), and barcheek pipefish (*S. exilis*). Thus, all could be synonymous with *S. californiensis*. Future work will further test these conclusions and our goal is to produce a more useful dichotomous key to California pipefishes based on updated taxonomy. We expect to add more pipefish localities and species sequence comparisons and extend what we learn to improve characterization and identification of juveniles. The results from this study will be beneficial to fishery biologists working in the field to improve pipefish identification.

#### **FRI-625**

##### **HERITABILITY OF BRIGHT COLORATION IN THE PIPEVINE SWALLOWTAIL (*BATTUS PHILENOR*)**

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Two primary contexts for the adaptive evolution of bright coloration are competition for mates (mate choice) and avoiding predator attacks (warning coloration). Bright animal coloration can be iridescent, in which the surface appears to change color with changing viewing or illumination angle. Bright animal coloration can also be produced by pigments, which do not appear to change color with changing viewing or illumination angle. The pipevine swallowtail, *Battus philenor*, is unique in having both sexual signals and warning coloration that include iridescent and pigment components, both of which are variable in color. The aim of our study was to examine the role genes play in producing this variation, providing a sense of potential indirect benefits of female choice. We tested the hypothesis that color variation has a genetic component. We predicted that in a full-sib analysis there should be greater variation in the coloration of the sexual and warning signal among families than within families. We reared *B. philenor* under standard laboratory conditions and analyzed heritability using a full-sib analysis.



We collected reflectance measurements for components of the sexual and warning signal iridescence using a spectrophotometer and CLR to extract brightness, hue, and chroma values. We used a multivariate ANOVA to analyze the warning signal variation, and a generalized linear mixed model to analyze the sexual versus warning signal variation in males with significance value of 0.05 (IBM SPSS, v. 21). Our results indicated a genetic component to coloration, implicating indirect benefits in *B. philenor* female mate bias.

#### **SAT-633**

##### **EVOLUTIONARY REFERENCE POINTS FOR THE CONSERVATION OF LEEDY'S ROSEROOT, A RARE AND ENDANGERED CLIFF-DWELLING PLANT**

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Plants in the genus *Rhodiola* are interesting because of their biogeography, their potential medicinal uses, and the rarity of some *Rhodiola* taxa. We studied 3 North American *Rhodiola* taxa: *R. rhodantha*, an alpine species native to the central and southern Rocky Mountains; *R. integrifolia* ssp. *integrifolia*, an arctic and alpine species of western North America and Siberia; and *R. integrifolia* ssp. *leedyi* (Leedy's roseroot), a rare and endangered cliff dwelling plant known in four populations in Minnesota and 2 populations in New York. We tested the genetic variability of Leedy's roseroot populations and estimated their effective to actual population size ratios ( $N_e/N$ ). We compared 10 microsatellite markers from Leedy's roseroot (134 individuals, 4 populations), *R. integrifolia* ssp. *integrifolia* (16 individuals, 4 populations), and *R. rhodantha* (31 individuals, 6 populations). Preliminary analyses reveal 18 alleles for Leedy's roseroot and  $N_e/N$  ratios ranging from 0.1 to 0.9 (95% CI of 0.03- $\infty$ ). *R. integrifolia* ssp. *integrifolia* and *R. rhodantha* have 45 and 55 alleles,  $N_e/N$  ratios of 0.89 (95% CI of 0.64-1.76) and 0.59 (95% CI of 0.74-1.39) respectively. More microsatellite markers are needed to reduce the 95% confidence intervals. The restricted range of Leedy's roseroot, and its relatively small population sizes (200 – 6,000), along with the lower levels of genetic variability suggest that the populations are losing genetic variability and might be at risk of inbreeding depression. Leedy's roseroot habitat should be protected, seedbanks should be established, and Leedy's roseroot populations should be monitored for signs of numerical decline.

#### **FRI-628**

##### **PREY SELECTION DYNAMICS OF NATICIDAE GASTROPODS ON ARCOIDEA BIVALVES**

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Size-selectivity exhibited in nature is rooted in the relationship between the cost of obtaining a prey and the subsequent energetic rewards rendered by its consumption. Using this theory, we hypothesized that the predation patterns of shell-drilling Naticidae gastropods were mandated by the size of Arcoidea bivalves, a well-known prey. A random sample of bivalve shells was collected from Otter Island (a state-protected island in South Carolina), and measurements of shell length and borehole diameter were taken from digital images using ImageJ software. Gastropod size and borehole size are assumed to be proportional, as literature previously

states. Although the field data is still undergoing analysis, we predict the correlation between the size of Naticidae gastropods and the size of Arcoidea will confirm the presence of size-selectivity.

#### **FRI-630**

##### **BIRD CALLING FREQUENCY VARIES WITH HABITAT, WEATHER, AND TIME OF DAY IN A COSTA RICAN TROPICAL FOREST**

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Bird vocalizations were studied during the rainy season at Parque Nacional Volcán Tenorio in northwestern Costa Rica. Vocal communication among birds is of particular importance but may be impeded by weather patterns and other environmental factors. Our goal was to understand how bird species distributions and calling behavior are affected by short-term weather changes and habitat in a tropical forest environment. The site is particularly interesting for its high diversity of bird species and rapidly shifting weather conditions. A total of 100 one-minute recordings were made in a stratified random design, stratified by time of day. Calls of 21 bird species were recognized from the recordings, as compared with 28 bird species directly observed in the field. The number of calls per minute ranged from 0 (21% of the total sample) to 53. The forest site had fewer bird calls (mean = 11.0 calls per minute) than the open site (mean = 24.6 calls per minute). Calling frequency varied with time of day; the highest levels were in the early morning. The frequency of bird calls decreased or stopped altogether during rainy weather conditions. The density of calls per minute did not conform to a random dispersion, but showed a clumped pattern in time. Sound spectrograms of bird calls from open and forest sites were compared.

#### **SAT-720**

##### **EFFECTS OF SENSORY MODALITIES ON MATING SUCCESS IN THE *DROSOPHILA NEOCORDATA* AND *DROSOPHILA AUSTROSALTANS***

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Reproductive isolation is a combination of mechanisms that prevents 2 different species from reproducing. One behavioral mechanism, courtship, consists of transmitted signals along with behavioral patterns. Different sensory modalities convey these signals and some of the messages being transmitted carry information about the readiness and quality of an individual that has come into contact with a potential mate. Species within the genus *Drosophila* vary in how much they rely on each sensory modality to communicate. These sensory channels include vision, gustation (taste), touch, olfaction (smell), and audition (hearing). In our lab, we have been studying the relative use of different sensory modalities within the *Drosophila saltans* group because these species differ greatly in their courtship song signals and the necessity of courtship song for mating success. This project focused on *D. neocordata* and *D. austrosaltans*. To compare the importance of each sensory modality, we ablated vision by covering the eyes,

gustation by removing foretarsi (the location of gustatory receptors), touch by removing midtarsi (involved in females touching males), olfaction by removing antennae, and audition by removing aristae. Even though both species have unique courtship, males in both rely on their ability to use foretarsi in order to taste the female. When foretarsi are removed, the latency between contact and initiation of courtship is longer than the control. We will be able to compare the results from *D. neocordata* and *D. austrosaltans* to the other saltans species to gain further insight into the evolution of reproductive isolation in *Drosophila*.

## ENVIRONMENTAL SCIENCE/STUDIES

### FRI-613

#### COMPARISON OF SEEDLING REGENERATION AND LIGHT AVAILABILITY IN AN EXPERIMENTAL CLEAR CUT AND REFERENCE FOREST STAND IN THE HUBBARD BROOK EXPERIMENTAL FOREST, NH

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We studied the course of regeneration for tree seedlings following an experimental clearcut at the Hubbard Brook Experimental Forest. We compared the present day seedling layer in lower- and mid-elevation herb plots between a 30-year-old clear cut and a 100-year-old stand. We posed the question: does light availability affect seedling regeneration in terms of seedling composition and abundance? A total of 500, 1 m by 1 m plots will be analyzed for their composition and seedling demography. We relate seedling density and diversity to leaf litter and light availability in addition to stand age. We also present the sequence of seedling regeneration in permanent plots over the 30 years post clear cut in the experimentally cut forest. It is essential to understand how an ecosystem will rehabilitate in the case of a natural or man-made disaster. Studying the regeneration of tree species allows the scientific community to aid in rehabilitating disturbed areas. We expect to find a direct correlation between seedling regeneration and canopy composition.

### SAT-618

#### WHAT IS STRESSING OUT OUR STREAMS?

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The conversion of forest into other uses such as agriculture is known to cause harmful effects to streams in the surrounding area, including increased water temperature and changes in organic matter inputs (e.g., woody debris). This study sought to assess the independent and interactive effects of organic matter input on ecosystem processes such as primary productivity in a tropical montane stream system. We hypothesized that changes in woody debris inputs associated with agricultural activity would increase rates of ecosystem processes, particularly primary productivity. To test this hypothesis, we conducted a controlled experiment using

streamside flow-through mesocosms within the secondary forest of the Las Cruces Biological Station in San Vito, Costa Rica. Our mesocosm experiment contained 8 flow-through channels. Treatments consisted of either rock substrate or rock, leaf litter, and woody-debris substrate. These treatments simulated agricultural and forested stream substrates, respectively. We then estimated primary productivity by measuring algal biomass within each mesocosm once a week for a total of 2 weeks. We expect that decreases in organic matter inputs increase primary productivity, which in turn increased the algal biomass.

#### **FRI-600**

##### **USE OF HONEY MESQUITE AS A POTENTIAL PHYTOREMEDIATOR OF 2,4-DINITROTOLUENE (2,4-DNT): ELECTROANALYTICAL STUDIES**

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The chemical 2,4-dinitrotoluene (2,4-DNT) is a precursor of the explosive trinitrotoluene (TNT), and it is widely used in the manufacturing of dyes, munitions, and plastics. Due to its common use, several sites around the world are contaminated with this chemical. *Prosopis glandulosa*, commonly known as mesquite, has been used in heavy metal phytoremediation. Mesquite produces large amounts of biomass, grows quickly, and has a large transpiration rate. Because of its deep root system, this plant may have the ability to accumulate other contaminants. The aim of the present work is to determine if mesquite is able to uptake and accumulate 2,4-DNT inside its tissues and to apply cyclic voltammetry as a complementary technique for the fast identification of 2,4-DNT. Mesquite plants were grown in a hydroponic system and exposed to 2,4-DNT at  $1.0 \times 10^{-3}$  M and  $1.0 \times 10^{-4}$  M. Extracts from roots, stems, and leaves were analyzed separately by cyclic voltammetry using a glassy carbon electrode (GCE). Extracts obtained from 2,4-DNT at  $1 \times 10^{-3}$  M treatment show higher peaks in the voltammogram revealing some interactions compared with voltammograms from control plants. Physical changes were observed in treated plants and compared with control plants. Chlorophyll content was measured in mesquite leaves from all treatments. Chlorophyll content in leaves from plants exposed to 2,4-DNT at  $1.0 \times 10^{-4}$  M was an average of  $32.3 (\pm 8.1)$  and  $18.2 (\pm 5.0)$  for plants exposed to 2,4-DNT at  $1.0 \times 10^{-3}$  M compared to  $18.66 (\pm 13.1)$  in control plants. Further analysis will be done using high pressure liquid chromatography (HPLC) to quantify 2,4-DNT in plant extracts.

#### **SAT-607**

##### **TAXONOMIC ASSESSMENT OF PERIPHYTON COMMUNITY IN THREE SUBTROPICAL STREAMS OF PUERTO RICO**

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The periphyton community composition plays an important role as a biological indicator of nutrient impairment in streams and rivers. Other abiotic factors could regulate stream composition and structure such as geomorphology, light, temperature, grazers, and flood disturbances that vary with the seasons of the year, spatial factors, and natural phenomena. In

this study, three rivers contrasting in nutrient conditions were assessed: Mameyes, with the least nutrient concentrations and the most clean watershed; followed by Guanajibo and Río Piedras which have the highest nutrient levels, but low dissolved oxygen and fecal coliforms caused by human recreation. Periphyton presented a possible method to define chemical differences in these streams. Periphyton was colonized on concrete blocks as the growth media with a 6 cm diameter PVC on the upper surface. Then, the outer area of the cylinder was scrubbed, and the material inside the cylinder was poured into a 500 ml amber bottle and preserved with 10% formaldehyde or 2% glutaraldehyde. The artificial substrates were installed, and samples were collected after 3, 7, and 10 d and a month of colonization. Many species were identified. Their relative abundance (individuals/mL) and biodiversity, using Shannon's index, were determined. The Guanajibo and Río Piedras sites exhibited an abundance of periphyton, as opposed to the Mameyes site due to its nutrient limitation. The Heterokontophyta group (diatoms) dominated the communities on artificial substrates within the first 10 days of colonization; after a month, the communities on the artificial substrates were similar in composition to those of naturally occurring substrates (rocks).

#### **FRI-607**

##### **SOIL DEVELOPMENT ON SHALES OF THE SAN SEBASTIAN FORMATION, PUERTO RICO**

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The Susquehanna Shale Hills Observatory (Penn State) links a latitudinal transect of shale soils in different climates from Wales to Puerto Rico. The aim of the Puerto Rico research is to serve as the southernmost anchor for analysis of the development of shale weathering profiles in a humid, tropical climate. A small stream in a ravine has shown low concentration and removal of cations and soluble ions from the study area. Field work at the site near the Juncal community includes two, 2-meter pits and two trenches distributed within the study area. Physical descriptions of these soil profiles show that red clay dominates the soil formation, matching previous descriptions that the area soils are ultisols. The soil profile is more than 6 meters deep, and chemical analysis of the soil samples vs. shale bedrock showed a loss in cations, such as K<sub>2</sub>O (0.65%) and CaO (0.35%), with increases in Al<sub>2</sub>O<sub>3</sub> (17.67%) and Fe<sub>2</sub>O<sub>3</sub>T (10.14%). From bottom to top in the soil profile, cations are higher (K<sub>2</sub>O, about 0.92%; CaO, about 16.41%) and sesquioxides are less abundant (Al<sub>2</sub>O<sub>3</sub>, about 9.27%; Fe<sub>2</sub>O<sub>3</sub>T, about 4.31%). The chemical compositions of the soils in the Juncal area behave similarly to 3 of the U.S. transect sites (Alabama, Tennessee, and Virginia) that also show high accumulation of sesquioxides (Al<sub>2</sub>O<sub>3</sub> about 15% - 20% and Fe<sub>2</sub>O<sub>3</sub>T, about 7% - 10%) and a low percentage of cations (CaO, about 0.1% - 10% and K<sub>2</sub>O, about 0.5% - 4.2%). Climate and location appear to be the key factors to understand the soils in this study area where weathering processes develop faster and soil profiles tend to be deeper and thicker than farther north.

**FRI-610****QUANTITATIVE ANALYSIS OF CURLY-TOP VIRUS WITHIN CHILE PEPPER FIELDS IN NEW MEXICO**

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Curly-top disease in New Mexico chile pepper fields has a negative impact, causing financial hardship for chile-pepper farmers. Curly-top virus strains are vectored by leafhoppers, *Circulifer tenellus*, that survive on weeds such as London rocket, *Sisymbrium irio*. The leafhopper moves into chile fields and transmits the virus to the pepper within minutes of feeding on the plant making pesticides ineffective. Weeds surrounding chile fields are reservoirs of the virus and leafhopper, making weed removal a potential control method for disease reduction. We believe that weed removal will decrease disease occurrence; however, it is unknown to what distance from the field weeds need to be removed. To study this, we examined the correlation of virus strain and quantity in weeds near infected chile plants. We recorded locations for both weeds and infected chile plants. Leaf samples were collected in Dona Ana County, New Mexico. Chile peppers collected showed symptoms of curly-top disease, and weed samples were taken from weeds closest to infected chile plants. DNA was extracted from the samples and tested using polymerase chain reaction (PCR) and quantitative PCR specific for the coat protein region. Results gave us quantities and strain identifications of curly-top virus. Infected chile peppers and weeds were mapped to identify patterns of curly-top disease infection in relation to weed location. Our findings provide recommendations to chile farmers for more productive control measures in managing curly-top disease in the near future.

**FRI-601****CONCEPTS OF WATER TREATMENT CHEMISTRY USING FERRATE IN A SMALL TREATMENT SYSTEM**

Albert Baxter<sup>1</sup>, Joseph Goodwill<sup>2</sup>, David Reckhow<sup>2</sup>.

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Reservations have small water treatment facilities that are at an inherent disadvantage due to their small size and, in some cases, remote location. Also, limited funding and a shortage of technical expertise create maintenance concerns for these treatment facilities. In collaboration with the University of Massachusetts Amherst, Haskell Indian Nations University took on the challenge of evaluating a cleaner, simpler and economically viable chemical reagent that can help with water treatment systems. Facilities on the reservations have an opportunity to use iron (VI) ferrate as a chemical reagent to clean raw water for human consumption more effectively. The focus of the study was to evaluate water treatment with ferrate, which is potentially more effective and less prone to the unwanted side effects of traditional procedures for water treatment. Also, the water treatment's impact on land contamination and its effect on the environment were considered. We tested for quality from the water supplies of 2 different locations in Kansas, the Potawatami and the Kickapoo reservations. Water treatment parameters of interest included testing for pH, hardness, alkalinity, iron, and manganese levels before filtration with the treatment of ferrate, metal fractionation of the raw water before and

after filtration, and the absorbance of ultraviolet light as a surrogate measurement for organic carbon. Results indicate ferrate is a powerful oxidant and disinfectant. It reduces the use of other chemicals such as coagulants, caustic substances, and oxidants such as chlorine. In this way, ferrate can provide a more simple solution for cheaper, safer water.

#### **SAT-600**

##### **SINGLE-WALLED CARBON NANOTUBES (SWCNTS) IMPACT THE CLASSIC EFFECTS OF CHEMICAL CONTAMINANTS: A MECHANISTIC EXAMINATION OF CO-EXPOSURES TO ETHINYLESTRADIOL AND SWCNTS IN FISH**

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Single-walled carbon nanotubes (SWCNTs) are a type of nanomaterial (NM, < 100 nm) used in numerous industries including electronics, energy storage, and biomedicine. As the use of NMs increases, their potential adverse effects on ecosystems have come into question as we have limited understanding of associated health impacts. As SWCNTs are highly sorbative, they may interact with chemical contaminants in the environment, thereby altering their biological effects. Ethinylestradiol (EE2) is a synthetic estrogen of birth control pills found in surface waters and linked to feminization of fish and altering reproduction through activation of estrogen receptors (ERs). Based on these observations, we hypothesized that SWCNTs would alter the defined activity of EE2 by limiting availability through sorption to SWCNTs. To test this, we determined the impact of SWCNTs on EE2 binding and activation of the largemouth bass (LMB) ER using *in vitro* fluorescence polarization binding affinity and luciferase reporter gene assays, respectively. Our findings showed that SWCNTs effectively bound EE2, rendering it unavailable for binding and activating the ER. To determine if similar responses occurred *in vivo*, LMB were gavaged with mixtures of EE2 and SWCNTs. We are currently measuring the expression of *vitellogenin* (*Vtg*), a gene normally induced by EE2, by qRT-PCR. We anticipate that EE2-increased *Vtg* mRNA will be markedly repressed by SWCNTs. Overall, results of this study suggest that SWCNTs can alter steroidal-based responses in aquatic models and advance our understanding of the interactions of NMs and environmental contaminants, which is important for developing effective environmental risk management strategies.

#### **FRI-604**

##### **ASSESSING THE EFFECTS OF NUTRIENT ENRICHMENT IN ARCTIC AQUATIC ECOSYSTEMS**

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As a result of Arctic warming trends, permafrost soils are thawing at lower depths than historic records show, consequently releasing more nutrients into freshwater ecosystems. This, along with evaporation caused by higher temperatures, has resulted in higher nutrient concentration in Arctic aquatic ecosystems, which has the potential to increase aquatic production. Primary producers in freshwater ecosystems such as phytoplankton and periphyton are typically nutrient limited by nitrogen (N), phosphorus (P), or a combination of nitrogen and phosphorus (NP), which can be the result of frequent changes by N and P limitation over time. Phytoplankton depends on nutrients from the water column. In

order to assess pelagic algae nutrient limitation, we completed *in situ* studies on the Arctic tundra. Water was collected from the water column at three different sites during the summer of 2013. Water was released into 500 ml bottles that were attached to a PVC frame that suspended them 20 cm below the water surface. The nutrient addition treatments consisted of 400 µg/L KH<sub>2</sub>PO<sub>4</sub> (P), 400 µg/L NH<sub>4</sub>NO<sub>3</sub> (N), a combination of both (NP), and a control (C). Phytoplankton samples were collected by filtering 500 ml of water through GF/C filters. Results confirmed that pelagic algae are now P or NP co-limited, as opposed to 40 years ago when they were only P limited. In conclusion, the enrichment of nutrients has caused changes in algal community structure. Future studies will look at both warming and nutrient effects in a factorial experimental design.

#### **SAT-602**

##### **DIFFERENTIAL RESPONSES OF TWO ECOLOGICALLY SIMILAR TO VARIATION IN TEMPERATURE AND RESOURCES**

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Ecosystems experiencing rapidly changing climates have raised important ecological questions concerning species response to shifting environmental conditions. Species with complex life cycles, such as dragonflies, allow the potential impacts of environmental variation to be well examined since the influence of aquatic rearing conditions may alter terrestrial life stages. We examined the effects of rearing temperature and resource level on larval survival of 2 ecologically similar species, *Erythemis collocata* (western pondhawk) and *Pachydiplax longipennis* (blue dasher). Within high (26 °C) and low (21 °C) temperatures, we crossed species and resource level and reared larvae individually. We predicted that warmer tanks would decrease survival, higher resource availability would increase survival, and the species response would be similar. We found that temperature affected survival, with lower survival rates in tanks at higher temperatures. There was an interaction between temperature and species; western pondhawk was more sensitive to temperature than blue dasher. Resource level did not appear to affect survival in either species. These results suggest that these 2 species might not respond similarly to changing environmental conditions. Thus, global climate change might be expected to affect interactions between these 2 sympatric, ecologically similar species, with potential consequences for community composition.

#### **SAT-616**

##### **COMPARISON BETWEEN DIATOM AND BACTERIA ASSEMBLAGES AND DIVERSITY IN UPSTREAM AND DOWNSTREAM REACHES OF A TROPICAL SYSTEM**

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Diatoms are microscopic, photosynthetic organisms found in every body of water and contribute 20% of global oxygen via photosynthesis. Next to bacteria, they are the second most abundant organism found on earth. Diatoms and bacteria coexist in aquatic ecosystems, functioning in primary production and nutrient cycling. Previous research suggests that periphytic diatoms may be used as bioindicators of riparian ecological conditions and may



provide insight into how water quality is contingent on forest integrity and health. In this study, periphytic diatom assemblages and diversity relative to bacteria diversity was investigated in both upstream and downstream sites. Upstream sampling sites are located within secondary and primary forests of Las Cruces Biological Reserve in Coto Brus County, Costa Rica. Downstream sampling sites lie below the town of San Vito, population 5,509. Bacteria samplings were taken from surface water at each site; bacterial cultures were grown and categorized by morphology; diatom samplings were collected from randomly selected rocks at each site. Samples were analyzed to determine diversity by characterizing diatom assemblages and bacterial diversity. Environmental factors measured in the study include elevation, land use, disturbance, water quality, riparian vegetation and canopy cover. Diatom diversity relative to bacteria diversity is expected to be related to watershed-based stressors. The findings of this study are expected to suggest greater diatom diversity upstream than downstream of San Vito. Diatom diversity and bacterial diversity are expected to be negatively correlated.

#### **SAT-604**

##### **DESERT DUST STORMS, DIAPAUSE, AND DISPERSAL**

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The American Southwest is characterized by synoptic dust storms. These events carry particles deflated from dry lake beds in northern Mexico as well as the Southwest. Along with lake sediments, the resting stages of aquatic organisms are carried long distances. Here, we investigate the role of dust as a dispersal mechanism for aquatic biota. We characterized rehydrated dust from 14 dust storms during 2012 - 2013 at sites near El Paso, Texas, for both particle size, structure, and biodiversity. Specifically, we extracted DNA from dust samples (total DNA) as well as from animals rehydrated from dust samples. Using traditional and next generation sequencing, we identified aquatic organisms using DNA databases and the QIIME software pipeline. In rehydrated samples, monogonont and bdelloid rotifers, gastrotrichs, nematodes, tardigrades, ostracods, copepods, and branchiopods were found. Bdelloid rotifers occurred in 71% of samples; partial COI sequences show at least 3 species: *Philodina acuaticornis*, *P. rugosa*, and *Adineta vaga*. Nematodes were found in 21% of samples, and gastrotrichs and branchiopods in 14%. Preliminary analyses of environmental sequences from water and sediment show <1-12% of OTU arrays were identified as aquatic invertebrates other than nematodes. For 3 dust samples analyzed, sequences for arthropods, nematodes, and rotifers were obtained, but with relatively few representative sequences. Overall, these methods demonstrate regional transport of aquatic biota via wind in arid regions. Continued sequencing of rehydrated dust samples and expanded environmental sequencing will enhance our understanding of anemochory and its effects on biogeographic ranges of these organisms.

**FRI-602****EVALUATION OF QUANTITATIVE PCR ON T4-LIKE MYOVIRUS COMMUNITIES**

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Marine viruses are highly abundant pathogens that rely on host infections for reproduction. Among marine viruses that infect bacteria (bacteriophages) are myoviruses, distinguished by their contractile tails and characterized genetic diversity. T4-like myoviruses contain a gene, *g23*, used to predict amplification and diversity analysis of sequences from the environment. In order to obtain a closer approximation of the true dynamics of T4-like myovirus groups over time, we developed and evaluated a quantitative polymerase chain reaction (qPCR) assay for T4-like viruses. We tested *g23* primers against available T4-like myovirus genomes and observed that 75% of the T4-like isolates would be successfully amplified. Fifteen clones were selected from genomic libraries containing 2 clones per major grouping. Each clone was re-grown, its plasmids quantified and diluted, and subsequent PCR reactions performed. All selected clones amplified as expected with PCR products doubling with each cycle at an average efficiency of 96%. Unexpectedly, a slight positive relationship was observed between PCR fragment size and amplification efficiency, most likely the result of an artifact or unknown bias. Results obtained in this study provided confidence that the qPCR assay would work when applied to environmental samples. Using a standard clone with an average threshold cycle that would most closely approximate real environment samples, our next goal is to couple the qPCR assay with T4-like diversity assessments from the San Pedro ocean time series (SPOT) and ultimately determine how these viruses vary in conjunction with potential host populations.

**FRI-618****DNA FINGERPRINTING TO EVALUATE GENETIC DIVERSITY OF *XYLELLA FASTIDIOSA* FOUND IN TEXAS**

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Pierce's disease (PD) in grapevines is caused by *Xylella fastidiosa*, a Gram-negative bacillus that grows in the xylem of vines and is fatal within 1 year. PD is a problem in Texas, limiting the expansion of the state's grape industry. One of the critical issues to be understood is how PD moves from vineyard to vineyard and from one region of the state to another. To address the epidemiology of PD spread we plan to analyze small sequence repeats (SSR) from *X. fastidiosa* cultures extracted from vineyards in different counties. SSRs change more rapidly than other areas of the genome and can help us determine how bacteria spread on short time scales (months, years). Eleven bacterial cultures were extracted from vines in multiple counties. DNA will be extracted from these cultures, SSRs determined, and a cluster diagram built to visualize genetic variability within and between counties. This study will allow a better understanding of how the bacteria move within Texas and hopefully prevent future PD outbreaks.

**SAT-614****THE CORRELATION BETWEEN FATIGUE AND PILOT SIMULATOR PERFORMANCE**

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With flight largely considered the preferred way of travel, data analysis of pilot performance becomes a necessity to provide a safe atmosphere for travelers. The purpose of this project is to collect fatigue data from pilots participating in a flight simulator study. The study focuses primarily on the correlation of sleep history and the pilot's performance on the simulator, concentrating on their outcomes based on these patterns. The methods used to collect the data are primarily through surveys to determine sleep quality and timing along with recent sleep history and jet-lag. Through this continuing study, researchers hope to gain understanding of the affect that fatigue has on the pilot's reactions throughout the study as well as insight to circadian rhythm variation based on fluctuating routines and schedules.

**SAT-609****APPLIED ELECTROCHEMISTRY FOR THE ANALYSIS OF HEAVY METALS IN VIEQUES' SOILS**

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In this study, the concentration of heavy metals (Pb, Hg, Cd, Zn, and Cu) on the island of Vieques was scrutinized using an electrochemical method. The purpose of this work was to prove the effectiveness of this method for the direct extraction of the heavy metals in the land adjacent to the SWMU 6 on the west side of the island, thus finding a method for the complete extraction from the area. The method consisted of creating a template method to develop to apply the electrodes to create deposition of these metals directly from the studied soil. After the extraction of the platinum (Pt) electrons, a digestion of 50% v/v nitric acid was used to dissolve the heavy metals deposited on the electrodes. Then, the evicting electrochemical technique was used to corroborate the presence of these metals in the soil, making a sweep to more positive potentials. The evicting current of each metal is proportional to the concentration of the solution of the study. In all of the soil samples studied, mercury (Hg) was found along with an unknown substance. The greater the depth of the sample (B2 and C2), the higher the amount of Hg found. Hence, we conclude that the electrochemical method of extraction may be effective for the extraction and analysis of heavy metals in the soil of Vieques.

**FRI-605****SLUDGE INCORPORATION IN SOIL-COMPOST MIXTURE FOR CORIANDER (*CORIANDRUM SATIVUM*) PLANT GROWTH AND DEVELOPMENT**

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Agricultural soils have been degraded as a result of anthropogenic activities and indiscriminate use of pesticides. At present, it is a priority need to restore soils for agricultural production. Utilization of some recyclable wastes such as sewage sludge waste as compost is an alternative to recycle nutrient elements to improve soil quality. This research project is aimed at recycling sludge from water treatment plants and using it as an amendment in tropical soils, specifically in Puerto Rico. Recycling solid waste residues will be a cost-effective practice and sludge landfill disposal will be avoided. *Coriander sativum* was cultivated in a system of compost-soil-sludge at different proportions. Coriander cultivated at 25% compost/50% voladora soil and 25% river sludge show the best growth and development. Root length in coriander roots was an average of  $11.92 \pm 0.4$  cm while stem length was  $2.4 \pm 0.1$  cm compared to control plants:  $10.60 \pm 0.4$  cm and  $2.3 \pm 0.6$  cm, respectively. The highest chlorophyll content ( $33.01 \pm 0.8$ ) was for the coriander cultivated in 25% compost/62.5% coloso soil/12.5% river sludge compared to the chlorophyll content of the control plants ( $32.59 \pm 0.7$ ). The lowest root length and stem length measurements were for plants cultivated at 25% compost/ 62.5% coloso soil/12.5% river sludge:  $10.95 \pm 0.4$  cm and  $1.62 \pm 0.06$  cm respectively, and the lowest chlorophyll content was at 25% compost/ 50% coloso soil/25% river sludge ( $26.35 \pm 0.8$ ). Further analysis will be done to evaluate the mineral content in coriander stems using ICP-MS.

**FRI-608****KINETIC ANALYSIS OF THE PHYTOREMEDIATION OF FLUOROQUINOLONES USING *MIMOSA PUDICA***

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The presence of antibiotics in water bodies and wetlands has increased significantly over the years. High demand for these medicines to aid the ill has led to their improper disposal, resulting in contamination. Two commonly used antibiotics are the fluoroquinolones Ciprofloxacin and Norfloxacin. Ciprofloxacin and Norfloxacin water, and acid and basic solutions were used to study the phytoremediation capacity of *Mimosa pudica* in Gurabo, Puerto Rico. The maximum absorption wavelength (275.80 nm) in the UV region was determined for Ciprofloxacin and Norfloxacin different solutions (30 µg/mL, 15 µg/mL, 7.5 µg/mL, 3.75 µg/mL, 1.5 µg/mL, and 0.75 µg/mL). Two mL samples were analyzed and kinetic assays were conducted using a Shimadzu 1800 UV-Vis spectrophotometer. *M. pudica* degraded Norfloxacin in water solution after 180 minutes. Ciprofloxacin's concentration was reduced after 45 minutes. *Mimosa pudica*'s related microorganisms were isolated from the root's nodules and exposed to the same fluoroquinolone's solutions in Petri dishes. In the lowest concentrations, bacterial growth was observed. With these results, more studies have to be conducted as a clean

technology application to remove fluoroquinolones from water bodies and wetlands in the tropical regions.

#### **FRI-612**

##### **DETERMINING CONCENTRATIONS OF CO<sub>2</sub> AND CH<sub>4</sub> TO UNDERSTAND GREENHOUSE GAS DIFFUSIVE FLUXES INTO THE ATMOSPHERE**

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California's water system is at risk of being obliterated. In the Sacramento area, these once-marshlands are now lands carved down to 12 meters below sea level in some places. Scientists have converted sites to wetlands through flooding. In the making of a wetland, the soil will gradually build back up through the decomposition of vegetation. Further, a wetland site seems to take up significant amounts of CO<sub>2</sub> rather than produce it. The objective of this study is to determine the concentrations of CO<sub>2</sub> and CH<sub>4</sub> in the surface waters of the restored wetland sites in the Sacramento Delta area and to understand how they relate to the diffusion of these gases into the atmosphere. This was done by collecting 2 water samples from the vegetation and 3 water samples from the open water at 4 different sites. The water samples were then processed with nitrogen and the headspace concentrations were put through an LGR. The LGR output data was then used to determine the exact water concentration using Matlab. Preliminary data shows that CO<sub>2</sub> and CH<sub>4</sub> concentrations vary slightly within the same site, even when looking at concentrations in open water versus near vegetation. However, when comparing across different sites, there are large differences in CO<sub>2</sub> concentrations, and even more so for CH<sub>4</sub>. Concentrations also varied over time in both CO<sub>2</sub> and CH<sub>4</sub>. Understanding gas concentrations in the water will help in reading net CO<sub>2</sub> and CH<sub>4</sub> fluxes from the eddy covariance method at these sites.

#### **SAT-611**

##### **REACTIONS OF ALCOHOL AMINES WITH ATMOSPHERIC OXIDANTS NO<sub>x</sub>, H<sub>2</sub>O<sub>2</sub>, AND O<sub>3</sub> ANALYZED THROUGH A PARTICLE-INTO-LIQUID SAMPLER COUPLED TO DUAL ION CHROMATOGRAPHS**

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Gaseous alcohol amines are emitted into the atmosphere through various sources, including carbon sequestration technologies for power plants. However, little is known about how gas-phase alcohol amines interact with atmospheric oxidants, such as NO<sub>x</sub>, H<sub>2</sub>O<sub>2</sub>, and O<sub>3</sub>, to form particulate matter. This study is important because particles formed from volatile organic compounds such as alcohol amines; which include: monoethanolamine, 2-(methylamino) ethanol, and N, N-dimethylethanolamine; may have short and- or long-term adverse health effects. In this study, ion chromatography separations of the potential reaction products of the target alcohol amines were performed with standards to make a calibration curve from which the concentrations of the target species could be calculated. Then a particle-into-liquid sampler coupled to dual ion chromatographs (PILS-ICs) was used to analyze the water-soluble ion

component of the particulate matter formed. The experiments were conducted in an environmental chamber at the Center for Environmental Research and Technology, College of Engineering, University of California, Riverside (CE-CERT/UCR). The chamber is designed to emulate real environmental conditions allowing the reactions to proceed in a controlled environment. As of now, there is little knowledge of how the alcohol amines will react. The experiments will provide data revealing any potential hazards caused by alcohol amines released by carbon sequestration technologies.

#### **SAT-605**

##### **MANURE INCORPORATION TO COMPOST-SOIL SYSTEMS AS A SOURCE OF NUTRIENTS IN TOMATO PLANT FARMING**

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As human populations grow, the demand for food is also increasing. Restoration of land for agricultural practices is essential, particularly in tropical areas where soil organic matter (SOM) has been degraded by crop production. One of the greatest challenges of the 21<sup>st</sup> century will be to meet the food population demand without compromising arable land. Application of organic manure such as animal manure and composted material has been a good soil management practice in several regions of the world. Soil acidity, salinity, and steep slopes contribute to SOM decline. Higher temperatures in tropical regions lead to faster turnover rates of microbial biomass and soil organic matter in comparison to temperate climatic conditions. The aim of this work is to incorporate animal manure to soil-compost systems in tropical soils in order to recycle nutrient elements as well as to improve soil quality. Chicken manure was chosen because chickens only retain 40% of the nutrients consumed; therefore, 60% of the nutrients are found in the manure. Previous studies demonstrated that the incorporation of 25% w/v compost to tropical soils increased plant growth and nutrient uptake in basil and coriander herbs. Manure was incorporated in several soil-compost systems at different quantities (5 g, 10 g, 15 g, and 20 g). Plant germination, growth, and development will be evaluated by physical and chemical analysis of tomato plants and fruits. Macro and micronutrient uptake will be quantified using ICP-MS. Research outcomes will establish the feasibility to use compost as an amendment in tropical soils for integrated nutrient management.

#### **SAT-613**

##### **THE EFFECTS OF BIODIVERSITY AND LOCATION ON LEAF LITTER DECOMPOSITION IN PRIMARY AND SECONDARY TROPICAL FORESTS**

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A central challenge in ecology and conservation biology is to understand how changes in species composition affect ecosystem processes. The biodiversity-ecosystem functioning theory (BEF) suggests that ecosystem processes increase with species richness. The home-field advantage theory (HFA) suggests that the performance of a species (e.g., growth rate and

decomposition rate) should decrease as that species moves from its home range into new territory. This study questions the role of both theories in determining the rate of leaf litter decomposition in old-growth and secondary forests. In the context of HFA, we hypothesized that a leaf litter species will decompose faster in its home environment than a different environment. We also hypothesized that a more diverse mixture of leaf litter will decompose faster than the decomposition rates of a single leaf litter species. To test these hypotheses, we created all possible combinations of single and mixed leaf litter species from a pool of three litter species. Litter species included one common to a tropical montane old-growth forest (*Chrysochlamys glauca*), a second one common to a tropical montane secondary forest (*Miconia trinervia*), and a third species common to both (*Palicourea padifolia*). We put all treatments in mesh bags in plots in both the old-growth and secondary forest. After four weeks, we measured decomposition rate of each treatment. We expect the results to support both theories and to be among the first to test these major ecological hypotheses in a tropical environment.

#### **FRI-616**

##### **SORPTION OF MICROCYSTIN-LR BY NATURAL AND MODIFIED CLAY MINERALS**

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Microcystins are toxins produced by cyanobacteria that are associated with harmful algal blooms and eutrophic surface water. Microcystin contamination in drinking water is a problem worldwide and has been linked to various health problems. Microcystin-LR is the most common and among the most acutely poisonous cyanotoxins. Commonly used water treatment methods are ineffective or impractical for the removal of microcystins. The goal of this project is to investigate the efficacy of several materials for the removal of microcystin-LR from water. Microcystin-LR sorption isotherms will be constructed using several media including clay minerals, organoclays, and organoclays modified with tannins. After the sorption procedure, microcystin-LR in solution will be measured using liquid chromatography coupled with a mass detector. The Freundlich isotherm equation will be used to obtain the sorption coefficient of the microcystin-LR in the media used. We hypothesize that the sorption coefficient of microcystin-LR will vary with the type of material used. Organoclays are expected to be the least effective sorbents followed by the natural clays. The organoclays modified with tannins are expected to be the most effective material for sorbing microcystin-LR because microcystins are polypeptides, and tannins have the ability to precipitate proteins. Many conventional methods for removing microcystins from water are considered impractical; thus, it is imperative to find new ways to accomplish this goal. Tannins and organoclays are promising materials to consider. Treatment facilities utilizing these materials could potentially eliminate the risk of health problems associated with microcystin contamination and reduce the cost of public water supplies.

**FRI-606****GROWTH RATES OF A MARINE GROUP I THAUMARCHAEA ENRICHMENT CULTURE UNDER REDUCTION OF VIRAL PRESSURE, INCREASED GRAZING PRESSURE, AND EXPOSURE TO NATURALLY OCCURRING MARINE MICROBES**

Vickie Trinh, Alma Parada, Jed Fuhrman.

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Until 1992, the domain Archaea was generalized to be extremophilic prokaryotes living in harsh environments. Recent studies have revealed that Archaea are also found in moderate environments such as the Marine Group I Thaumarchaea, which are ubiquitous throughout the world's oceans and abundant in mesophilic waters. These organisms have been shown to be ammonia oxidizers that oxidize ammonia to nitrite as a source of energy to fix carbon dioxide. Their ability to oxidize ammonia, the first and rate-limiting step in nitrification, and their abundance suggest that they are important players in the nitrogen and carbon cycles; however, the niches they fill within marine microbial communities and the environmental controls on their abundance are poorly understood. Studying Marine Group I Thaumarchaea in culture can reveal how Archaeal abundance is controlled by their interactions with Archaeal viruses and other microorganisms. For example, we have found that the growth rates of a Thaumarchaeal enrichment culture, CN25, increases when viral pressures are reduced by dilution with 0.02 micrometer filtered seawater media, as indicated by the faster accumulation of nitrite. Adding the enrichment culture to seawater containing grazers and monitoring the community growth will determine the rate at which Archaea are removed and show how the microbial community changes in response to the presence of Archaea. Studying the interactions of Thaumarchaea with other microorganisms is fundamental to understanding their role in the microbial community.

**SAT-608****CLASSIFYING LAND COVER COMPOSITION OF LA PLATA WATERSHED IN PUERTO RICO USING HISTORICAL SATELLITE IMAGING AND REMOTE SENSING RASTER GRAPHIC EDITORS**

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Reconstructing the transformation of tropical watershed allows for researchers to understand the possible causes of change and the spatial patterns that result from social and environmental changes. Puerto Rico has a rich history of aerial photographic surveys that allows for doing spatially explicit reconstruction of the history of landscape changes since the 1930s. This allows us to perform a historical land cover transformation analysis for the La Plata River Watershed in Puerto Rico. To analyze land cover transformation, we utilize satellite imaging for the years 1930, 1960, and 2010. In these images, we have created the land use classes of agriculture, forest, and anthropogenic utilizing the remote sensing raster graphic editor of eCognition. This program allows us to create the previously mentioned classes based on specific parameters and algorithms. Our aim is to determine or identify a possible pattern in the land cover transformation for our study area. The results show that agricultural valleys have been mostly urbanized, while mountainous regions have given way to forest. A fine scale analysis of



forest transformation shows clearly how remnants of previous uses, aspects, slope, and elevation affects the future composition of the forest. The understanding of the patterns of change on this time scale will provide a better understanding of forest and anthropogenic area transformation in Puerto Rico.

#### **SAT-610**

##### **IMPROVING UNDERWATER VISION WITH AMPHIBIOUS CONTACT LENSES**

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Improving underwater vision is greatly desired by water sport enthusiasts and, with the newly designed underwater amphibious contact lenses, clear vision is provided. The project's inspiration came by a simple and interesting adaptation in nature by the "four-eyed" fish *Anableps anableps*. The eyes of the fish contain 2 corrective regions: one for vision in air and the other below water. A human's eye is optimally designed for in-air viewing with perfect vision, requiring a power of 43 diopters of accommodation. Each environment requires a different power range, permitting the viewer to observe images focused clearly on the retina. The corrective crystalline lenses tested are asymmetric, unlike commonly used masks and goggles which limit the user's field of view. The lenses are specifically prescribed for the wearer's visual prescription to correct any defocus or astigmatism. They were tested in a number of environments and conditions for visual acuity and compared to goggles. Environments ranged from salt water to fresh water. The visual acuity was measured by a Snellen eye chart specific to the testing area. In addition to testing visual acuity at near and distant points, resolution limit, pattern detection and recognition, and color were tested. In Arizona at noon, the test results determined hyper-acuity reaching 20/12.5. This indicates that the wearer had improved visual acuity under water with the contact lenses than the wearer did above water in the same conditions. In addition to increased visual acuity, there was immediate awareness of a full field of view.

#### **SAT-617**

##### **ESTROGENIC ENVIRONMENTAL ENDOCRINE DISRUPTORS IN TURTLE MOUNTAIN AMERICAN INDIAN RESERVATION WATER**

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The United States Environmental Protection Agency (EPA) defines endocrine disrupting chemicals (EDCs) as exogenous agents that interfere with the production, release, transport, metabolism, binding, binding action, or elimination of natural hormones in the body responsible for the maintenance of homeostasis, reproduction, development, and/or behavior. Environmental EDCs' interference with critical body systems and pathways pose serious health risks. The health risks associated with estrogenic EDCs include reproductive cancers such as prostate and breast cancer, the onset of early puberty, and the development of reproductive organs in unborn fetuses. Sources of exposure to EDCs occur from industrial byproducts and

pollution, agricultural pesticides, water contamination, consumer products, pharmaceuticals, and phytochemicals. Routes of exposure occur through inhalation, ingestion, and transdermal access. The EPA has banned several persistent organic pollutants (POPs), but many EDCs are not regulated. This research focused on the presence of estrogen in tap water, source water and surface water on the Turtle Mountain American Indian Reservation. To indicate EDCs are present, the samples were tested using yeast estrogen screen (YES) assay. The human estrogen receptor (hER-  $\alpha$ ) were transferred to the yeast genome and, when exposed to an estrogen compound, formed a receptor-estrogen complex. The complex binds to the estrogen response within the promoter region of the *lac Z* gene. Positive samples could indicate contaminated water that could contribute to negative health outcomes. This is important when looking at the prevalence of certain diseases and illnesses within the Turtle Mountain Reservation

#### **FRI-611**

##### **POPULATION DYNAMICS OF THE SANTA ROSA ISLAND TORREY PINE**

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The Torrey pine, *Pinus torreyana insularis*, is the rarest pine species in North America, with its current populations limited to San Diego, California, and Santa Rosa Island (SRI), California. We completed a census on the SRI Torrey pine population to determine its population size and whether it is stable, growing, or declining; the spatial variation in population structure; the spatial patterning of trees in different life stages; the environmental factors that are related to seedling recruitment; and the conservation gains associated with non-native ungulate removal. In total, 26,009 individuals make up the SRI Torrey pine population, only 3,068 of which are sexually mature. The proportion of juveniles to adults for SRI is 8:1, compared to 1:2 for San Diego. Using a point density calculation with ESRI software, 6 distinct clusters of older trees were revealed. Smaller, younger plants are more frequently located on the edges of the groves, while larger, older plants make up the groves. Core samples were taken from 25 trees to find a relationship between diameter at breast height (dbh) and age in order to estimate the age of each plant. We continue to monitor the survival and growth rate of the juveniles in 45, 10 x 10 m permanent monitoring plots. With non-native elk, deer, and cattle removed from the island in 2012, this study provides baseline data to enable land managers to quantify the ongoing recovery of the Santa Rosa Island Torrey pine from over a century of population suppression.

#### **SAT-615**

##### **SALINITY TOLERANCE OF EPHYRA OF *CHRYSAORRA QUINQUECIRRHA***

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<sup>1</sup>Towson University, Towson, MD, <sup>2</sup>University of Maryland Eastern Shore, Princess Anne, MD.

Medusae of the scyphozoan *Chrysaora quinquecirrha* blooms in the mesohaline Chesapeake Bay during the summer. They are voracious predators on mesozooplankton as well as a nuisance to swimmers. There is limited information on the ephyra of the scyphozoan *C. quinquecirrha*. It is essential to understand the optimal and suboptimal conditions for the larval stage, specifically its salinity tolerance, which would help predict when the medusa bloom will occur. Ephyra were captured with a 200 plankton net at a public pier in Cambridge, Maryland. Ephyrae were exposed to 2 different salinity treatments (3 and 20) and compared with ephyrae

in ambient salinity (7). The ephyrae were then observed for their depth and pulsation rates in each sample. Mortality was 100% after 2 days in 3 trials at salinity of approximately 3. Mortality, depth, and pulsation rate were highly variable at ambient and high salinities. Ephyrae in low salinity experienced metabolic stress and did not survive throughout the observation period. Ephyrae in high salinity exhibited an above average pulsation rate. Ephyra appear to withstand higher salinities and do not survive in low salinities. Ultimately, when the salinity is low in the bay, the medusa bloom may be delayed because ephyra cannot tolerate these conditions.

### **SAT-603**

#### **THE EFFECTS OF PERMAFROST THAW ON LONG-TERM NUTRIENT RELEASE INTO ARCTIC TUNDRA PONDS**

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With warming in the Arctic, more nutrients are being released from thawing permafrost into Arctic aquatic ecosystems. The levels of nutrient release over time are largely unknown. With higher nutrient levels in Arctic ponds, microbial activity as well as lower trophic levels may be significantly altered. To examine long-term nutrient release from thawing permafrost, and the role of microbial activity in this release, permafrost cores collected from Barrow, Alaska were incubated for 8 weeks in a cold room at 2 different temperatures (7 °C and 15 °C) in beakers containing either DI water alone or DI and formaldehyde. Water samples were collected at 24 h, 48 h, 72 h, 168 h, 336 h, 672 h, and 1,776 h (8 weeks) to measure: total phosphorus (TP), total dissolved phosphorus (TDP), dissolved organic carbon (DOC), and total nitrogen (TN). A continuous increase in nutrient release was observed for all measured parameters; however, the impact of microbial activity differed among nutrients. Cores where microbial activity was inhibited had larger amounts of nitrogen release, but lower levels of phosphorus release. Understanding the release of nutrients from the permafrost over the long-term can help model nutrient concentrations that will be added to arctic freshwater ecosystems with climate warming.

### **SAT-606**

#### **CHARACTERIZATION OF ENRICHMENT CULTURES FROM 50- to 80-MILLION-YEAR-OLD DEEP SUBSEAFLOOR BASALTIC CRUST**

Jordan Hoese, Jason Sylvan.

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A large portion of the Earth's biomass is located in subseafloor marine sediments, and initial work indicates that an equally large biosphere exists in the basaltic crust underlying these sediments. Investigating the extent and limits of life in the subseafloor basaltic crust ecosystem is vital to understanding both local and global ecosystems, as well the evolution of life on Earth, and possibly other planets. In an effort to understand microbiology in old subseafloor basaltic crust, we used an enrichment incubation approach to culture and describe microbial communities in samples taken from Integrated Ocean Drilling Program (IODP) Expedition 330, which sampled 50 to 80 million year old seamounts. Samples collected during Expedition 330 were inoculated into vials containing either dilute marine broth or media that targeted sulfur-oxidizing bacteria. Enrichments were kept at 4 °C until sampling 0.5 to 3 years later, when some of the enrichment was transferred to new media and the rest filtered for subsequent DNA

extraction. Quantitative PCR was performed on each extraction to quantify bacterial *16S rRNA* gene abundance, and samples with greater than 103 gene copies were analyzed by 454 pyrotag amplicon sequencing of the V4V6 region. Initial analysis of DNA sequencing results shows presence of the genera *Reichenbachiella*, *Halomonas*, *Ralstonia*, *Cytophaga*, and *Mariprofundus*, among others. Previous studies suggest that species from these genera act as key members in ecosystems similar to the subseafloor basaltic crust ecosystem sampled here. Future efforts will allow us to more exactly determine the phylogeny and metabolic roles of organisms in these enrichments through metagenomic sequencing.

#### **FRI-609**

##### **UPTAKE AND TRANSPORT OF $\text{Fe}_3\text{O}_4$ AND $\text{Fe}_3\text{O}_4$ -DMSA NANOPARTICLES IN *PROSOPIS JULIFLORA* (MESQUITE) PLANTS**

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Nanotechnology research and commercial exploitation of nanomaterials is increasing worldwide. Regulations about disposal or manipulation of nanomaterials are not being well established. Due to this fact, the distribution of nanoparticles in the environment must be addressed. In this research, mesquite plants were evaluated for the uptake of magnetite ( $\text{Fe}_3\text{O}_4$ ) and  $\text{Fe}_3\text{O}_4$  covered with dimercapto succinic acid (DMSA) nanoparticles (NPs). Root average size from mesquite plants exposed to 1,000 ppm of  $\text{Fe}_3\text{O}_4$  NPs was lower by about 20% with respect to control plants ( $21.8 \pm 2.0$  cm and  $17.7 \pm 1.0$  cm respectively). Stems of mesquite plants showed a reduction in size by about 30% when 62.5 ppm of  $\text{Fe}_3\text{O}_4$  NPs were added to the media ( $6.0 \pm 0.2$  cm and  $4.0 \pm 0.8$  cm, respectively). Chlorophyll content was reduced in leaves from plants exposed to 1,000 ppm of  $\text{Fe}_3\text{O}_4$  NPs with respect to control plants ( $45.5 \pm 0.7$  and  $42.9 \pm 1.0$  respectively). Root average size from mesquite plants exposed to 1,000 ppm of  $\text{Fe}_3\text{O}_4$ /DMSA NPs was lower in size by about 19% with respect to control plants ( $19.8 \pm 1.0$  cm and  $13.4 \pm 0.6$  cm respectively). Stems of mesquite plants exposed to  $\text{Fe}_3\text{O}_4$ /DMSA NPs did not show a significant change in size ( $p \geq 0.05$ ). Chlorophyll content was lower in leaves exposed to 125 ppm of  $\text{Fe}_3\text{O}_4$ /DMSA NPs ( $47.7 \pm 1.0$  and  $43.0 \pm 2.0$  respectively). Iron and nutrient content will be quantified in roots, stems, and leaves of mesquite plant tissues by ICP-MS.

#### **FRI-614**

##### **IMPACTS OF LONG-TERM USE OF RECLAIMED WATER ON THE VIABILITY OF SOILS TO SUPPORT TURFGRASS GROWTH**

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Reclaimed water usage has become a worldwide practice, but especially in arid cities. To maintain green space, arid cities must rely on irrigation rather than rainfall because these environments have greater evaporation than precipitation. Reclaimed water has become a popular choice for irrigation in public areas because it is more affordable and reduces potable water usage. However, one of the main concerns is the high amount of salt ions in reclaimed water. Accumulation of salt ions may adversely affect plant growth. With Governor Brown's recent drought emergency announcement for the state of California, reclaimed water usage is expected to expand, but we need to examine the best management practices. At the University of California, Santa Barbara (UCSB), irrigation is now 90% reclaimed water. We will investigate whether or not reclaimed water usage will cause campus soils to become too saline

for plant growth in the future. To conduct this study, we collected and analyzed soil samples from 3 campus turfgrass sites for electrical conductivity (EC), sodium adsorption ratio (SAR), and cation exchange capacity (CEC). We will combine these measurements with irrigation water chemistry data to evaluate and model the soil salinization risk. We hope our findings will serve as a basis for recommendations of best practices, not only at UCSB, but also in other locations using reclaimed water.

## **SAT-612**

### **DOES RESTORATION OF URBAN STREAMS IMPROVE ECOSYSTEM FUNCTION**

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Urban streams are often channelized and polluted, which leads to flooding and poor water quality. Restoration efforts are being undertaken to return these ecosystems to a more natural state. Despite the high cost of urban stream restorations, few projects are assessed for their efficacy in improving the structure and function of the ecosystem. In our research, we are evaluating 6 restorations in Milwaukee, Wisconsin using integrative metrics such as whole-stream metabolism. Stream metabolism measures the gross primary production by autotrophs and ecosystem respiration by heterotrophs within a particular reach. In addition, we are quantifying watershed characteristics (e.g., impervious surface cover, land-use) and metrics of ecosystem structure (e.g., discharge, water chemistry, and algal biomass) that we expect to influence stream metabolism. At each site, we paired a restored reach with an unrestored concrete channel immediately upstream or downstream, which serves as an unrestored reference point. Furthermore, the study streams varied in size from small headwaters to mainstem rivers (10-400 L/s), which allow us to investigate how the location within a watershed may influence the effectiveness of restoration for ecosystem health. By integrating both watershed and in-stream characteristics, our functional metric approach will allow us to test the assumption that restorations improve ecosystem structure and function. Such quantitative assessments are essential to inform the planning and implementation of future restorations.

## **FRI-603**

### **EVALUATING THE RELATIONSHIP BETWEEN LAND USE AND WATER QUALITY IN NON-PRASA SYSTEMS USING SPATIAL ANALYSIS**

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Puerto Rico currently has more than 250 non-PRASA water systems, which are water systems that are not serviced by the Puerto Rico Aqueduct and Sewer Authority (PRASA). These non-PRASA systems have limited resources for water management and are often non-compliant with the United States Environmental Protection Act Safe Drinking Water Act. The majority of these systems are located on the rural parts of the island, which are, characteristically, areas of increased poverty. Due to their lack of resources, they are often unable to administer the proper treatments and testing for the water systems. This can be potentially hazardous to these communities since poor water quality can result in the proliferation of diseases and exposure to toxic compounds. Our goal was to use geographic analysis to determine the risks of these systems for water contamination. To evaluate how geographic factors could shape the water quality of non-PRASA systems, we organized the database on water quality from the Puerto Rico Health Department for 92 non-PRASA systems, defined the watershed area for each system

using ArcMap, and evaluated the human activities within the watersheds using Euclidean distance analysis. With our multiple variable analysis we were able to determine that a significant relationship existed between water quality and the distance of conservation areas, suggesting that systems that are found at distances less than 3,000 meters from a conservation area are at a lower risk of contamination.

## **FOOD SCIENCES/TECHNOLOGY**

### **FRI-1101**

#### **ASSESSING AND IMPROVING STUDENT FOOD HANDLING KNOWLEDGE AND PRACTICES AT CALIFORNIA STATE UNIVERSITY FULLERTON.**

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Fruit and vegetable consumption has numerous health benefits and United States health policy generally recommends increased consumption. However, fruits and vegetables can be contaminated with heavy metals, pesticides, and microbes, which can lead to food-borne illnesses. Although proper food handling practices can mitigate these concerns, many consumers do not know about or regularly practice safe food handling. Unsafe food handling practices appear to be particularly common in some sub-populations, including college graduates. Many students begin to cook for the first time in college; therefore, it is an ideal time to improve their food handling practices and knowledge. In this study, we sought to document produce handling knowledge and practices in undergraduate students at California State University Fullerton (CSUF). We administered a web-based survey to student volunteers on their produce handling knowledge and practices. Although CSUF students report they regularly wash produce in general, most neglect to wash fruits that are peeled before consumption, such as cantaloupe and bananas, but that still pose health threats. Students were most aware of chemical-based and microorganismal contaminants, but rarely acknowledged the possibility of heavy metal contamination. Reported produce handling practices did not differ between organic and conventional produce. We will extend this study to other sub-populations and use the information gathered from the surveys to develop interventions to improve student knowledge and practice of produce handling procedures.

## **FORESTRY SCIENCES**

### **FRI-619**

#### **IS THAT FOREST BREATHING: SOIL RESPIRATION ACROSS A GRADIENT OF DISTURBANCE SEVERITY AND FOREST DEVELOPMENT**

Julia Yang<sup>1</sup>, Chris Gough<sup>2</sup>.

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In the present era of global change, the release of carbon (C) from soils is a crucial determinant of the terrestrial C sink and thus atmospheric CO<sub>2</sub> concentrations. Past disturbances and the stage of ecosystem development may affect current ecosystem function and impact future trajectories of ecological change; however, the extent to which historical disturbances affect present-day C cycling has not been quantified for most ecosystems. Our objectives were to 1) quantify soil respiration over the course of forest development, and 2) determine whether different disturbance histories, clear-cut harvesting only versus both clear-cut harvesting and burning, affect rates of soil respiration. Our research was conducted at the University of

Michigan Biological Station within a chronosequence of clear cut and burn disturbance, a chronosequence of clear cut only disturbance, and three end-member stands of varying community compositions. We measured soil respiration over the course of five weeks using a LI-6400-09 CO<sub>2</sub> flux chamber. We expect respiration to increase with forest age because plant biomass and organic matter pools are larger; respiration to be highest in the mixed deciduous conifer forest because plant biomass is greater than in the conifer dominated forest; and respiration to decrease with higher disturbance severity because biomass and organic matter pools are smaller. We expect this last disturbance effect will persist across all stages of stand development. A better understanding of how forest age and disturbance history interact will improve our knowledge of the terrestrial C cycle and will have significant implications for forest management strategies in the future.

#### **SAT-619**

##### **A COMPARISON OF SOIL CO<sub>2</sub> EFFLUX OF MID-ROTATION LOBLOLLY PINE (*PINUS TAEDA L.*) EXPOSED TO FERTILIZER AND RAINFALL EXCLUSION AND THE PARTITIONING OF HETEROTROPHIC AND AUTOTROPHIC RESPIRATION**

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Future climate predictions associated with increased atmospheric CO<sub>2</sub> show an increase in temperature and more variable precipitation that could affect ecosystem productivity. Some areas, such as Oklahoma, are projected to experience less frequent, but more severe precipitation events which could lead to longer dry periods. Terrestrial ecosystems can sequester large amounts of carbon from the atmosphere. Once in the ecosystem, fixed carbon can be stored or respired back to the atmosphere. Belowground respiration occurs in two forms: autotrophic (roots) and heterotrophic (microbes). Loblolly pine plantations are common and highly productive ecosystems found throughout the southeastern United States. To understand how a more variable climate will affect loblolly pine ecosystem productivity under current plantation management practices, we must determine the effects of nutrient and water availability on soil CO<sub>2</sub> efflux. The objectives of this study were to measure soil CO<sub>2</sub> efflux under treatments of throughfall exclusion and fertilizer and to determine the amount of soil CO<sub>2</sub> efflux from heterotrophic and autotrophic components. Soil CO<sub>2</sub> efflux was measured using an infra-red gas analysis system (Li-Cor 8100, LiCor Environmental, Lincoln, NE). Measurements were conducted bi-weekly from June through August, 2014 concurrent with soil temperature measurements at 10 cm depth. Further, heterotrophic and autotrophic respiration was partitioned using measurements conducted within root exclusion collars. We hypothesized that rainfall exclusion and fertilizer will decrease soil respiration. Soil CO<sub>2</sub> efflux measurements collected over the summer of 2014 will be presented.

## GENETICS

### FRI-1104

#### GENETIC CONTROL OF CARDIAC INFLOW TRACT FORMATION

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In the *Drosophila* circulatory system, hemolymph enters the cardiac tube through specialized inflow tracts termed ostia. These cells express the orphan nuclear receptor gene *seven-up* (*svp*), as well as the signaling molecule wingless (*wg*), that activates a cascade that is responsible for gene expression. We studied the involvement *wg* has in activating other genes that are hypothesized to be required in ostia formation. We found that *wg* signals in an autocrine manner to promote inflow tract formation, and it must collaborate with the homeotic gene *abdA* to activate markers of the inflow tracts. In addition, we identify an alkaline phosphatase ortholog that is expressed in the ostia, and that may contribute to inflow tract development. There are many conserved genetic pathways between *Drosophila* and vertebrate species, and in particular *wg* has mammalian orthologs that are expressed in the developing heart, which makes our research important in defining pathways for heart development.

### FRI-1114

#### IDENTIFYING THE GENETIC CONNECTIVITY OF *COLOBOCENTROTUS ATRATUS* IN HAWAII

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The use of population genetics to monitor target species in ecologically sensitive areas is an effective management tool for understanding the structure of those populations. This study attempts to elucidate the population structure of the marine invertebrate species *Colobocentrotus atratus*, also known as the shingle or helmet sea urchin or Ha'uke'uke in Hawaiian. Ha'uke'uke inhabits wave-swept, rocky intertidal shores throughout the Hawaiian Archipelago, where it is recreationally harvested for the consumption of its gonadal tissues, also known as uni. Culturally, the Ha'uke'uke, which is mentioned in the Kumulipo, the Hawaiian creation chant, as one of the first organisms to be born, is harvested for its delicious taste and, less often, its medicinal properties. We will obtain tissue samples from multiple individuals along at least 2 different shorelines (i.e., north, south, east, and/or west) around the main islands of Hawai'i (Kauai, Oahu, Maui, and Hawaii). Lab work consisted of method development to extract DNA from Ha'uke'uke tissues to PCR amplify and sequence the *Cytochrome Oxidase I* gene, a commonly used population genetic marker. We predict that populations inhabiting different shorelines will exhibit structure due to their relatively short larval duration (typically one month). We hope to continue to investigate Ha'uke'uke population structure throughout the Hawaiian Islands in an effort to better manage this important cultural resource.



**SAT-343****IDENTIFICATION OF THE PERIOD GENE IN THE PRAYING MANTIS *HIERODULA PATELLIFERA***

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The clock protein PERIOD (PER) is a critical constituent of insect molecular circadian clocks, which control a number of biological rhythms from the cellular to the organismal levels of analysis, including peptide synthesis, egg deposition, and locomotion. Although much is known about the molecular constituents of circadian clocks in model organisms such as *Drosophila melanogaster* (fruit fly), understanding lesser-known insect models is critically important in that it provides novel insights into the ways that biological systems operate. These expanded approaches are becoming possible due to advances in molecular techniques and DNA sequencing technology. One example of a novel system is the praying mantis (Insecta, Mantodea). We study this system because of its unique constellation of complex motor behaviors and sensory and circadian systems. The molecular components of the mantis circadian systems are yet unknown. However, based on preliminary data, we hypothesize that the mantis circadian systems are similar to those of its sister taxon, the Blattodea (cockroaches). Using highly conserved regions of the PERIOD protein from the American cockroach, *P. americana*, we designed degenerate primers which have been used to successfully amplify 720 and 1,000 bp putative period fragments from our mantis cDNA. Once sequenced, these fragments will be used as templates for RACE (rapid amplification of cDNA ends) PCR to identify the *per* gene sequence in the mantis, *Hierodula patellifera*. Results from this experiment represent a significant step forward in our understanding of the ubiquity of the *per* gene and conservation of the genetic underpinnings of molecular clocks across taxa.

**FRI-1113****ANKRD11 TRUNCATION AND ITS PATHOGENIC MECHANISM LEADING TO KBG SYNDROME**

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KBG syndrome is a rare genetic disorder. Its features include short stature, intellectual disability, and skeletal anomalies. It is associated with mutations in ANKRD11, Ankyrin Repeat Domain-Containing Protein 11. The resulting protein from this gene inhibits ligand-dependent activation of transcription and is highly regulated during the cell cycle. Reported pathogenic mutations of ANKRD11 involve a nonsense mutation resulting in a truncated protein. These truncations include the deletion of 3 destruction boxes which are vital for the recognition of protein targets for ubiquitination and proteolysis. Therefore, this study proposes to determine whether the critical region of deletion is the final 3 destruction boxes, as well as determine if the pathogenic mechanism of mutated ANKRD11 is through disruption of ubiquitin-proteasome proteolysis. We predict that the loss of these destruction boxes will lead to reduced proteolysis and translocation of the protein into the nucleolus. To test these hypotheses, the desired truncation of ANKRD11 was constructed and transfected into Neuro-2a cells. To determine if

the protein is ubiquitinated, wild-type and mutant ANKRD11 protein will be co-transfected with HA-ubiquitin, immunoprecipitated, and tested on western blots. To determine if the mutant ANKRD11 leads to translocation of wild-type and mutant protein into the nucleolus, immunofluorescence will be performed to visualize co-localization of these two proteins.

#### **FRI-1116**

##### **DEVELOPMENT OF A REPORTER CONSTRUCT TO DETECT FRAME SHIFT ERRORS IN *ESCHERICHIA COLI***

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Some organisms use programmed frame shifts as a mean of gene regulation. This project is based on developing a screening method for sequences that promote ribosomal frameshifting. The immediate goal is to make a reporter gene that requires the expression of 2 different reading frames from a single transcript. We designed a *lacZ* that had a deletion of 42 codons (*lacZ* $\Delta$ 42) called *lacZ* $\Omega$ . This is necessary to provide an allele that is *lacZ* defective but can be complemented by *lacZ* $\alpha$ . To start the process for the reporter construct, we needed to make a fusion of the *lacZ* $\alpha$  domain to the *CAT* gene that confers resistance to chloramphenicol (Cm). This fusion has the *lacZ* $\alpha$  sequence inserted out of frame between the *CAT* promoter and the *CAT* open reading frame. Via recombineering, this reporter construct was inserted into the genome of *E.coli* and the phenotype resulted as expected, *lacZ*(-) and Cm<sup>r</sup>. However a sequence that promotes ribosomal frameshifting was inserted between the *CAT* promoter and the reporter construct. This caused the cells to suffer a phenotypical change, which made them chloramphenicol resistant and *lacZ*(+). Future plans with this construct are to develop an assay to easily detect +1 and -1 frameshifting using different sequences that will stimulate ribosomal frameshifting. We are currently in the process of inserting a poly adenine sequence that will facilitate a ribosomal slippage that we expect will express both *lacZ* $\alpha$  and Cm<sup>r</sup>.

#### **FRI-1102**

##### **IDENTIFYING REGULATORY ELEMENTS IN THE *TPNC41C* ENHANCER REGION RESPONSIBLE FOR FIBER-SPECIFIC EXPRESSION IN *DROSOPHILA MELANOGASTER***

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Similar to skeletal muscles in vertebrates, the somatic muscle of *Drosophila* is composed of different fiber types that vary in their structural and functional properties. An example of such muscles are the indirect flight muscles (IFMs) and jump muscles of the fly thorax. Although the early development of muscle tissue has been thoroughly studied, the mechanisms by which muscle fibers initially become specified into their different types remains unclear. To further our understanding of this mechanism, we studied the transcriptional regulation of the jump muscle-specific troponin gene, *TpnC41C*, of *D. melanogaster*. Analysis of the highly conserved genomic region directly upstream of the gene revealed a 300 bp enhancer sufficient for its proper expression. Two sequences within this region were analyzed as possible regulatory sites

essential for activation of *TpnC41C*'s tissue-specific expression. Using site-directed mutagenesis, we developed reporter plasmids with individual and combined mutations of these sequences within the *TpnC41C* enhancer placed upstream of a *LacZ* gene. Flies containing genomic insertion of these plasmids were examined for expression of the reporter protein  $\beta$ -galactosidase. Reporter activity tested through immunohistochemistry on cryosections and *in vitro* enzymatic assays showed that mutations in these sites greatly reduced enhancer activity. Of the two sites, one was confirmed through *in vitro* binding assays to specifically bind Myocyte Enhancer Factor-2. Identification of the transcription factors necessary for specific gene expression in model organisms such as *Drosophila melanogaster* provides us with knowledge of the evolutionarily conserved regulatory pathways of muscle formation in all animals, including mammals.

#### **SAT-1116**

#### **STUDY OF MISSENSE RAI1 MUTATION G3440A IDENTIFIED IN SMITH-MAGENIS SYNDROME PATIENTS**

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Smith-Magenis syndrome (SMS) is a contiguous gene syndrome associated with microdeletion within chromosome 17-band p11.2. Most of the symptoms are associated with neurobehavioral defects. That includes but is not limited to motor and speech delay, attention seeking, self-injury and hugging, and autistic features. In about 10% of SMS patients, no common deletions were identified; instead, mutations in a single gene, *Retinoic Acid Induced 1 (RAI1)* were found. *RAI1* plays important roles during development and neuronal function; however, the molecular role of *RAI1* is mostly unknown. Here we identified a new point mutation in SMS patients, c.3440G>A. The main goals of this research are the generation of a *RAI1* constructs carrying this mutation and the determination of the transactivation activity of this mutant protein compared to the wild type. The missense mutation was generated by direct mutagenesis using overlapping PCR. We will ligate this mutation to a pALTER-RAI1 expressing vector and transfect into N2A cells. Protein localization will be determined by immunofluorescence. Protein molecular weight will be checked by western blot, and mutant transcription activity will be tested using luciferase assay. Our study contributes to the understanding of *RAI1* function and the development of future therapy for SMS.

### SAT-1115

#### DEVELOPMENT OF AN ASSAY TO DETECT TRANSCRIPTION MISINCORPORATIONS IN *ESCHERICHIA COLI*

Jorge Irizarry-Caro<sup>1</sup>, Mary Ernst<sup>2</sup>, Alison Rattray<sup>2</sup>, Jeffrey Strathern<sup>2</sup>.

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Accurate transcription is an essential step in maintaining genetic information. However, the mechanisms controlling transcription fidelity and the biological consequences of transcription errors are poorly understood. Because of the transient nature of mRNAs and the lack of reliable experimental systems, the identification and characterization of defects that increase transcription errors have been particularly challenging. The principle is based on suppression of a mutation in the active site of the Cre recombinase. This assay is based on 2 parts: a source of Cre, which is actually the transcription misincorporation substrate, and a genetic reporter with a phenotypic change created by Cre-mediated recombination between lox sites. To develop a substrate for *E. coli*, we chose the galactokinase gene (*galK*) as our reporter. From an alignment of the galK protein from *E. coli*, *H. sapiens*, and *L. lactis*, we identified sites that might be able to accept a 12aa insertion encoded by the LoxP sequence without disrupting its function. We selected four different sites that were away from the *GalK* active site and on the surface of the protein. The project started with the strain MG1655, which is *galK*(+) and grows on glucose forming red colonies on a MacConkey galactose plate. Using recombineering, we first inserted a 7-base sequence which caused a frame-shift mutation, and the cells became *galK*(-). The insertion of this LoxP site was successful, putting the gene back in frame and making the cells *galK*(+). Active Cre recombinase can be detected by flipping the inversion to restore *galK* function.

### SAT-1108

#### CHARACTERIZATION OF A *DROSOPHILA* CRR-DOMAIN-CONTAINING GENE FOR SYNAPTIC DEVELOPMENT AND FUNCTION

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Synapses are critical for neuronal function and plasticity. The *Drosophila* larval neuromuscular junction (NMJ) has become a powerful genetic model system for studying the molecular mechanisms that regulate synaptic growth. The bone morphogenic protein (BMP) signaling pathway is a critical retrograde (muscle to neuron) growth signal that regulates synaptic development in *Drosophila* and mammals. BMP signaling is regulated by cysteine-rich repeat (CRR) proteins, which act as extracellular modulators. The molecular mechanism of how CRR proteins function during synapse formation is unknown. Previous studies in our laboratory have shown that a CRR-domain-containing gene induces synaptic overgrowth when misexpressed in muscles. Therefore, we hypothesized that this gene is working in the postsynaptic terminal to promote BMP signaling. The main goal of this project is to characterize mutant phenotypes of the gene through morphological, behavioral, and physiological studies. Synaptic morphology will be assessed by determining synapse number at the NMJ. The expected phenotype for the mutant gene is decreased synapse formation at the NMJ. The behavioral consequences of loss of CRR regulation of BMP signaling will be determined using *Drosophila* activity motors (DAMs),

a high-throughput locomotion assay. Finally, to assess physiology, we will use electroretinograms to analyze synaptic transmission at mutant synapses. This work can provide insight into the role of a CRR-domain-containing gene in regulating the retrograde BMP signaling pathway and identify novel genes required for synaptic growth.

#### **FRI-1112**

##### **NEXT-GENERATION SEQUENCING RH BLOOD TYPING: NATIONAL CHILDREN'S STUDY**

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Sickle cell disease (SCD) affects approximately 100,000 people in the United States. Many individuals with SCD require blood transfusions to increase their healthy red blood cell (RBC) count. Traditionally, clinicians have matched donor and recipient blood types through hemagglutination. This technique relies on the use of known antibodies, failing to account for lesser-known blood type variants in the *RHD* and *RHCE* genes that produce D antigen subtypes (i.e., weak D and partial D). We hypothesize that next-generation sequencing (NGS) will increase the resolution at which we type blood. This approach allows us to characterize and discover point mutations and copy number variants that impact antigen structure and function in the Rh system resulting in Rh subtypes. The Rh system alone contains approximately 400 different antigens, each clinically important, especially in chronically transfused patients who are prone to allosensitization. Utilizing both the Blood Group Antigen Gene Mutation Database and the University of California, Santa Cruz Genome Browser, our independent research project involves cataloging a number of genetic variants found in the Rh system (n = 393) along with the frequency of these alleles in various ethnic populations. Our established catalog will be used to characterize genetic variation within 30 whole genome sequenced trios (n = 90) generated through the National Children's Study. These analyses have both the potential to 1) identify patients' Rh blood types based on NGS sequencing data, and 2) classify novel Rh blood types that might have clinical significance in transfusion medicine, ultimately redefining the relationship between donors and recipients in transfusion therapy.

#### **SAT-1112**

##### **ASSEMBLY OF A GAL4-PBID EXPRESSION PLASMID FOR ANALYSIS OF PROMOTER ACTIVITY**

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Analysis of gene regulatory elements is approached using various *in vitro* and *in vivo* methods. *In vivo* analysis of gene expression has routinely been performed utilizing *Drosophila melanogaster* as the model organism. In particular, targeting plasmids have been employed to target the fly genome for the analysis of gene regulatory elements using P-element-based expression plasmid constructs such as pPTGAL4. Recent developments have yielded new classes of targeting constructs that rely on distinct DNA elements that, in turn, allow for site-specific integration of the targeting constructs in the genome at a landing pad. Currently, there are no suitable constructs available for GAL4-driven expression of reporter genes in an insulated system that also allows for site-specific integration into the genome. In light of this, we have

constructed a hybrid GAL4-based expression plasmid that provides an insulated background, allows for cloning of promoter fragments using a multiple cloning site, and allows for site-specific integration into the genome. This construct was generated by PCR amplification and cloning a GAL4-multiple cloning site DNA fragment into pBID, a site-specific integration plasmid. The functionality of this plasmid will be tested using the *Drosophila* KCNQ potassium channel promoters, which have been previously characterized and thus serve as a control set of promoters for characterization of this expression plasmid. The development of this plasmid will facilitate the analysis of gene promoter activity in an insulated background with a well-defined genomic location. This will provide a new tool for the analysis of gene activity in organisms such as *Drosophila melanogaster*.

#### **SAT-1114**

#### **GENOMIC ANALYSIS OF *CANDIDA ALBICANS* FOLLOWING SERIAL PASSAGE IDENTIFIES CANDIDATE VIRULENCE FACTORS**

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*Candida albicans* is a commensal fungus found in most human oral, gastrointestinal, and genitourinary tracts and is known to seed life-threatening infections in immunocompromised humans. In many microbial pathogens, the serial propagation of a strain within the host has been shown to increase the strain's virulence. However, most *C. albicans* isolates are well adapted to the mammalian environment, hindering microevolution events that could result in increased fitness or virulence. We hypothesized that extended passaging of clinical isolates of *C. albicans* would more readily allow the identification of novel fitness and virulence factors. There is limited knowledge around the microevolution of genes associated with pathogenicity in these cases, and our goal was to characterize the genetic differences between these pre-passaged and passaged strains of *C. albicans*. We used next-generation sequencing data generated on the Illumina HiSeq platform to study how isolates of 3 clinical isolates changed following passaging. Reads from the pre-passaged and passaged isolates were aligned to the *C. albicans* SC5314 reference using Burrows-Wheeler Aligner (BWA), and single nucleotide polymorphisms (SNPs), insertions, and deletions were detected using the GATK Unified Genotyper Variant Filtration. Given that we are particularly interested in identifying variants that reveal genetic differences between the pre-passaged and passaged isolates, we have begun to establish associations between shared genetic alterations and virulence. We have uncovered a number of initial candidate virulence factors, including transcriptional regulators of zinc cluster DNA-binding motif, putative GPI-anchored proteins, and ALS family proteins. These results may prove valuable for the future development of antifungal drugs.

**SAT-1111****CROSSING OVER: FINE-SCALE CHARACTERIZATION OF RECOMBINATION SUPPRESSION DURING THE EVOLUTION OF A YOUNG STICKLEBACK Y CHROMOSOME**

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Sex chromosomes evolve when recombination is suppressed between a pair of autosomal homologs. However, the details of these events are largely unknown in evolutionarily young sex chromosome systems. Threespine stickleback (*Gasterosteus aculeatus*) are particularly useful for studying these events because they have a relatively young (35 million years old) Y chromosome. Only 2 million years ago, an even younger neo-Y chromosome formed as the result of a fusion between an autosome and the ancestral Y chromosome in the Japan Sea population of threespine stickleback. Previous studies have indicated that suppression of recombination on the neo-Y occurs near the fusion event, contributing to divergence of the neo-X and neo-Y in the Japan Sea population. Although recombination suppression has been documented, the boundaries of recombination have not been finely mapped. Here, we construct a genetic linkage map of the neo-sex chromosomes by quantifying recombinant genotypes in approximately 600 total F1 progeny from 4 Japan Sea parent crosses. Microsatellite markers were genotyped at regular intervals across the ancestral and neo-sex chromosomes. Our results will reveal the extent and pattern of recombination suppression across the neo-sex chromosomes compared to ancestral sex chromosomes, shedding light on the earliest stages of sex chromosome evolution: namely, how recombination suppression in the Japan Sea stickleback sex chromosomes correlates with the evolution of male beneficial genes, and how mutations accumulate in the absence of recombination. Further analysis of these systems will provide an understanding of the role of recombination suppression in sex chromosome evolution and species diversification.

**FRI-1105****CHARACTERIZING THE GENETIC CHANGES OF AN OUTBRED LABORATORY POPULATION OF *NASONIA VITRIPENNIS* UNDER INDIVIDUAL AND GROUP SELECTION FOR NUMBER OF OFFSPRING**

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Phenotypic changes in laboratory organisms have been demonstrated as a response to group selection, but the extent to which group selection affects genomic variation is still poorly understood. *Nasonia vitripennis* (Pteromalidae) is a parasitoid wasp found worldwide. Due to the haplodiploidy sex determination system, ease to maintain lab populations, availability of a sequenced genome, and short generation time, *Nasonia* has become a model organism to study evolution and genetics including molecular evolution of adaptive traits and sex ratio evolution or co-evolution with endosymbionts. These attributes also make *Nasonia* a desirable system to investigate selection operating across multiple levels of biological organization. Here, we describe genetic variations among nine populations of *Nasonia vitripennis* for 10 microsatellite loci. We detected variations across all loci and also obtained the heterozygosity

for each locus. We bred these 9 populations to create a single genetically diverse lab strain. This population was subjected to both individual and group selection treatments, selecting on increased number of offspring per host. In the group selection treatment, the single group in each of the 3 replicates that produced the most offspring was selected for the next generation. In the individual selection treatment, the single female in each of three replicates that produced the most offspring was selected for the next generation. We then characterized the consequences of artificial selections on this genetically diverse strain by calculating heterozygosity and selection coefficients.

#### **SAT-1107**

##### **USING BIOINFORMATICS AND RNA-SEQ TO EXAMINE IRON DEFICIENCY CHLOROSIS IN SOYBEAN**

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Bioinformatics has become a necessary tool for research in the biological sciences. Analyzing RNA-seq data is especially crucial for completing studies that correlate phenotypic results to gene expression. In this study, we analyzed RNA expression in 2 different soybean lines, in 2 different tissues, at 2 time points, and under iron deficient and sufficient conditions. With 4 biological replicates per sample, we analyzed 48 different RNA-seq files, each with more than 10 million sequences. Therefore, we developed a user-friendly pipeline for analyzing the data. We used PuTTY to connect to a bioinformatics server, transfer, uncompress RNA-seq data files, and organize the project. Once on the server, we used a variety of publicly available programs to trim adaptors and remove low quality sequences. We then assembled the reads to the soybean genome. After the files were order, we used the statistical package R to identify genes differentially expressed in response to iron treatment in the 2 lines. An important feature of this pipeline is that we could use R to visualize our data and identify problems in our analyses and in the samples. With this information, we will be able to identify candidate genes for controlling plant response to nutrient stress that could be used for the improvement of soybean and other crops. Further, this becomes a resource for biologists to learn how to analyze RNA-seq data.

#### **FRI-1103**

##### ***C.ELEGANS* VS. *C.BRIGGS*AE LIN-3/EGF GENE COMPARISON**

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Cell signaling networks are important regulators of cell division and growth. Our research focuses on understanding how cell-signaling networks can function differently in distinct species. The formation of the vulval organ in *C. elegans* is relatively the same as in the related nematode *C. briggsae*. However, experimental studies show that there are important differences between the two species with respect to the epidermal growth factor (EGF)



pathway. The purpose of this project is to characterize the function of the signal gene, *lin-3*/EGF, in *C. briggsae* and compare it to *C. elegans*. One approach utilizes molecular analysis that is based on the observation that in *C. elegans*, the *lin-3* gene includes different splice variants, thus resulting in distinct proteins that are membrane-attached, or diffusible. We will evaluate the structure of *C. briggsae* *lin-3* cDNAs to determine whether they differ from *C. elegans* in the relative abundance of these forms. The second approach utilizes genetic analysis. In a genetic screen, we have identified 6 *C. briggsae* mutants with vulval development defects expected if the *lin-3* gene is disrupted. We are using DNA sequence analysis to determine whether any of the strains includes a mutation in the *lin-3* gene. If none of the strains carries a mutation in *lin-3*, we will use gene-targeting methods to generate a *lin-3* mutant. The results of this project will determine whether the observed differences between the species reflect differences in *lin-3*/EGF processing or diffusion, and will allow for functional comparison of *lin-3* mutants.

#### **FRI-1107**

#### **UNDERSTANDING GENOMIC FUNCTION THROUGH GENE ANNOTATION**

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Annotation is the process of describing the function of genes in a DNA sequence. Our aim is to develop an annotation pipeline that will allow us to effectively identify genes and their functional significance in order to better understand genomic divergence and function. The sequenced data used for this project came from the red lionfish (*Pterois volitans*) and *Heliconius* butterflies. The red lionfish is an effective invasive species across the Caribbean. However, it is not understood what gives them the potential to expand and establish effectively in new environments. Different populations of the *Heliconius erato* butterfly vary drastically in wing color patterns. To identify gene function in regions of high genomic divergence between populations may provide insight into the genes involved in adaptation and in wing color patterns. The lionfish data from sequenced material was aligned to a general nucleotide database in order to filter the sequences that mapped to the Actinopterygii (lionfish class), while a database protein search was done for the *Heliconius* data, obtained from a reference genome, in order to match nucleotide sequences with proteins. With the results from the lionfish data, we would like to generate a network of gene families and their functions. For the *Heliconius* butterflies, however, we were able to organize the data into the genome using the Artemis annotation tool. We are expecting that, with the results of the gene annotation together with results of population genomic analyses, we will be able to determine the genes responsible for the peaks of divergence.

**FRI-1115****CHARACTERIZATION OF RESPIRATORY PATHWAYS IN *SHEWANELLA ANA-3***

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Arsenate-reducing bacteria are intimately involved in processes that facilitate the release of arsenic from sediments and into groundwater, thereby causing arsenic contamination of water. Under aerobic conditions, arsenate is typically immobilized onto mineral surfaces. However, under anoxic conditions, microbes can respire the solid-phase arsenate producing arsenite, which is more toxic and mobile than arsenate. The facultative anaerobe and metal-reducing bacterium, *Shewanella sp. ANA-3* has been used as a model organism to study the regulation of arsenate respiration metabolism. Unlike *E. coli*, *Shewanella* does not use typical anaerobic regulators such as *fnr* and *arcA*. For this reason, it is hard to determine the regulation of arsenic respiration. A transcriptome experiment using RNA sequencing was done which identified a number of highly expressed genes associated with arsenate respiration conditions. It was hypothesized that these genes are potential candidates for the arsenate respiratory pathway and may be essential for arsenic respiration in *ANA-3*. To test this hypothesis, insertion mutations were systematically constructed within the coding region of 20 different candidate genes in order to disrupt their function. These mutants were grown anaerobically, respiring either arsenate or fumarate (control conditions) as terminal electron acceptors. Of the mutants tested, the putative thiol-disulfide interchange gene showed the most significant growth defect under arsenic conditions and grew similar to wild type on fumarate. To further study the importance of this gene in the arsenic respiratory pathway, biochemical studies will investigate how the thiol-disulfide interchange gene is directly involved in arsenic respiration.

**SAT-1110****CREATING THE FIRST DRUGGABLE GENOME**

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Genetic techniques such as gene knockout and knockdown have been enormously useful for understanding gene function, but they require many cell divisions, and therefore they enable secondary adaptations to become engaged. Secondary adaptations can be avoided by using small molecule inhibitors, but they are too expensive or even impossible to produce for genome-wide applications. Here we develop a new genome-wide method that would allow all genes of interest to be inactivated in response to a single small molecule. The method involves tagging each gene of interest with a small degron domain that causes rapid ubiquitylation and degradation of the entire protein in response to binding auxin. We developed a high-efficiency method of tagging these genes with the auxin-inducible degron (AID) and expressing the AID-specific E3 ubiquitin ligase (TIR1). Using the *PAN1-AID* gene as model, we optimized the concentration of the auxin analog, 1-naphthaleneacetic acid (NAA), which can be used to detect growth inhibition. Preliminary results showed that 25 out of 25 transformants correctly target the gene and confer sensitivity to NAA in the range of 50 - 100  $\mu$ M. Much higher concentrations inhibited growth of control cells, measured after just one day of incubation. However, we

expect the AID system of protein depletion will not work for all genes, particularly if the product is localized to an organelle. In summary, we have shown our method can be used to efficiently tag and inactivate many, but not all, gene products in yeast. This is the first step toward creating the first druggable genomes.

#### **SAT-1113**

##### **THE EPIGENOMIC AND EVOLUTIONARY IMPACT OF DNA METHYLATION SPREADING IN SOYBEAN**

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DNA methylation is an important mechanism for regulation of gene expression in plants. While methylation in the CG context is generally associated with gene expression, the methylation of transposable elements (TEs) occurs in three contexts (CG, CHG, and CHH, H = A, T, or C), which leads to their transcriptional silencing. Recent studies have shown that DNA methylation can spread from TEs to neighboring genes causing their transcriptional repression. However, the extent of this phenomenon and its impact on genome evolution is not well understood. To address this question, we conducted an epigenomic comparative study between domesticated soybean (*Glycine max*) and its wild relative (*Glycine soja*) using the whole genome methylome. In this study, we showed evidence that thousands of genes in domesticated soybean have been silenced during the last few million years due to the spreading of DNA methylation.

#### **SAT-1109**

##### **THE EFFECTS OF DEVELOPMENTAL ETHANOL EXPOSURE ON COURTSHIP BEHAVIOR IN *DROSOPHILA MELANOGASTER***

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Developmental ethanol exposure causes a collection of developmental abnormalities in mammals, collectively known as fetal alcohol syndrome (FAS) or fetal alcohol spectrum disorders (FASD). While the cause of FASD is known, the precise molecular pathways that are disrupted by developmental ethanol exposure are not well understood. We have developed a *Drosophila* model of FASD, and have previously shown that we can successfully model both the growth and development effects of ethanol and neurobehavioral abnormalities associated with developmental ethanol exposure. Courtship behavior in flies is a complex, yet hard-wired behavior, any disruption of which indicates abnormal neurological development. Our preliminary data indicates that expression of fruitless (*fru*), the master regulatory gene for this behavior, is disrupted by larval ethanol exposure. We are therefore characterizing courtship behavior as a model for the effects of ethanol on neurological development. We hypothesize that developmental ethanol exposure will result in changes in the performance of the courtship ritual. To test this hypothesis, we assay courtship latency (the time it takes males to begin courtship) in male flies reared in 7% ethanol-containing food. Behavior will be filmed for five minutes and the videos analyzed for the length of time before males begin to perform wing song. Significant changes in this latency indicate changes in behavioral responses to stimuli. We

will present the results of this analysis, as well as our examination, using GFP reporters in ethanol-reared flies, of the neural circuitry that regulates courtship. (This research was supported by NSF-REU Grant# DBI 1004350.)

### **SAT-1103**

#### **TARGETED DELETION OF ZEBRAFISH lncRNA IS18 WITH TALENS**

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Long, non-coding RNAs (lncRNAs) are important players in epigenetic regulation of gene expression during development and disease. A number of mechanisms have been proposed for lncRNA action; however, few functional studies of lncRNAs have been described. We are using transcription activator-like effector nuclease (TALEN) technology to create targeted deletions and conditional alleles of lncRNAs in order to investigate lncRNA function in development and cancer. The McGrail group has isolated a zebrafish retinal tumor model linked to a mutation in the lncRNA gene *lncRNA-cbx1a*. The goal of our project is to isolate a new deletion allele of the zebrafish *lncRNA-cbx1a* gene. To do this we will use two TALEN pairs to simultaneously target double-strand breaks to exons 2 and 5 of *lncRNA-cbx1a* in zebrafish embryos. Repair of the double-strand breaks by the non-homologous rejoining pathway will fuse exon 2 to exon 5 and the intervening genomic sequence will be lost, creating a new deletion allele. This strategy has been successfully employed to create a large deletion in the swine LDK receptor gene. The *lncRNA-cbx1a* deletion allele will provide a new genetic tool to study the role of lncRNA in zebrafish development and tumorigenesis.

### **SAT-1117**

#### **TRANS-SPLICING IN THE FLATWORM: THE EFFECT OF THE SPLICED LEADER 3'-TERMINAL AUG ON GENE EXPRESSION**

Ana Saucedo, Scott Roy.

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One area of growing interest to evolutionary geneticists is the process of spliced leader (SL) trans-splicing, which occurs in a number of eukaryotes including flatworms. When spliced leader trans-splicing occurs, a short sequence of RNA called the spliced leader is attached to the 5' end of some of an organism's pre-mRNA transcripts. Some functions of SL trans-splicing and their affect on gene expression, as well as other functions, are clearly identified. A consistent characteristic of the *Schistosoma masoni* SLs not fully understood is the existence of a terminal AUG at the 3' end of the sequence. This begs the question of whether or not this AUG could be used as a translation initiator methionine, and subsequently, what other effects this might have on gene expression if the AUG is translated. Our lab obtained *S. masoni* cDNAs from NCBI Sequence Read Archives and is now using bioinformatics analysis to examine this data. A small percentage of cDNAs have shown evidence of the SL sequence at the 5' end of the assembled transcripts. Of this group, we are working to identify instances when the terminal SL AUG extends into the main open reading frame of the transcript in order to determine the cases where this AUG could be required for translation initiation. Preliminary results have shown

cases where this occurs. These results and subsequent further analysis will allow us to continue to explore and better understand this possible additional function of SL trans-splicing in flatworms and its affect on gene expression.

#### **SAT-1102**

##### **GENETIC VARIABILITY OF THE METABOLIZATION OF COPPER IN GENE *ATP7B***

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Wilson's disease is an autosomal recessive genetic disorder caused by a deficiency in copper metabolism, which then accumulates in body tissues such as the liver or brain. Neuropsychiatric and hepatic symptoms are observed in subjects suffering from this disease. However, symptoms may be misdiagnosed as psychiatric or hepatic problems such as dementia or cirrhosis, with subsequent mistreatment and aggravation of the disease. Wilson's disease has been associated with mutations located on the *ATP7B* gene, which codes for a copper transporter to the bile, and ceruloplasmin, the major copper-carrying protein in blood. In most cases (60%), subjects are homozygous for a loss-of-function mutation in this gene. Otherwise, the subject may be heterozygous (30%) or carry no detectable mutation in *ATP7B* (10%). Two mutations have been found in a subject from southwestern Puerto Rico who appears to be heterozygous for Wilson's disease and slightly affected by copper transportation deficiency. One of them is an A-to-G transition at position 2731 of the mRNA based on GenBank accession number NM\_000053.3. This mutation abolishes a splice site. Another mutation located at position 3551, seems to cosegregate with the 2731 mutation, but it is located within an intron and believed to have no effect. We have established a major part of the genealogy of the subject and will be studying closely related family members that may be suffering from this condition to confirm the association of these mutations with the disease. We will also study the frequency of these mutations in different regions of Puerto Rico.

#### **FRI-1109**

##### **EFFECT OF TRP 64 ARG MUTATION IN HUMAN BROWN ADIPOSE TISSUE IN RELATION TO OBESITY AND ITS SECONDARY METABOLIC COMPLICATIONS**

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Obesity is a leading public health problem in the United States. New strategies to prevent obesity and increase the expenditure of energy are especially important. One potential target to explore in this approach is brown adipose tissue (BAT), which has the ability to dissipate energy by producing heat, rather than storing energy as triglycerides. A definite correlation between human obesity and BAT activity has not yet been made, but understanding how defective, human, brown fat cells relate to obesity is a critical step in elucidating new therapeutic strategies. In human white fat cells, the Trp64Arg mutation in the Beta-3 adrenergic receptor gene ( $\beta_3AR$ ) has been associated with diabetes mellitus type 2, increased capacity to gain weight, fat accumulation, insulin resistance, and an inability to break down fat. We aim to

understand the effect of this mutation in human, brown adipocytes. To do so, the genome editing system clustered regularly interspaced short palindromic repeats (CRISPR)-Cas9 will be used to design a mutant human embryonic stem cell line. Several CRISPR sequences will be analyzed to assess which construct functions most efficiently. The construct will then be introduced into the stem cells and differentiated to brown adipocytes. The generation and isolation of a functional Trp64Arg CRISPR construct and competent mutant BAT cell line will enable further studies of the importance of BAT cells in obesity.

#### **FRI-1106**

##### **DETERMINING THE ROLE OF TRANSLATION DURING THE CELL CYCLE IN *C. ELEGANS* EMBRYOS**

Alex Villarreal, Ahna Skop, Megan Gnazzo.

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Cell division is one of the most basic events required by all living organisms to accomplish growth, repair, and reproduction. Because this process is so vital, the smallest defects in cell division can lead to complications in cells such as becoming multinucleated, which is a driving factor behind tumor formation and conditions like cancer. It was assumed that translation within cells is temporarily inhibited during cellular division and rapidly resumes within each daughter cell immediately on entering the G1 phase of the cell cycle. However, several RNA-binding proteins have been identified, such as CAR-1, that function during cytokinesis. How CAR-1 is functioning during the cell cycle is unclear, although we suspect that CAR-1 could mediate the translation of localized mRNAs during cell division. The goal of this project is to determine if translation is necessary during the cell cycle in early *C. elegans* embryos. We plan to determine the critical concentrations of translation inhibiting drugs (puromycin and cyclohexamide) on permeable *C. elegans* embryos. We will then visualize the treated embryos using *in vivo* video microscopy to determine the cellular consequences of these drugs. We are particularly interested in observing cell division and cell cycle defects. This research may provide evidence that translation plays a role during the cell cycle.

#### **FRI-1110**

##### **DEVELOPMENT OF A SELECTION MARKER FOR AUTOMATED GENOME CONSTRUCTION**

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Selectable markers have been essential tools of genetic engineering for some time. They are commonly used for plasmid maintenance, engineered conjugation, and genome manipulation. On the other hand, counter-selectable markers are also useful for a handful of techniques. These applications include scar-less gene deletion, plasmid curing, and engineering double-crossovers. Since selectable and counter-selectable markers both have practical applications that are very useful, development of dual-selectable markers is desirable. As in the case of counter-selectable markers, dual-selectable markers also suffer from high counter-selection escape; this is one of the primary complications of finding suitable dual-selectable markers. In this project, we will attempt the development of a selection marker for automated genome construction. We will be working with the enzyme thymidine kinase /deoxyuridine kinase (tdk)

and demonstrate whether it can be used for coselection multiplex automated genome engineering (coS-MAGE). We will be alternating between Azt & Fdu through the cycles and determining where the break-out point lies. An effective, dual-selectable marker is one that can manage to run through various cycles without breaking down. (This research is supported in part by SHURP award NSF DBI-1263215 and an award from the Biogen-IDEF Foundation.)

#### **SAT-1104**

##### **LOCALIZATION OF THE PROTEIN CODING GENE *CG1674* WHOSE FUNCTION REMAINS UNKNOWN**

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In *Drosophila melanogaster*, the study of muscle formation and structure can be used to gain a better understanding of the factors that trigger muscle disease in humans. Our current goal is to determine if the protein CG1674 is a component of the sarcomere and if it is required for muscle structure and function. The protein coding gene *CG1674* was discovered through proteome sequencing of dissected flight muscles. This sequencing data suggests that our protein is a functional component of the flight muscles of *Drosophila melanogaster*. We are currently generating a CG1674-GFP fusion protein to determine localization of our protein within the muscle cell. In parallel, we are trying to determine the requirement for *CG1674* in normal muscle formation by using RNAi. When crossing CG1674-RNAi with the drivers Mef2Gal4 and 1151Gal4, the flies are flightless. We are currently in the process of staining sections of these flies to examine their muscle morphology. We predict malformation of the muscles, specifically in the myofibril structure. By finding the cellular location of *CG1674*, we hope to determine its function in muscle development.

#### **SAT-1101**

##### **IDENTIFYING GENETIC FACTORS AFFECTING FIBER LOSS IN AGING MUSCLES**

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Sarcopenia is age-dependent muscle atrophy and loss. This loss of muscle mass is a direct result of loss of individual muscle fibers. Although the consequences of sarcopenia have been identified, the mechanisms that lead to this particular condition are unknown. This study investigates the roles of the transcription factors Rbf1 and Dp in age-related muscles fiber loss in the jump muscle of the fruit fly *Drosophila melanogaster*. The jump muscle in flies consists of 20 to 30 individual fibers that are gradually getting lost over the lifespan. We quantified the extent of fiber loss by counting jump muscle fibers in young and aged flies. In experimental flies we decreased expression of either Dp or Rbf1 in jump muscles through the genetic knockdown technique. We found that downregulation of Rbf1 and Dp results in an improved fiber retention in aging jump muscles, as compared to control jump muscles. Dp and Rbf1 are known transcriptions factors, collaborating with each other to make a regulatory complex to control gene expression. We propose that Dp and Rbf1 could be involved in human sarcopenia, as they have readily identifiable human homologs. In our studies, *Drosophila* proved to be a good model for identification of novel factors that contribute to muscle aging, and we anticipate that in the future more such factors will be revealed.

**SAT-1106****TRANSCRIPTONAL ANALYSIS OF GLYCOLYSIS, BETA-OXIDATION, AND PROTEOLYSIS IN RESPONSE TO LOCALIZED TISSUE DAMAGE IN *D. MELANOGASTER***

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Organisms that suffer tissue damage during development must undergo delay and allocate resources toward correcting injuries before proceeding toward later stages, otherwise complications may rise later in development, including death. The mechanisms underlying this phenomenon are largely unknown. It is likely that localized injury leading to developmental delay will increase the energy needs of the organism and upregulate anabolic pathways. We are examining changes in gene expression following wing precursor tissue damage in the fat body of the third instar larval stage of *Drosophila melanogaster*, commonly known as the fruit fly, to understand the metabolic response to injury during development. The metabolic needs of developing larvae are met largely by the fat body, an organ analogous to the human liver and important in the storage, synthesis, and transportation of amino acids, fatty acids, and carbohydrates. We use microarray analysis of RNA isolated from larval fat body to identify genes in various metabolic pathways that are differentially expressed following injury. Pathways of interest include glycolysis, beta oxidation, and proteolysis because of their importance in energy and metabolite homeostasis. Understanding the changes in gene expression and metabolic changes in injured larvae can lead to a greater understanding of complications that develop early in development of complex Eukaryotes.

**SAT-1105****EVOLUTION AND FUNCTION OF *QUERCUS LOBATA* PROTEINS: PEPSIN RETROPSIN, REC, CCT, NUDIX HYDROLASE, LEA\_2, RETROPEPSIN LIKE, AND PMD**

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The California valley oak (*Quercus lobata*) is endemic to the state of California and is currently a threatened oak tree species. This study focuses on determining the function of proteins from the valley oak. These proteins come from the genes from 3 “contains” generated from the genome. The entire genome of the *Quercus lobata* was sequenced through Illumina Next Generation Sequencing using Solexa technology. Contigs are assembled with the use of De Bruijn graphs in order to construct the entire genome. For the study, 3 “contains” were used in the preliminary annotation. DNASubway was used to produce gene predictions for proteins and their functions through the use of Wolfpsort, InterProScan, and NCBI. The peptide sequences and top BLAST results were used to assemble a maximum likelihood phylogeny tree through the use of MEGA 5 for each of the peptide sequences taken from the gene predictions. The “contains” contain the genes for pepsin retropepsin, REC, CCT, nudix hydrolase, LEA\_2, retropepsin like, and PMD. There is little known about REC and PMD in plants because they were only recently discovered in eukaryotes. REC is a signal receiver domain and it was



originally thought to be unique only to bacteria, but has been found in eukaryotes. PMD was discovered in 2006, but there is little information about the role it plays in oak trees.

#### **FRI-1108**

##### **TRANSCRIPTOME-WIDE EXPLORATION OF THE RELATIONSHIP BETWEEN SECONDARY RNA STRUCTURE AND RNA MODIFICATIONS**

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Despite the fact there are over 100 different types of modifications that can occur on RNA, little is known about their function and impact on the RNA's life cycle. Pseudouridine and N6-methyladenosine are 2 of the most abundant RNA modifications, and although their discovery occurred decades ago, little is known about the factors governing which precise substrates are subjected to the modifications. The development of a sequencing method that combines dimethyl sulfate (DMS) labelling of non-structured RNAs with RNA sequencing provides transcriptome-wide information on RNA secondary structures in yeast. We hypothesized that RNA secondary structure might play a role in guiding catalysis of RNA modifications at specific sites. To test this hypothesis, we created a pipeline that allows examination of secondary RNA structures in relation to the location of modified nucleotides. The pipeline extracts secondary structure in a window of 200 nt centered around modified nucleotides and allows studying the secondary structure either at a per-modification level, or across all modified sites (meta-modification analysis). Sequence and expression controls are employed to account for sequence-level artifacts. We initially found a strong secondary structure for pseudouridine, which we subsequently determined to reflect a sequence-dependent artifact. Analysis of structure in the context of N6-methyladenosine is ongoing. Our analysis should help resolve longstanding questions regarding the factors governing RNA modification substrate specificity, as well as potentially shed light on their function.

#### **FRI-1111**

##### **DEVELOPMENT OF A KARYOTYPE FOR *ARACHIS HYPOGAEA* L. (PEANUT) USING REPETITIVE SEQUENCE FISH PROBES**

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Since its domestication approximately 3,000 years ago, the species *Arachis hypogaea* L. (peanut;  $2n = 4x = 40$ ) has been a crop species of considerable importance particularly for the United States, the third largest peanut producer in the world. In addition to its importance as an international food, the peanut is known for its array of uses and high nutritional content, including proteins (25% per 100 g), vitamins B, C, and E, CoQ10 and antioxidant contents rivaling many fruits. The remarkable nature of the peanut is only further realized by its ability to grow in a substantial variety of climate conditions; however, many promising aspects of the *A. hypogaea* crop are overshadowed due to both the limited genetic information available and the lack of a karyotype. Here, we present progress in developing a karyotype for the

peanut. We conducted FISH in order to develop a better understanding of peanut genetics, using probes that target abundant repeat sequences throughout the peanut genome. Ultimately, this work will complement the sequencing of the peanut genome and may facilitate a more thorough understanding and aid in better cultivation of peanut.

#### **SAT-327**

##### **DISEASE-RELEVANT MUTANT VCP DYSREGULATES NF- $\kappa$ B ACTIVATION, AND ITS IMPACT ON THE EXPRESSION OF UBIQUITIN E3 LIGASES IN C2C12 MYOBLAST CELLS**

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Inclusion body myopathy with Paget's bone disease and frontotemporal dementia (IBMPFD) is an autosomal dominant disease caused by mutations on the valosin containing protein (VCP) gene. Over 80% of patients with VCP mutations develop progressive muscle weakness and wasting. Its underlying pathogenic mechanisms, however, remain largely unknown. Previously, we have shown that the disease-associated mutant VCP (R155H and A232E) prolongs NF- $\kappa$ B activation in C2C12 myoblast cells following an acute LPS stimulation. We hypothesize that the impaired resolution of NF- $\kappa$ B activation leads to aberrant transcriptional alterations, including up-regulation of inflammatory-related genes and muscle-specific ubiquitin ligases, which further promote degeneration of muscle cells. We first examined the changes in muscle-specific ubiquitin E3 ligases, Murf 1 and Atrogin 1, following the acute LPS exposure to C2C12 cells. Our preliminary immunofluorescence data indicates an increase in expression of Atrogin 1 protein levels, while no significant difference has been noticed in Murf 1 levels after NF- $\kappa$ B activation. To test whether VCP mutation exacerbates the expression of Atrogin1 and Murf 1 in comparison to wild-type VCP, we will transfect murine myoblast C2C12 cells with plasmid containing wild-type VCP, VCP-R155H or VCP-A232E. Transfected cells will then be incubated for 1 hour with 1  $\mu$ g/mL LPS as NF- $\kappa$ B activator, followed by a 1 hour incubation for recovery without LPS. Protein levels will be quantified through western blot and intensity analysis of immunofluorescence staining. We expect greater protein levels of Atrogin1 and Murf1 in mutant VCP which may help to understand the underlying mechanisms of muscle degeneration in IBMPFD patients.

#### **FRI-1117**

##### **PIRFENIDONE: TREATMENT FOR IPF**

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Idiopathic Pulmonary Fibrosis is a progressive fibrotic pulmonary disease that carries a 50% survival within 5 years of diagnosis. Currently there is no FDA approved treatment for this disease. Pirfenidone has been studied for the treatment of Idiopathic Pulmonary Fibrosis. Pirfenidone is an anti-fibrotic and anti-inflammatory medication that inhibits the production and release of inflammatory cytokines. Pirfenidone has been shown to weaken fibroblast proliferation and therefore slow the advancement of this disease. Recent clinical trials comparing Pirfenidone to placebo demonstrate a decreased disease progression by 43% and possible a decreased mortality rate in the patients with IPF. This data has lead us to hypothesize that treatment with the drug Pirfenidone could slow the progression of the disease and prolong the life of the patient with Idiopathic Pulmonary Fibrosis. This drug is currently being considered by the FDA for approval.

This summer, the sponsor of this trial, InterMune implemented an early access program to Pirfenidone. Once the patient is screened through preliminary inclusion/exclusion criteria and accepted they will begin an 18 month drug therapy program; where Pirfenidone is titrated to 2403 mg/day over an initial 14 days. This program will allow patients with Idiopathic Pulmonary Fibrosis to begin therapy with this drug while it is being considered for FDA approval. This access to Pirfenidone offers hope to patients with IPF.

## MARINE SCIENCES

### FRI-704

#### BIOGEOGRAPHIC SHIFTS AND SPECIES DENSITY OF ECHINOID (SEA URCHIN) SPECIES ALONG THE SOUTHERN CALIFORNIA BIGHT ASSESSED USING GEOGRAPHIC INFORMATION SYSTEM

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The expansion of the ocean's oxygen minimum zones is a concern because it influences oceanographic boundaries for many species, which may either expand or contract their habitat range. Evidence from terrestrial fauna and flora suggests that species distribution has been continuously adjusting to changing climate conditions. However, we currently lack an understanding of how deep sea animals are responding to these conditions. Over the last 25 years there has been a 20-30% decline in oxygenation of the upper slope off southern California. This study evaluates how decreases in oxygen concentration have altered the depth distribution and density of the sea urchins *Strongylocentrotus fragilis* and *Lytichinus pictus* in this region. Sea urchins are found on the sea floor all over the world, and often are a keystone species; they comprise most of the megafauna in the Southern California Bight (SCB). The Southern California Coastal Water Research Project (SCCWRP) and the Bight Program have surveyed the SCB and collected megafauna via benthic otter trawls every 4 to 5 years from 1994 through 2008. Our research uses ArcGIS version 10.1 to visualize and interpolate data to understand the trends that these species are exhibiting in the SCB. We predict that *Strongylocentrotus fragilis* will expand their depth distribution since they thrive in low oxygen and elevated CO<sub>2</sub> waters and *Lytichinus pictus* will contract their depth distribution in response to declining oxygen concentrations. Such information allows us to understand how deep sea animals respond to hypoxia.

#### **FRI-724**

##### **IDENTIFICATION OF SUBSEAFLOOR IRON REDUCERS AND SULFUR OXIDIZERS FROM EXTINCT SEAMOUNTS**

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While a majority of the living space in the ocean is deeper than light can penetrate, known as the aphotic region, very little is known about the microbes who survive without sunlight. The largest aquifer on Earth can be found within the seafloor basaltic crust, and it holds an undetermined amount of biomass. Seawater flows through seafloor basaltic rock, carrying with it nutrients that can sustain microbes. Because basalts are rich in iron (Fe) and sulfur (S), it is hypothesized that seafloor basalts should harbor microbes that perform redox reactions with Fe and S for respiration. To test this hypothesis, subsurface samples were taken during Integrated Ocean Drilling Program (IODP) Expedition 330, which sampled 50 to 80 million year old seamounts along the Louisville Seamount Trail in the southwest Pacific Ocean, and kept *in vitro* in media that encourage growth of iron reducers and autotrophic sulfur oxidizers. Enrichments were kept at 4 °C until sampling 0.5 to 3 years later, when some of the enrichment was transferred to new media and the rest filtered for subsequent DNA extraction. Their DNA was extracted and analyzed via quantitative polymerase chain reaction (qPCR) of the bacterial *16S rRNA* gene, a microbial genomic fingerprint, to determine relative biomass in the incubations. *16S rRNA* gene counts ranged about  $7 \times 10^2$  to  $7 \times 10^8$  copies for 70 enrichment incubations analyzed. Enrichments with greater than  $10^3$  gene copies were analyzed by amplicon sequencing of the *16S rRNA* gene. Results of this sequencing, which inform us of the Fe and S cycling microbes present in old, seafloor basaltic crust, are discussed here.

#### **FRI-723**

##### **THE USE OF VITELLOGENIN AS A BIOMARKER IN WHITE PERCH (*MORONE AMERICANA*)**

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Due to the impact of endocrine disrupting compounds (EDCs) and estrogens in the environment, white perch within the Chesapeake Bay have experienced disruption in their endocrine system. Biomarkers, such as vitellogenin (VTG), are early warning signals of exposure to EDCs. VTG is synthesized and secreted in the liver in response to endogenous estrogens in female fish. It is released into the bloodstream and stored in oocytes where it is converted to egg yolk proteins. In males, the presence of vitellogenin shows there has been exposure to estrogenic compounds or EDCs. The EDCs and estrogenic compounds are problematic because they are the cause of increased incidences of reproductive disorders, developmental abnormalities in wildlife, including fish, and reduced fertility in human males. The source of these EDCs is widespread and includes anthropogenic as well as agricultural inputs. The liver of the male white perch was used to establish the presence of vitellogenin within 3 tributaries and 3 seasons. Each tributary was classified based on its land-use pattern: developed, agriculture, and forested. Fish livers were sonicated in 100 µl of phosphate buffered saline in the presence

of protease inhibitors. The soluble proteins containing vitellogenin were recovered by centrifugation and extracted. Presence of vitellogenin will be determined using ELISA. Determining the presence of vitellogenin in the liver will contribute to understanding the disruption of the endocrine system of white perch due to land-use patterns and seasonal variations.

#### **SAT-724**

##### **OCEAN BITEMAP A PROTOCOL FOR SIMPLE, STANDARDIZED ASSAYS OF MARINE PREDATION INTENSITY**

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The marine realm covers 70% of our planet. These key ecosystems and their related biodiversity are critical for life, producing oxygen, regulating climate, breaking down wastes, recycling nutrients, purifying water, and providing food. Therefore, it is necessary to understand what constitutes a healthy and balanced marine ecosystem. MarineGEO is a global monitoring system assessing near-shore communities across the globe. To understand the patterns of marine predation and their grazing intensity over space and time we are participating in a bicoastal experiment to compare coral reefs in Kaneohe Bay, Hawaii and Fort Pierce, Florida. We measured the feeding of carnivorous, herbivorous, and omnivorous fish. Specifically, a series of plastic rods were baited with dried squid and fresh kale, placing them in sandy bottom, reef flat, and the reef slope on the windward and leeward side of Coconut Island. Feeding was scored completely consumed, partially consumed, or untouched, over a 24 h period. To determine which species were eating the bait underwater Go Pro cameras filmed feeding activity. Upon completion of these current experiments data will be analyzed and compared between the Hawaii and Florida sites. Healthy communities support abundant sea life capable of finding and capturing food within relatively short periods of time. Therefore, these types of standard assessments of marine communities will reveal important attributes about the absence and presence of fish and their feeding patterns. Understanding these patterns and how they fit into a global pattern is essential to help restore near shore communities highly impacted by human population.

#### **FRI-717**

##### **OOCYTE DEVELOPMENT IN WHITE PERCH (*MORONE AMERICANA*)**

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White perch (*Morone americana*) is one of the most abundant species of fish in the Chesapeake Bay. It serves important roles both ecologically, in its intermediate trophic level, and economically, as a recreational and commercial fishery. Despite its abundance, little is known about the effect of increased levels of exposure to endocrine-disrupting compounds from developed and agricultural land use on the fish's reproductive development. During 2010 and

2011, white perch were collected from 6 different Chesapeake Bay tributaries, each associated with agricultural, developed, or forested land use. The ovaries from these fish were embedded and sectioned to create histological slides, and a sample of oocytes' development was staged based on developmental classifications. Preliminary results have shown that from 2010 to 2011 fish from some of the tributaries have experienced a significant increase ( $p < 0.05$ ) in number of oocytes at the highest classification of development. This serves as an indicator of an increasing number of oocytes undergoing vitellogenesis, a biomarker of exposure to endocrine-disrupting compounds. Continued research and results from this experiment may demonstrate significant differences in the level of development of oocytes of white perch from different tributaries with varying levels of endocrine disrupting compounds. Developmental differences in white perch may lead to changes in population structure, behavior, and the overall ecological role that these fish play in the unique Chesapeake Bay ecosystem.

#### **SAT-721**

##### **EFFECTS OF *VIBRIO* BACTERIA IN GLOBAL FISH TRADE INDUSTRY**

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Ornamental fishes are the third most common pets in the United States and are largely imported from harvest locations and aquaculture facilities in Southeast Asia. Disease along shipment routes is a major obstacle to fish welfare and industry profitability, yet little is known about the microbial communities associated with these fish shipments. The objective of this research is to further understand the behavior of potential bacterial pathogens while transported from one location to another, and the major role they play in microbial communities, the environment, and fish and human health. Our research will focus on the genus *Vibrio*, a known bacterial fish pathogen. The proposed methods are to measure and contrast the diversity of *Vibrios* using next-generation DNA sequencing data. Our analyses will determine whether any increases in pathogenicity occur during shipment both inside and outside fish in transit and upon arrival to pet shop aquaria. We hypothesize that, due to stressful conditions of fish shipments, more pathogenic *Vibrios* will be found after transit. The findings of the research will provide clues to fish disease in trade and hopefully influence regulatory measures to control the treatment and handling of ornamental fishes that carry such potential pathogens.

#### **SAT-703**

##### **EFFECTS OF PREY AVAILABILITY ON CONDITION AND SETTLEMENT TIMING OF LARVAL NORTHERN ROCK SOLE (*LEPIDOPSETTA POLYXYSTRA*)**

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Northern rock sole (*Lepidopsetta polyxystra*), an economically important species in the Gulf of Alaska and Bering Sea, have pelagic larvae that develop into benthic juveniles. The larvae

disperse passively from hatching sites before settling in nursery habitats and undergoing metamorphosis to become juveniles. While the substrate preference of newly settled juveniles is well studied, settlement patterns observed in the field are annually variable and often deviate from predictive habitat models. Therefore, the drivers of settlement are still unclear. We addressed the hypothesis that planktonic prey availability impacts the condition of northern rock sole larvae and affects the timing of settlement. We raised larvae from hatch in both high and low prey treatments. When fish began to settle in the tanks, we measured the standard length and dry mass of both the settled and pelagic larvae within each treatment and compiled those data into a linear regression model. The residuals of the length-dry mass relationship were used to measure conditions. Preliminary results of the analysis of the residuals suggest that larvae from the high food treatment were in better condition than those in the low food treatment. The data also indicates that settled larvae were in better condition than the pelagic larvae in both food treatments. Based on these results, we postulate that some level of condition is necessary before larvae are competent to settle. This competence may be advantageous for surviving the energetic demands of metamorphosis and adapting to a new benthic lifestyle and its associated foraging challenges.

#### **SAT-704**

#### **THEN AND NOW: A 40-YEAR TROPHIC ECOLOGY COMPARISON OF COASTAL ELASMOBRANCH SPECIES IN ELKHORN SLOUGH, CALIFORNIA**

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Sharks and rays are apical predators that inhabit Elkhorn Slough, a tidally influenced estuary in Moss Landing, California. These elasmobranchs utilize the slough as habitat, feeding grounds, and a nursery area in the spring and summer when the waters are warm. Elkhorn Slough is subject to anthropogenic impacts such as agricultural runoff and erosion due to the dredging of Moss Landing Harbor. As sharks and rays are upper trophic level predators, they may be threatened by changes in their habitat, especially to their food source. Leopard sharks (*Triakis semifasciata*), bat rays (*Myliobatis californicus*), and thornback rays (*Platyrrhinoidis triseriata*) were used to evaluate how trophic positions and food web relationships have changed over time using previous studies for comparison. Ten replicates per species of liver and white muscle tissue were analyzed for trophic position using stable isotope analysis (SIA), and stomach-gut content analysis (SCA) was used to visually analyze the stomach contents. Additionally, whole frozen prey items underwent SIA for trophic position to provide a basis for the food web. Comparing the results from SIA and SCA identified whether elasmobranch diets were benthically or pelagically sourced and what percentage of their diet is dependent on prey items available within the Elkhorn Slough. The results will determine if and how trophic relationships are changing in a key estuarine habitat and assist with management decisions and conservation of elasmobranch species.

**FRI-737****DETERMINING AGE AND BODY SIZE DISTRIBUTION OF ENDANGERED NORTH PACIFIC LOGGERHEAD TURTLES (*CARETTA CARETTA*) AND EAST PACIFIC GREEN TURTLES (*CHELONIA MYDAS*) AT AN EAST PACIFIC BYCATCH HOTSPOT**

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Stranding rates along the coastline of areas highly utilized by fishing industry can give an indication of the magnitude of at-sea mortality for local wildlife. Studies have shown that multiple sea turtle species use the Pacific coast of Baja California Sur, Mexico, as an important foraging ground, and bycatch from both industrial and artisanal fishing in this area results in a high rate of mortality, significantly impacting sea turtle populations. The focus of the present study is to determine the age of endangered sea turtles, specifically North Pacific loggerheads (*Caretta caretta*) and East Pacific green turtles (*Chelonia mydas*), utilizing this high bycatch area. This research is part of an ongoing study examining the life history and habitat-use patterns of marine turtles in the Eastern Pacific. The size distribution of loggerhead turtles (n = 26) and green turtles (n = 25) gathered from stranding events along the coast of Baja Mexico from 2001 to 2013 are quantified using skeletochronology techniques. Skeletochronology ages marine turtles and back-calculates carapace length by identifying and measuring the annual growth rings in their humerus bones. Results from this research will later be coupled with stable isotope analysis to understand habitat-use patterns. The goal of this study is to better describe the size and age distribution of 2 species of marine turtles along the Pacific coast to improve the efficacy of present conservation efforts.

**SAT-740****PASSIVE ACOUSTIC MONITORING OF NORTH ATLANTIC RIGHT WHALES**

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North Atlantic right whales, *Eubalaena glacialis*, are a critically endangered species facing significant threats from ship strikes and entanglement in fishing gear. The migratory patterns between their summer feeding grounds off the northeast coast of the U.S. and their winter calving grounds off the southeast coast of the United States are poorly understood. To increase our understanding of the routes and timing of migration through the mid-Atlantic region, we deployed 5 marine autonomous recording units (MARUs) to monitor right whales migrating past Cape Hatteras, North Carolina. The MARUs were deployed in a line extending from near shore out to the shelf break at 5, 10, 20, 30, and 40 km. The units collected acoustic data continuously from October 2013 to February 2014. The MARU closest to shore was released from its mooring during a storm, and severe weather did not permit retrieval. The acoustic data from the four remaining units was analyzed using an automated baleen whale call detection system and manual review of spectrograms. Right whale up-calls were detected on 28% of the total number of days recorded, with all detections occurring between December and February. The most up-calls were detected on the two recording units located 10 and 20 km off the coast



of Cape Hatteras, suggesting that the migratory corridor is in close proximity to shore. From these results, we show that passive acoustic monitoring is an effective way to study North Atlantic right whale migration through this region.

#### **FRI-718**

##### **THE EFFECT OF OCEAN ACIDIFICATION ON INVESTIGATORY BEHAVIOR OF TWO JUVENILE ROCKFISH SPECIES**

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The recent rise in atmospheric carbon dioxide (CO<sub>2</sub>) has led to increased absorption of CO<sub>2</sub> into the oceans and a drop in ocean pH that may impact marine organisms. Many studies have shown that ocean acidification negatively affects shell-forming invertebrates, but there are few studies that investigate how fish are affected. Newer studies have reported that changes in pH can alter fish behavior and that some species seem to be more resistant to future pH conditions than others. This study examines the boldness and curiosity of juvenile fish from 2 temperate species: copper rockfish (*Sebastes caurinus*) and blue rockfish (*Sebastes mystinus*). Individuals were acclimated to one of 4 different pH treatments (7.2, 7.5, 7.8, and 8.0) for 16 weeks. Each individual was exposed to a novel object, and the time each fish investigated the object was measured over a 10 minute period. We predict that a decrease in pH will affect investigation time for copper, but not for blue rockfish, which may affect fitness and, in turn, lead to changes in the structure of fish communities on temperate reefs.

#### **FRI-739**

##### **INSIGHT INTO THE ESTABLISHMENT OF THE INTRODUCED MANILA CLAM IN A BAY AT THE SOUTHERN END OF ITS INTRODUCED RANGE**

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Abundance of the introduced Manila clam (*Venerupis philippinarum*, Veneridae) are increasing in Southern California estuaries, likely due to various local sources of planktonic larvae and adults and spread from established populations farther north over decades. The clam has been present but sparse in Mission Bay since the 1990's but has recently been observed as common. Our project, therefore, tests the influences on establishment of the clam within this region. During summer 2013, we sampled 8 paired sites, adjacent reaches of tidal flat with and without hard substrate (e.g., rip rap). We measured likely environmental influences (e.g., soil properties, salinity, distance to bay mouth, and inflows). Preliminary data show that the Manila clam is associated with hard substrate and fine organic sediments and is often found in high abundances with fewer native venerids. Our results will reveal the distribution of the clam and environmental influences on its establishment within Mission Bay. Lessons will provide insight into the management of the species such as the conditions under which it is likely to establish.

#### **SAT-734**

##### **POTENTIAL EFFECTS OF ENDOCRINE DISRUPTING CHEMICALS ON FISH COMMUNITIES IN LOWER NEWPORT BAY, CALIFORNIA**

Prarthana Shankar, Evelyn Ruelas, Arthur Barraza, Angela Castanon, Brian Rivas, William Hoesel, Kristy Forsgren.

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Endocrine disrupting chemicals (EDCs) are anthropogenic, exogenous compounds that alter the endocrine system, affecting hormone-regulated functions including reproduction and growth. There is growing concern for EDCs entering the aquatic ecosystem via urban runoff and impacting local fish populations. We studied the potential effects of EDCs on fish in Lower Newport Bay, CA. We hypothesized there would be no differences in the standard length, weight, and reproduction of fishes collected via beach seines at three eelgrass bed sites (2 receiving runoff via nearby storm drains and a reference site without a storm drain). We found no significant differences in the length or weight of black surfperch and shiner surfperch among sites. Spotted sand bass were significantly longer ( $p = 0.0424$ ) at one of the storm drain sites but showed no difference in weight ( $p > 0.05$ ). Topsmelt and giant kelpfish were significantly larger ( $p < 0.0001$ ) at one storm drain site and smallest at the other storm drain site. A subset of fishes is further being assessed for reproductive health. Interestingly, 59% of male black surfperch had only 1 testis. Black surfperch had a male-skewed sex ratio at all sites (expected 50:50 sex ratio,  $p = 0.0020$ ). Our findings are consistent with previous research linking EDCs with skewed sex ratios and differences in length and weight of fish. Additionally, the absence of one testis in black surfperch is unusual and may be an effect of EDCs. Continued monitoring of fish populations in Lower Newport Bay is important to further our understanding of the impact of EDCs via urban runoff.

#### **SAT-718**

##### **THE STUDY OF ULVOID BLOOMS OVER TIME AND THEIR EFFECTS ON THE SALT MARSH COMMUNITY IN ELKHORN SLOUGH ESTUARY**

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Anthropogenic inputs into coastal ecosystems such as nitrogen and phosphorous represent a significant threat to the functioning of these ecosystems. Coastal estuaries are particularly susceptible to the impacts of increased nutrient input due to their role as a buffer between coastal and terrestrial ecosystems. In this study, the effects that nutrient driven growth of *Ulva* has on *Salicornia* sp., the predominant salt marsh plant in the Elkhorn Slough Estuary, will be examined. In particular, this study will determine whether temporal and spatial variation in *Ulva* blooms affect the growth and survival of *Salicornia* in the Elkhorn Slough Estuary. This study will be conducted in three distinct parts. The first aspect of the project includes viewing historical, aerial photos of Elkhorn Slough to estimate *Ulva* sp. abundance from 1930s to present day and correlate these values with nutrient data. *Ulva* sp. abundance and nutrient levels are expected to have a directly proportional relationship. The second part of this study is

a field experiment testing the effects of *Ulva* sp. coverage on *Salicornia* by using two quadrat types; *Salicornia* free of algae and *Salicornia* covered by algae. The last component of the study, monitors algae distribution along the salt marsh edges of the estuary. Since *Salicornia* is a major component of the salt marsh, it is important to understand its current response to algal coverage. Loss can lead to the decline of both plant and animal abundance and diversity as well the loss of key ecosystem services within the slough.

#### **FRI-740**

##### **NATICIDAE GASTROPODS PREDATOR-PREY RELATIONSHIP RELATED TO SIZE-SELECTIVITY**

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In nature, animals commonly select prey based on the costs and benefits associated with its capture and consumption. For example if a larger predator pays a lower cost for feeding on a large prey item than a smaller predator then the difference in cost will influence the feeding preferences. This study examined the relationship between prey size (surf clam, Matridae) and predation patterns (moon snails, Naticidae). A random sample of predated surf clams (n = 477) was collected from Otter Island, South Carolina in December 2013. Predated shells were identified by the presence of a borehole, the size of which is correlated with the size of the moon snail predator. The measurements of the shells and their boreholes were obtained from digital images using ImageJ software. The results indicate there is a positive correlation between predator size and the size of the prey, which supports the hypothesis that moon snail predators' exhibit size selectivity on their prey choice. This pattern is expected if different sized predators feed on prey of sizes similar to their own.

#### **SAT-723**

##### **MONITORING SPECIES OF INTEREST IN THE ROCKY INTERTIDAL: AN EVALUATION OF THE ACCURACY OF CITIZEN SCIENCE DATA COMPARED TO EXPERTLY COLLECTED DATA WITHIN MONTEREY BAY**

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The citizen science movement involves the use of a person who is not paid and does not necessarily have a science background who is trained by a researcher to collect data and handle equipment and made its debut in 1900 with the annual National Audubon Society Christmas bird count. As researchers have recognized the benefits of large-scale data collection by volunteers, the use of citizen scientists has gained powerful momentum with institutions such as Cornell University and the National Science Foundation leading the charge. With the potential power to influence environmental policy and research conclusions, data collected by citizen science should be subject to careful scrutiny, especially if the data is detailed. Two organizations, the Partnership for Interdisciplinary Studies of Coastal Oceans (PISCO) and the Long-term Monitoring Program and Experiential Training for Students (LiMPETS) monitor the rocky intertidal along Monterey Bay sharing several of the sites where they collect transect and

quadrat data. PISCO has a team of trained experts to collect the rocky intertidal data while LiMPETS training for identifying and recording species in the intertidal lasts three days and the team is composed entirely of volunteers as young as high school freshmen. We propose to use data sets from both PISCO and LiMPETS that were recorded at a shared location within a month of one another to analyze and determine if there is a statistically significant discrepancy between the species count data. We predict there will be no statistically significant discrepancy between the PISCO and the LiMPETS data sets.

#### **SAT-717**

##### **DEVELOPMENT OF A MARSH WEIR TO ASSESS SEA LEVEL RISE IMPACTS IN CALIFORNIA SALT MARSHES**

Cindy Fajardo, Christine Whitcraft, Jesse Dillon.

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Coastal habitats such as salt marshes are predicted to be directly impacted by sea level rise (SLR) over the next few decades. However, little is known about the impacts of SLR on salt marsh ecosystems. To simulate the effects of sea level rise in salt marshes, we are developing a weir box (1/4) that will be inserted into the sediments to increase inundation by holding the incoming tide longer than normal after the tide recedes. There will be 3 treatments (natural inundation control, +3 h, and +6 h of inundation per day), and each treatment will have its own set of replicate (n = 6) weirs. The weirs were constructed out of PVC foam sheets and are currently being tested in the Colorado Lagoon located in Long Beach, California. If preliminary testing is satisfactory, the weirs will then be placed in other California salt marshes. Each weir will surround a single clump of *Spartina foliosa* (cordgrass) and will directly impact both the aboveground plants and the sediments below. Changes in plant, invertebrate and microbiological community composition, and function will be monitored in each inundation treatment. This will provide important predictive data about the impact of SLR on salt marsh ecosystems and how it will affect the surrounding communities.

#### **FRI-703**

##### **EFFECTS OF PRIMARY PRODUCTION OF CHLOROPHYLL-A ON REPRODUCTIVE STRATEGY IN THE SOUTHERN LINE ISLANDS**

Brian Phan, Scott Miller, Scott Hamilton.

*Moss Landing Marine Laboratories, Moss Landing, CA.*

Coral reefs fringing the uninhabited islands of the Southern Line Islands in the Pacific Ocean are among the most pristine coral reefs in the world, allowing studies of the natural drivers of ecosystem function to be conducted in the absence of confounding human impacts. The 5 islands span a strong oceanographic gradient, with islands closest to the equator having greater primary production, using chlorophyll-a as a proxy. These variations in bottom-up processes can have indirect effects on the fish communities on these reefs. One such effect on lower trophic level species (e.g., surgeonfish) could be intra-specific differences in reproductive strategy, measured by the degree of maturation and gonadosomatic index (GSI). To examine the degree of maturation and GSI, we dissected 2 species of fish (*Acanthurus nigricans* and *Ctenochaetus*

*marginatus*) that were collected from the Southern Line Islands to obtain gonad size and overall size for the degree of maturation and GSI. We predict fish from islands with lower primary productivity will have a lower degree of maturation and smaller GSI than fish from islands that rest in more productive seas. Having a baseline of reproduction in lower trophic fish species can be used for the study of natural drivers of reproduction for conservation in coral reef ecosystems.

#### **FRI-722**

##### **THE EFFECTS OF URBAN POLLUTION ON THE REPRODUCTIVE PHYSIOLOGY OF CALIFORNIA HALIBUT (*PARALICHTHYS CALIFORNICUS*)**

Matthew Scanlon, Kristy Forsgren.

*California State University Fullerton, Fullerton, CA.*

Anthropogenic influence on coastal ecosystems is increasing as our population grows. Urban pollution sources (e.g., runoff, wastewater effluent, gasoline leaks from boats) may contain compounds that affect fishes in a variety of ways. Endocrine disrupting compounds (EDCs) that mimic sex steroid hormones are of particular concern and have the potential to alter the reproductive physiology of teleost fishes. California halibut (*Paralichthys californicus*) is a benthic, euryhaline fish that spends most of its adult life in the ocean. As juveniles, halibut inhabit more sheltered areas such as bays and estuaries that are more susceptible to anthropogenic influences. Of particular interest to this study are the EDCs from boat pollution and urban runoff. It is likely that harmful compounds from these sources settle in the sediment and influence juvenile halibut by direct contact and bioaccumulation via benthic food sources. Juvenile halibut were collected from 3 sites of differing anthropogenic-influence (i.e., Los Angeles Harbor, Newport Back Bay, Catalina Island) and their reproductive physiology was assessed by measuring blood sex steroid hormone levels and examining gonadal tissue histologically. We hypothesized that halibut found in more pollution-heavy sites would have more indicators of reproductive dysfunction (altered steroid levels, unhealthy reproductive tissues) than fish collected in less influenced areas. Addressing this hypothesis will increase our understanding of how EDCs affect economically important fish species, such as halibut, in Southern California.

#### **FRI-738**

##### **NATURAL VARIATION IN CONDITION OF SURGEONFISHES FROM CENTRAL PACIFIC CORAL REEF ECOSYSTEMS**

Katherine Neylan, Scott Miller, Scott Hamilton.

*Moss Landing Marine Laboratories, Moss Landing, CA.*

Coral reefs are threatened ecosystems, yet little is known about the role of natural variation in oceanographic conditions that structure these ecosystems. Most studies on coral reefs to date have been conducted in areas that have been degraded by anthropogenic factors. To reduce these confounding influences, this study was conducted in the Southern Line Islands, a chain of 5, remote, uninhabited atolls in the central Pacific Ocean. These islands span a strong productivity gradient, using chlorophyll a as a proxy. This results in variation of bottom up

processes among the different islands, potentially indirectly affecting the fish communities through oceanographic-driven changes in their prey base. A variable that can be affected by this variation is fish condition. In order to investigate the condition of these fish, individuals of 2 species of surgeonfishes were collected from the 5 Southern Line Islands and brought back for dissections to measure the Hepatosomatic index (HSI), Fulton's condition factor (K), and relative weight of fat stored in the body. We expect to find that fish from islands located in more productive waters will have higher HSI, higher Fulton's K values, and larger fat globules relative to fish size. We expect this because the fish in more productive areas will have food more readily available, allowing them to select preferred prey more often. This study will help us understand natural variation of coral reef fish condition, and is important for acquiring baseline data that can be used in resource management assessments and strategies.

#### **FRI-734**

##### **BIODIVERSITY AND ABUNDANCE OF BENTHIC MACROFAUNA IN THE STREAMS AT LAS CRUCES RESTORATION AREA**

Cherie Kauahi, Patricia Esquete.

<sup>1</sup>*University of Hawai'i at Hilo, Hilo, HI*, <sup>2</sup>*Universidad de Vigo, Vigo, Pontevedra, ES*.

Benthic stream macroinvertebrates are key to the freshwater stream ecosystems which they inhabit. They serve as indicators of water quality, secondary producers, food resources for higher trophic levels and more. In this study, we examined the diversity and abundance of benthic macroinvertebrates within two river systems at Las Cruces Biological Station in southern Costa Rica. Benthic substrates of interest were rock and gravel along two adjacent land use types, primary and secondary forest restoration areas. Three replicate samples were collected from each site and substrate type, with a total of 30 samples. Rock and gravel samples from a control site within the primary forest, distant from restoration areas were also collected for comparison. Sample substrates were brushed to loosen any organic material in the direction of the river flow and were caught in a Suber Net. Faunal samples were preserved in 70% ethanol, sorted, and identified to the lowest possible taxonomic level using dissecting and compound microscopes. The expected results are that: macroinvertebrate diversity and abundance will be greater on larger rock substrate types, macroinvertebrate diversity will be greater in the secondary forest reaches, and abundance will be characterized by higher dominances of fewer species. The results of this study will provide an idea of how primary and secondary forest restoration areas ultimately help to regain macroinvertebrate diversity within tropical forests.

#### **SAT-739**

##### **GENETIC DIVERSITY AND HEALTH OF TEXAS OYSTER POPULATIONS IN GALVESTON BAY**

Courtney Knauer, Christopher Bird.

Texas A&M University-Corpus Christi, Corpus Christi, TX.

Nearly 85% of oyster populations have decreased significantly in the past several years. These important keystone species provide not only economic benefits for humans, but also assist in a healthy diverse ecosystem and provide food and habitats for many other marine organisms.

Population declines, like that of the oyster, are normally characterized by a decrease in genetic diversity. This study looks at the genetic diversity of oysters in Galveston Bay to find consistent population differences within different locations to determine the relative health and diversity within an ecosystem. We hypothesize that oysters in different locations will indeed contain a distinct genetic make-up that differs from those in different locations in the bay. Samples will be collected from back water locations with a lower salinity content, at the mouth of the bay with a higher salinity content, and from the middle of the bay to produce a gradient in which to study. Three replicates of 48 oysters per location will be collected from the bay. The genomes will be sequenced by the RADseq protocol in order to observe 20,000 loci. Within these loci, single nucleotide polymorphisms (SNPs) will be observed to identify genetic differences and local adaptations in the oysters. Results will support the determination as to whether extreme populations are being selected for, thus reducing the genetic diversity of the bay overall. This will help assess the health of the bay and if changes need to be made in conserving the oyster populations.

## MICROBIOLOGY

### FRI-1131

#### INCREASED EXPORT OF HETEROLOGOUS PROTEINS BY MUTATING THE TYPE 3 SECRETION SYSTEM IN *SALMONELLA*

Elias Valdivia, Kevin Metcalf, Danielle Tullman-Ercek.  
*University of California, Berkeley, Berkeley, CA.*

We have engineered a protein pump in *Salmonella* to secrete proteins that can be easily recovered from the media. Heterologous proteins are made by bacteria with recombinant DNA methods for therapeutic and industrial purposes, but purification from the cell is difficult. The proteins can also aggregate to form insoluble inclusion bodies in the cytoplasm when they are overproduced. However, many pathogenic bacteria use a type III secretion system (T3SS) to pump proteins out of the cell. In this work, we have made genomic point mutations in the *prgI* gene, which encodes for the T3SS needle, of *Salmonella enterica* subsp. *enterica* serovar Typhimurium that increases the secretion of heterologous proteins into the media. To determine which mutation resulted in the highest protein secretion, we compared the secreted protein titer by western blot. With genomic engineering methods, we have been able to express the T3SS mutations from the genome, enabling the protein pump to assemble properly, and 2 mutations, *prgI*<sup>WT</sup>::*prgI*<sup>P41A</sup> and *prgI*<sup>WT</sup>::*prgI*<sup>Q48A</sup>, have increased the titer of secreted protein.

**FRI-1130****BACTERIOPHAGES AS A THERAPEUTIC STRATEGY TO TARGET ADHERENT, INVASIVE *ESCHERICHIA COLI* ASSOCIATED WITH INFLAMMATORY BOWEL DISEASE**

Jessica Tsui, Jonathan Jacobs, Jonathan Braun.

*University of California, Los Angeles, Los Angeles, CA.*

Crohn's disease is a form of inflammatory bowel disease that affects millions of people worldwide. While the cause is not known, it is suspected that specific intestinal microbes may be able to incite disease in genetically susceptible individuals. One candidate bacterial trigger is adherent, invasive *Escherichia coli* (*E. coli*) (AIEC). AIEC adheres to the patient's ileal epithelium, invades the *lamina propria*, and then proliferates within macrophages. AIEC is a candidate target for antibiotic treatment for Crohn's; however, antibiotics may also target beneficial microbes in the gut. Since bacteriophages (phages) naturally have high specificity for their bacterial hosts, our objective is to determine if phages can be used as a therapeutic strategy for specifically targeting AIEC in Crohn's disease patients via the phage's lytic cycle. Five different strains of *E. coli* phages underwent ultraviolet-induced mutation, and selection followed by cloning to isolate mutant phages with enhanced ability to target AIEC. The selected phages and AIEC were co-cultured with human epithelial cells to test the potency of these phages against AIEC *in vitro*. Results suggest that each of these phages can effectively target both non-adherent and adherent AIEC. A combination of all 5 phages was also tested but did not show synergistic activity relative to the single most potent phage. Long-term co-culture experiments will be conducted to assess for AIEC resistance to phages and synergistic activity exhibited by phages. These promising early results support continued investigation into the suitability of phages directed against AIEC as a therapeutic strategy for Crohn's disease treatment.

**FRI-1132****MLSB ANTIBIOTIC RESISTANT GENES ENCODING FOR ANTIBIOTIC-INACTIVATING ENZYMES ARE FOUND IN ENVIRONMENTAL STRAINS OF *STAPHYLOCOCCUS***

Marisol Zuniga, Andrey Tatarenkov, Luis Mota-Bravo.

*University of California, Irvine, Irvine, CA.*

*Staphylococci* cause approximately 30% of hospital-acquired bacterial infections. Macrolide, lincosamide, and streptogramin<sub>B</sub> (MLS<sub>B</sub>) antibiotics are commonly used against *staphylococcal* infections. However, application of MLS<sub>B</sub> drugs is hampered by the emergence of antibiotic resistance. Our objective was to determine the incidence and diversity of antibiotic inactivating genes in strains of *Staphylococcus* isolated from public areas. The bacteria were collected from beaches of Southern California, filtered, grown on selective media, and identified using MALDI-TOF. PCR was used to screen for *ereA*, *vgbA*, *vgbB*, *InuA*, *InuB*, *mphC*, *vatA*, *vatB*, and *vatC* genes. PCR products were sequenced and analyzed through Mega5 and DNAsp programs. Genes *InuA* and *mphC* were detected in 13% and 34% of isolates, respectively; other genes were not detected. Most *Staphylococcus* strains with *mphC* had nearly identical alleles, but one strain was highly divergent (7.7%). The identical alleles were observed in diverse *Staphylococci* species. Three moderately divergent *InuA* alleles were uncovered in our samples that corresponded to *InuA* lineages known worldwide. Combined analysis of our data and Genbank



data revealed that European farms harbored the highest *InuA* diversity, probably a result of regular use of lincosamide antibiotics. The worldwide distribution of *InuA* and *mphC* alleles suggests high gene flow, whereas their occurrence in diverse bacteria species indicates extensive horizontal gene transfer. The high incidence of *InuA* and *mphC* genes in Southern California far from agricultural areas suggests that the natural environment is important in accumulating, harboring, and reshuffling antibiotic resistant genes, resulting in new combinations that may later emerge in clinical settings.

#### **FRI-1127**

#### **DETERMINING CARBON CONTENT OF HYPER-SALINE SEDIMENTS FROM THE GREAT SALT LAKE DESERT**

Christopher Matthews, Kennda Lynch, Nohemi Almaraz.  
*Colorado School of Mines, Golden, CO.*

While there is a rather large amount of information and studies on hypersaline aquatic habitats, there is an inherent lapse in what is known about hypersaline sediments and soils. Organic carbon is a standard indicator of microbial productivity and species richness in any given environment. Inorganic carbon can also be an indicator of microbial ecology as microbes often mediate the precipitation of evaporite minerals in hypersaline systems. Hence, determining both organic and inorganic carbon of hypersaline soils and sediments allows for further characterization of the microbial ecology of these environments. In this study, we present the preliminary results of inorganic and organic carbon content as determined by coulometric titration, along a defined study transect in the Pilot Valley Basin of the Great Salt Lake Desert.

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**SAT-1139****DETERMINING THE ROLE OF TRANSCRIPTION FACTOR LMO2 ON ANTIBODY CLASS SWITCH RECOMBINATION**

Christopher Hinojo<sup>1</sup>, Ramiro Verdun<sup>2</sup>.

<sup>1</sup>Iowa State University, Ames, IA, <sup>2</sup>University of Miami, Miami, FL.

LMO2 is a cytosine-rich protein of 156 amino acids containing 2 zinc-binding LIM domains and is required for adult hematopoiesis through its ability to regulate gene expression by facilitating the creation of multi-part DNA-binding complexes. This protein is expressed in healthy B cells and upregulated in diffuse large B cell lymphomas (DLBCL). While the role in LMO2 in lymphoma patients has been explored because of its early diagnostic capabilities for DLBCL, its role is unclear in B cells. Here we show that LMO2 plays an essential role during repair of DNA breaks in class switch recombination (CSR), an essential process for the diversification of the immune response. CSR is a DNA recombination between 2 DNA breaks, a process that allows changing the antibody isotype. Using mouse CH12F3 B cells, we found that specific inactivation of the LMO2 protein decreases the efficiency of CSR. Specifically, LMO2 is required for the microhomology-dependent repair of the DNA breaks induced during CSR. Our results show that LMO2 plays an essential role in the repair of DNA breaks during CSR and possibly influences the choice of DNA repair pathway in this essential physiological process.

**FRI-1140****VISUALIZATION OF PHOTOSYSTEM II DISTRIBUTION IN ENCAPSULATED *CHLAMYDOMONA REINHARDTII* UNDER HIGH AND LOW LIGHT CONDITIONS**

Aysha McClory<sup>1</sup>, David T. Hanson<sup>2</sup>, Jerilyn Timlin<sup>3</sup>.

<sup>1</sup>University of New Mexico, Los Alamos, Los Alamos, NM, <sup>2</sup>University of New Mexico, Albuquerque, NM, <sup>3</sup>Sandia National Laboratories, Albuquerque, NM.

Properties of photosynthetic cells are not uniform within leaves or between environmental conditions. Cells near the top of the leaf receive high light and shade those below them. This gradient within the leaf causes functional differentiation of cells, with cells near the top being optimized for avoiding high light damage and lower cells optimized for light capture. Furthermore, leaves grown in high light are generally thicker than those in low light, which accentuates the gradient. We have encapsulated dense cultures of algae in a tetramethyl orthosilicate (TMOS) silica sol gel to prevent cell growth and movement while maintaining metabolic function. Our gels are similar in thickness to thick leaves and have a similar cell density but lack internal air spaces. Therefore, we expect to see a similar pattern of photosynthetic adjustment with depth as we would in leaves. To determine this, we used hyper spectral imaging to examine the chlorophyll a and b ratios and photosystem distribution of *Chlamydomona reinhardtii* with depth in the gel for cultures grown at two light levels and thicknesses. We hypothesize an increase in antennae size in the thinner samples under low lighting and an even greater increase in antennae size in the thicker samples under low lighting.

infected cells as compared to mock infected cells after treatment with PX12. These studies will provide new information on redox regulation and novel targets to treat KSHV infected cells.

#### **SAT-1139**

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**FRI-1124****COMPARING DEEP CAVE BACTERIA WITH MARS SIMULATION SURVIVING BACTERIA:  
IMPLICATIONS FOR LIFE DETECTION ON EXTRATERRESTRIAL BODIES**

Krystal Charley, Diana E. Northup.

*University of New Mexico, Albuquerque, NM.*

Caves on Mars are a likely place to host extant or fossil microbial life. These caves would provide shelter from harsh surface environments. Lechuguilla Cave, in southeastern New Mexico, is a good analog site for Mars because the microorganisms exist in an aphotic, oligotrophic environment, and in the absence of flowing water. Previous studies have not directly compared cultures from Mars analog sites to cultures that have survived under simulated Martian conditions. Our study uses bacterial cultures from a prior NASA-funded project that tested the ability of cave and surface bacteria to survive simulated Martian conditions. We hypothesized that cultures from the Mars simulation experiments will be similar to those found in deep caves and they would share metabolic strategies. R2A medium plates were inoculated with ferromanganese deposits obtained from Lechuguilla Cave in 2013 from the Far East Branch in the Ruby Chamber. Cultures were stored in a cave temperature incubator (20 °C). Using an established protocol to subculture our samples, we obtained 30 putatively pure subcultures. These subcultures have been characterized morphologically and form the core set for comparison to the Mars survivor cultures. The bulk of the subcultures are white in coloration and vary from mucoid to crusty. We are currently working on identifying the bacteria using the full-length *16S rRNA* gene sequences (a bacterial fingerprint), which provide what metabolic strategies these microorganisms may employ in these very low-nutrient environments. This culture-based approach will assess whether caves in New Mexico are good analogs for Martian caves.

**SAT-1121****STRUCTURAL AND ELEMENTAL CHARACTERIZATION BY SCANNING ELECTRON MICROSCOPY  
OF HYPERSALINE MICROBIAL MATS FROM THE GREAT SALT LAKE DESERT**

Nohemi Almaraz, Christopher Matthews, Kennda Lynch.

*Colorado School of Mines, Golden, CO.*

The Great Salt Lake Desert (GSLD) is an example of an ancient paleolake that has transitioned to a modern evaporite basin full of hypersaline sediments. Though hypersaline systems are characterized as extreme environments, they tend to yield very diverse microbial communities. Despite this, hypersaline soils and sediments systems like the GSLD, remain understudied. Therefore, it is necessary to further analyze and characterize these environments to understand the development of microbial communities within. The characterization of this environment is important to understanding hypersaline environments on Earth as well as ancient aqueous environments on Mars. Here we present the first macro- and micro-scale investigation of microbial mat structures discovered in the hypersaline sediments of the Pilot Valley basin. In this study we used scanning electron microscopy to analyze the microstructure and elemental abundance of these microbial mats. Our study has revealed the presence of artifacts that might have developed as a result of microbial activity as well as laminar layering with different

structural formations. We see filaments embedded within the sediments and extracellular polymeric substances which are abundant in some layers but not in others. A wide diversity was also observed at the macro scale throughout different regions of the Pilot Valley basin. Through this research we have been able to assess the morphological diversity that characterizes the microbial community in this hypersaline environment.

#### **SAT-1119**

##### **SYNERGISTIC INTERACTIONS OF *PSEUDOMONAS AERUGINOSA* AND *STAPHYLOCOCCUS AUREUS* IN AN *IN VITRO* WOUND MODEL**

Stephanie Deleon, Kendra Rumbaugh.

*Texas Tech University Health Sciences Center, Lubbock, TX.*

Microbes within polymicrobial infections often display synergistic interactions that can enhance their colonization, virulence, or persistence. One of the most prevalent types of polymicrobial infection occurs in chronic wounds, where *Pseudomonas aeruginosa* (PA) and *Staphylococcus aureus* (SA) are the 2 most common causes of infection. Although they are the most commonly-associated microbial species in wound infections, very little is known about their interspecies relationship. Evidence suggests that PA and SA coinfections are worse than monoculture infection with either species; however, difficulties in growing these 2 pathogens together *in vitro* have hampered attempts to uncover the mechanisms involved. Here we used a simple and clinically relevant *in vitro* wound model, which supported concomitant growth of PA and SA. We observed that being together increased the ability of PA and SA to survive antibiotic treatment, as did the presence of host-derived matrix components. Our data indicate that PA and SA may mutually benefit by coinfecting wounds.

#### **FRI-1141**

##### **EVALUATION OF THE ANTIMICROBIAL ACTIVITY OF *RHODIOLA ROSEA*, A TRADITIONAL MEDICINAL PLANT**

Wafa Zeidan, Sweta Sharma, Christine Case.

*Skyline College, San Bruno, CA.*

*Rhodiola rosea*, commonly called golden root, is a native plant of the circumpolar soils. *R. rosea* is used in traditional Native American medicine to treat intestinal disorders and tuberculosis. The traditional use suggests that the plant has antibacterial components. Our purpose is to test the hypothesis that *R. rosea* is antimicrobial and to identify its specific antimicrobial compounds. A commercial alcohol-free root extract was mixed with water, 100% ethyl acetate, 100% methanol, and 95% ethanol. These extracts were screened against bacteria and fungi in agar diffusion assays to determine antimicrobial activity. The ethyl acetate and aqueous extracts inhibited *Staphylococcus aureus*, *Escherichia coli* and *Mycobacterium phlei* bacteria, but did not inhibit *Penicillium notatum* or *Candida albicans* fungi. The minimum bactericidal concentration against *S. aureus* is 0.063 µL/µL, while *E. coli* was inhibited but not killed at 0.125 µL/µL. The extract does not cause cell lysis. Characterization of the antibacterial properties is in progress. We conclude that *R. rosea* has antimicrobial properties and may provide source material for a new antimicrobial.

**FRI-1143****REVERSE ENGINEERING OF THE OMPR GENE NETWORK**

Jay Pinilla, Amelia Abdullah, Sweta Sharma, Desmond Lun.  
*Rutgers University, Camden, NJ.*

The reverse engineering problem for gene regulatory networks involves developing a model that utilizes -omics data to decipher the wiring diagram consisting of the functional relationships in regulation of genes. Due to the poor accuracy of network predictions from statistical and machine learning methods that have been submitted thus far for DREAM challenges, we developed a theoretical model that uses gene expression data from networks under various conditions. We have previously shown through computational experiments based on *in silico* data that, given simplifying assumptions about the network topology, identification is achievable and feasible for small networks consisting of a few hundred genes. To validate our model, we attempt to reverse engineer the ompR regulatory sub-network in *E. coli* MG1655. The outer membrane protein Regulator (ompR) gene is well studied, however its role in gene regulation within *E. coli* MG1655 strain is not fully understood. We probe the network by modifying the expression level of genes sensitive to ompR regulation and measuring the corresponding expression profiles. Through this process, we seek to determine the regulatory relationships of the genes in the ompR subnetwork. With this knowledge, we may be able to understand how changes in the extracellular environment that activate ompR propagate through its regulatory subnetwork to confer changes in cell phenotype.

**FRI-1135****ENHANCED IMMUNOGENICITY OF A GENETICALLY-STABILIZED LIVE ORAL ANTHRAX VACCINE**

Ivan Albino Flores, Manuel Osorio.

*Center for Biologics Evaluation and Research, United States Food and Drug Administration, Bethesda, MD.*

*Bacillus anthracis*, the etiological agent of anthrax disease, is a proven weapon of bioterrorism. The principal component of the current anthrax vaccine is the protective antigen (PA) protein. Although safe and efficacious, this vaccine has some limitations: it requires 6 injected doses over 18 months to stimulate protection, requires the cold chain, and has been associated with adverse events. Thus, there is a need for a new generation of anthrax vaccines that are easier to administer, more stable, and induce protection with fewer doses. We are using the attenuated *Salmonella typhi* strain Ty21a as a vector to deliver PA for development of an oral vaccine against anthrax. The PA expression cassette consists of a gene encoding PA under the control of the constitutive, highly expressed lpp promoter, and genes encoding necessary components for PA secretion. This cassette was inserted into the *Salmonella* Ty21a chromosome via standard  $\lambda$ -red recombineering techniques. The resulting integrants were evaluated for genetic stability and stable production of PA. Immunogenicity of the vaccine constructs was studied by immunizing mice with three bi-weekly doses given via the intraperitoneal route. Chromosomal integration of a PA expression cassette resulted in a genetically stable vaccine construct capable of maintaining PA expression for at least 100

generations of growth. This vaccine construct induced strong antibody responses to PA in vaccinated mice. We are now evaluating the protective efficacy of these vaccine constructs by challenging vaccinated mice with aerosolized spores of the *B. anthracis* Sterne strain.

#### **FRI-1137**

##### **GENETIC VARIATION AND GENEALOGICAL STRUCTURE AMONG *ERIOPHORUM VAGINATUM* ECOTYPES USING NEXT GENERATION SEQUENCING**

Armando Lerma, Ming-Ying Leung, Michael Moody, Jon Mohl.

*University of Texas at El Paso, El Paso, TX.*

*Eriophorum vaginatum* is an ecologically important Arctic plant lineage and it serves as a model for understanding home site advantage in light of climate change. Ecophysiological research has recognized distinct ecotypes from the north and south of its range in Alaska. This research employs double digest restriction associated DNA (RAD) sequencing, a next generation sequencing technique, to identify single nucleotide polymorphism (SNP) data for distinguishing the ecotypes at the genetic level. The RAD sequence data is filtered through the FASTX sequence preprocessing tools and then loci are assembled using the STACKS pipeline followed by the identification of SNPs. Finally, a model based clustering program (Structure) and a tree building program (Geneious) are used to evaluate genetic variation, structure, and relatedness between ecotypes. Distinguishable genetic structure between ecotypes from the north and south end of the range is expected with genetic distance between populations correlating with geographic distance. A high number of ecotype specific SNPs are expected to be discovered for use in large-scale population genetic studies of the group in the Arctic.

#### **SAT-1137**

##### **THE ORAL CAVITY AS AN EXTRAVAGINAL RESERVOIR FOR BACTERIAL VAGINOSIS-ASSOCIATED BACTERIA**

Anthony Lopez<sup>1</sup>, Erin dela Cruz<sup>1</sup>, Jeanne Marrazzo<sup>1</sup>, David Fredricks<sup>2</sup>.

<sup>1</sup>University of Washington, Seattle, WA, <sup>2</sup>Fred Hutchinson Cancer Research Center, Seattle, WA.

Bacterial vaginosis (BV) is the most common vaginal infection among women of reproductive age and is associated with increased risk of premature labor, pelvic inflammatory disease, and both acquisition and transmission of HIV. BV is characterized by a change in the vaginal microbiota: most notably, a decrease in dominant *Lactobacillus* species coupled with a 100 to 1,000-fold increase of anaerobic bacterial populations. Many facets of BV pathogenesis remain unclear. For example, although antibiotics generally alleviate symptoms, BV recurs within 6 months in approximately 50% of women treated. Our study attempts to understand such recurrence by characterizing a possible extrvaginal reservoir for bacterial vaginosis-associated bacteria (BVAB) in the oral cavities of male sexual partners. Gingival swabs were obtained from a cohort of 23 men and their female partners. Female partners were assessed for BV at baseline; women found to be BV positive were treated with antibiotics and followed for approximately 1 month to monitor treatment outcome. We will use species-specific quantitative PCR on bacterial DNA extracted from gingival swabs to test for BVAB colonization in the oral cavities of male partners. From these assays, we expect to estimate the prevalence

of oral BVAB colonization, quantify the bacterial load of individual BVABs, and determine whether these measurements correlate with BV status of female partners. Establishing the oral cavity in male partners as an extravaginal reservoir for BVAB would have implications for BV treatment and may suggest cunnilingus as a possible mode of BV recurrence.

#### **SAT-1120**

##### **EFFECTS OF HOST ACUTE STRESS RESPONSE ON THE REPLICATION AND ADHESION PROPERTIES OF *STREPTOCOCCUS PNEUMONIA***

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An acute response to infection is the release of stress hormones such as norepinephrine (NE). Studies in the field of microbial endocrinology generally indicate that NE increases bacterial growth rate and promotes invasive disease. In the case of *Streptococcus pneumoniae* (the pneumococcus), NE inhibits invasive disease yet paradoxically provides protection to the organism against an increased neutrophil response to infection. Neutrophils are a key component to the host response to bacterial infections by controlling the infection through production of exogenous reactive oxygen species. *S. pneumoniae* naturally has protection against exogenous reactive oxygen species through contribution of pyruvate oxidase (SpxB). We propose that NE regulates the pneumococcal SpxB protein thereby increasing its resistance to neutrophil killing. Utilizing 2D and 1D gel electrophoresis combined with western blot analysis, we will verify the effect of NE on pneumococcal production of SpxB. Further, *in vitro*, killing assays using HL-60 neutrophil differentiated cells will allow us to determine NE enhancement of protection on the pneumococcus. Current 2D gel assessment suggest that NE regulates pneumococcal production of the SpxB protein. Further, assessment of killing assays will provide evidence as to the protection provided to *S. pneumoniae* through NE exposure. Our current, findings allow us to suggest that SpxB participates in pneumococcal survivability to innate immunity.

#### **FRI-1133**

##### **MUTATIONS IN CELL SURFACE PROTEINS OF *RICKETTSIA PARKERI* LEAD TO ALTERED INVASION EFFICIENCY**

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*Rickettsia* are obligate intracellular pathogens that cause potentially lethal diseases including spotted fever and typhus. They primarily invade endothelial cells by subverting actin assembly pathways that are typically required for cell motility, cell shape, and cell-cell interactions. We hypothesize that bacterial cell surface proteins play a crucial role in invasion efficiency. To test this, we are taking advantage of existing transposon insertion mutations in genes encoding cell surface proteins of *Rickettsia parkeri* (*R. parkeri*). We are evaluating these mutants in host cell invasion assays to assess bacterial invasion efficiency relative to wild-type strains. We expect to find mutants for which there is increased as well as decreased efficiency. This will lead to the identification of new proteins in *Rickettsia* that are required for adhesion and actin mobilization



during invasion. In the longer term, elucidating the mode of invasion may be beneficial for devising new strategies to prevent disease and improve treatment for *Rickettsia* infections.

#### **FRI-1134**

##### **GENE KNOCKOUT IN *TOXOPLASMA GONDII***

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*Toxoplasma gondii* is a parasite that is found worldwide and can infect a huge range of warm-blooded animals through various routes. The event of differentiation between tachyzoites and bradyzoites in the life cycle of the parasite is the main concern of infection with *Toxoplasma gondii*. The ability of the parasite to convert between the tachyzoite and bradyzoite stage is the main cause of life-long infection in hosts. To study how *Toxoplasma gondii* maintains a lifelong infection, we plan to knockout genes thought to be important for establishment and maintenance of the bradyzoite life stage and to study their effects. Using previous data from RNAseq analysis of *Toxoplasma gondii* during acute and chronic infection in mice, it was decided to knockout the gene *TGME49\_290980*, known as Glycine C acetyltransferase (GCAT). To accomplish this, we have designed flanking sequences of *TGME49\_290980*, cloned them into a storage vector, performed test digests, and sequenced positive clones. Future work to accomplish this experiment will be to insert the flanking sequences into our knockout vector, electroporate the vector into *Toxoplasma gondii*, and screen for parasites that have the gene of interest removed. Once a gene knockout strain has been produced we will infect mice with the strain of *T. gondii* and determine if there is a defect in persistence of the parasite. Finding a non-persisting strain of *T. gondii* would be pivotal for vaccine development.

#### **SAT-1134**

##### **ELUCIDATING THE ROLE OF HYPOXIA INDUCIBLE FACTOR DURING LATENT KSHV INFECTION**

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Kaposi's sarcoma-associated herpesvirus (KSHV) is the infectious agent of Kaposi's Sarcoma, a tumor that is the most prevalent cancer found in untreated HIV-infected individuals worldwide. KSHV establishes predominantly latent infection both in cells *in vitro*, as well as in KS tumors. KSHV, like all viruses, lacks an independent metabolism. It dramatically alters host cellular metabolism, specifically in carbon utilization pathways. We have previously shown that, similar to cancer cells, latent KSHV-infected cells require increased glucose uptake and glycolysis for survival. Hypoxia-inducible factor 1 $\alpha$  (HIF-1 $\alpha$ ) and HIF-2 $\alpha$  are 2 homologous alpha subunits of the heterodimeric transcription factor HIF. In cancer cells, HIF induces aerobic glycolysis to enhance energy production and prevent cancer cells from damage via hypoxic stress. However, it is still unknown if latent KSHV infection requires HIF protein, and if the HIF pathway is the direct cause of the observed induction of glycolytic gene expression and downstream metabolism. We hypothesize that during latent KSHV infection, HIF-1 $\alpha$  and HIF-2 $\alpha$  are the master regulators of the altered, host cellular metabolism. We utilized an shRNA knockdown

approach to determine the protein expression of glucose transporter-3 and hexokinase-1, essential glycolytic enzymes that are known to be upregulated by KSHV infection. If stabilized HIF is the master regulator of cellular metabolism (i.e., glycolysis), we would expect the results to show significantly lower protein expression during latent KSHV infection when HIF production is inhibited. This study has the potential to reveal important drug targets for future strategies to inhibit and treat latent-KSHV infection and ultimately KS tumors.

#### **SAT-1125**

##### **GROWTH DYNAMICS OF *WILLIOPSIS SATURNUS* RELATED TO EXOPOLYSACCHARIDE PRODUCTION**

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A yeast-bacterium co-culture was isolated in R2A agar plates from a low pH hydrogen-producing bioreactor with compost. Overgrown cultures in solid media showed the formation of gas bubbles that were persistent and resistant to physical manipulation. GC analysis of the bubbles' gas space identified the significant enrichment of hydrogen, most probably produced by the prokaryotic component of the co-culture, while the growth of the isolated yeast showed the production of an exopolysaccharide (EPS) directly related to the formation of the bubbles. Preliminary characterization of the EPS using Fourier transformed infrared spectroscopy (FTIR) showed a significant similarity to cellophane, a polymer known for its low gas permeability with several potential industrial applications. The production of the EPS by the yeast, presumptively identified as *Williopsis saturnus*, has been related to the growth dynamics of the organism by measuring the content of EPS secreted to the media during different stages in the yeast growth.

#### **FRI-1129**

##### **PHYSIOLOGICAL RESPONSE OF *OSTREOCOCCUS* TO NUTRIENT DEPLETION**

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Phytoplankton are an important primary producer, populating all of the oceans on Earth. One of the most important environmental variables that control population growth of phytoplankton is nutrient availability. With rising levels of carbon dioxide in our atmosphere and increasing density stratification due to warming oceans, the nutrients available to phytoplankton in the euphotic zone will change. To further understand the nutrient limitations of phytoplankton, we are investigating how the growth rate and elemental quotas of the pico-phytoplankton *Ostreococcus* respond to the nutrient depletion of nitrogen and phosphorus. We are addressing this question by monitoring the growth of *Ostreococcus* cultures in multiple nutrient conditions (nutrient replete and deplete) using flow cytometry. In addition to calculating growth rates, we are collecting samples for cellular elemental quotas from the different treatments and across different phases of growth. These results will provide insight into the physiological plasticity of phytoplankton, which is a poorly characterized parameter in current biogeochemical models. Ultimately, the results of this study will give us a deeper

understanding of the role of phytoplankton in marine biogeochemical cycles and how their populations may be affected in the future.

#### **SAT-1132**

##### **TL1A-DR3 SIGNALING PATHWAY IN DIABETES**

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Inflammation plays a central role in diabetes-associated vascular complications such as impaired wound healing, nephropathy, cardiomyopathy, and atherosclerosis. Better understanding of the molecular mechanisms that drive inflammation in diabetic disease is essential to prevent diabetes vascular complications, reducing the risk of amputations, blindness, and death. TL1A is a cytokine member of the tumor necrosis factor superfamily (TNFSF) of ligands expressed in several organs, suggesting that it participates in tissue homeostasis. TL1A exerts its function through binding to the DR3 receptor. Its activity is regulated through sequestration by the decoy receptor DcR3. The role of TL1A-DR3 signaling in diabetes has not been previously investigated. Previous work from our group has demonstrated that TL1A expression is increased by exposure of endothelial cells to high glucose and in specific tissues of diabetic mice. Accordingly, we hypothesize that DR3 and DcR3 receptors are expressed in diabetic disease. We analyzed heart and kidney samples obtained from the diabetic mouse model db/db for the expression of DR3 and DcR3 by western blot and qPCR. Our results show that DR3 protein expression is significantly upregulated in both diabetic hearts and relative to control animals. DR3 RNA was upregulated in diabetic hearts. However, no significant changes were observed in diabetic kidneys. The expression of DcR3 protein in diabetic kidneys and hearts was not significantly different from control. However, it showed a reducing trend in diabetic hearts. We are currently performing immunohistochemistry studies to determine the cellular localization of both DR3 and DcR3 in diabetic kidneys and hearts.

#### **FRI-1121**

##### **GLUTAMINOLYSIS IS REQUIRED FOR LATENT KAPOSI'S SARCOMA HERPES VIRUS INFECTION**

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Kaposi's Sarcoma (KS) is the most common tumor of AIDS patients. Our lab studies how the etiologic agent of KS, Kaposi's sarcoma herpes virus (KSHV), alters host cell metabolism. Similar to cancer cells, virally infected cells have altered metabolic requirements. Our lab published a global metabolomic analysis of latent KSHV infection revealing that KSHV infection increases glucose and glutamine levels. Increased glycolysis and glutaminolysis are hallmarks of cancer and required for tumor cell survival. Glutaminolysis involves the conversion of glutamine to glutamate and alpha-ketoglutarate ( $\alpha$ KG) through 2 key enzymes, glutaminase (GLS) and glutamate dehydrogenase (GDH). The  $\alpha$ KG can enter the tricarboxylic acid cycle (TCA) and support ATP production. Cancer cells often require glutamine to replenish the TCA cycle depleted from increased glycolysis. Interestingly, glutamine starvation significantly induces cell

death of KSHV infected cells compared to uninfected cells. These preliminary data show that exogenous glutamine is required for latent KSHV infection. We hypothesize that glutamine is required during latent KSHV infection to replenish the TCA cycle. Our research showed that inhibition of glutaminolysis using BPTES, a drug inhibitor of GLS, also leads to significant cell death of KSHV infected cells. In future experiments, we will supplement BPTES treated and infected cells with TCA cycle intermediates, such as pyruvate or  $\alpha$ KG, to determine if glutaminolysis is required to replenish the TCA cycle. Our data indicate that glutamine/glutaminolysis is required during latent KSHV infection to replenish the TCA cycle. Through our metabolic studies of KSHV infection, we are identifying potential targets for KS therapy.

#### **FRI-1120**

##### ***STREPTOCOCCUS PNEUMONIAE* ADHESION TO A549 EPITHELIAL CELL UNDER NOREPINEPHRINE REGULATION OF SPXB**

Marisa Gonzales, Cody Blackstone, Xavier Gonzales.

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*Streptococcus pneumoniae*, also known as the pneumococcus, is the primary cause of bacterial pneumonia in children. Pneumococcus can exist asymptotically in the nasopharyngeal cavity, however, in some individuals it can invade the lungs and the blood. Systemic release of norepinephrine (NE) is a component of the acute host response to infection and studies in the field of microbial endocrinology generally indicate that NE increases bacterial growth rate and promotes invasive disease. However, NE attenuates experimental invasive pneumococcal disease by decreasing its capabilities to adhere to epithelial cells. The NE regulation of pneumococcal adherence to lung epithelial cells is associated with the bacterial iron uptake mechanisms. We propose that NE inhibits pneumococcal adhesion through regulation of the iron associated surface protein that participates in adhesion, SpxB (pyruvate oxidase). In this study, we utilize proteomic analysis through 2D and 1D gel electrophoresis along with antibodies raised toward SpxB protein. Further, *in vitro* adhesion assays with A549 lung epithelial cells and *spxB* mutant pneumococcus with and without NE treatment are performed. Currently, 2D gel assessment suggest that NE decreases pneumococcal production of the SpxB protein. Further, assessment of adhesion assays will provide evidence for acceptance or rejection of the proposed hypothesis. We conclude that pneumococcal SpxB is regulated by NE.

#### **FRI-1119**

##### **BIOCHEMICAL CHARACTERIZATION OF THE FOLATE BIOSYNTHETIC PATHWAY IN A RICKETTSIAL ENDOSYMBIONT OF *IXODES PACIFICUS***

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*Ixodes pacificus* ticks have been identified as the paramount vector for Lyme disease and anaplasmosis in North America. Recently, a novel *Rickettsia* species classified as phylotype G021 has been identified as living within the tissue of *I. pacificus*. Its genome contains the 6 genes (*folA*, *folC*, *folE*, *folK*, *folP*, and *ptpS*) required for *de novo* folate biosynthesis. Since *I.*

*pacificus* cannot produce folate nor obtain it from blood, it was hypothesized it obtains this essential nutrient from the *Rickettsia* endosymbiont. To address this hypothesis, recombinant protein expression of these enzymes was used to study *de novo* folate biosynthesis. The 6 rickettsial folate genes were PCR amplified and cloned into a pET-41a(+) expression vector. The clones were transformed into competent non-expression NovaBlue *E. coli*, and later into a competent high-expression BL-21 *E. coli* strain. The clones were verified by digestion, and the correct open reading frame for each gene was verified by sequencing. *FolA*, *FolC*, *FolE*, and *PtpS* have been overexpressed and optimized by different incubation temperatures, induction time, and IPTG concentrations. The amount of soluble and insoluble portions of the overexpressed proteins were determined and analyzed by SDS-PAGE. We found that the genes were successfully amplified and cloned into the expression vector in the correct reading frame and 4 of them have been successfully expressed for protein analysis. This study has shown that folate genes exist in the genome of a novel rickettsial endosymbiont of *I. pacificus* and may be capable of producing functional enzymes, providing fitness advantages to the host.

### **SAT-1123**

#### **GROWTH, ABUNDANCE, AND CHARACTERIZATION OF ANAEROBIC, THIOSULFATE-REDUCING MICROORGANISMS ISOLATED FROM A SALT LAKE, LA SAL DEL REY, IN DEEP SOUTH TEXAS**

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La Sal del Rey (the King's Salt) is a naturally-occurring salt lake in Hidalgo County, Texas, and part of the Lower Rio Grande Valley National Wildlife Refuge. Salt lakes may contain high concentrations of oxidized sulfur compounds; thus, microorganisms may be essential to the cycling of sulfur and other elements in the lake. Our research objective was to isolate and characterize halophilic microorganisms from La Sal del Rey that could grow using oxidized sulfur as an electron acceptor in anaerobic respiration. Water samples were collected from the lake; temperature, salinity, pH, and rudimentary chemistry were measured. Laboratory minimal media were prepared with salinity matching the lake water and with thiosulfate as the only respiratory electron acceptor. Lake water was diluted and spread onto agar plates to isolate individual organisms. Most probable numbers (MPN) analysis was used to determine the density of thiosulfate halophiles present per milliliter, and the growth rate of thiosulfate-halophiles was estimated using a spectrophotometer. Results showed that the water salinity was approximately 320 ppt (32%), mean water pH was 7.51, and mean water temperature was 25.2 °C. Growth rate analyses showed that the organisms grew slowly in media with thiosulfate and 320 ppt NaCl and were still in exponential growth phase after 12 days. Very small colonies of microorganisms were observed growing anaerobically on solid media with thiosulfate. Cultured microorganisms were characterized phenotypically and identified using commercial test strips and 16S rRNA sequencing, respectively. Next-generation DNA sequencing was used to compare meta-genomic information from the lake microbial thiosulfate community.

**FRI-1128****CHARACTERIZATION OF A NOVEL, SMALL-MOLECULE INHIBITOR OF ANTHRAX LETHAL TOXIN**

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Anthrax is an infectious disease caused by the spore-forming bacterium *Bacillus anthracis* and is classified by the Center for Disease Control as a Tier 1 bioterrorism agent. The bacterium secretes a binary toxin called lethal toxin (LT), comprised of 2 protein subunits, protective antigen (PA) and lethal factor (LF). PA binds to receptors on host cell membranes and mediates endocytic uptake of LF. Acidification of the late endosome induces a conformational change in PA, resulting in the formation of a pore in the endosomal membrane and entry of LF into the cytosol where it exerts its virulent effects upon the host cell. The objective of this study is to further elucidate the intoxication pathway by investigating the mechanism by which a novel compound, RC1, prevents LT-induced cell death in murine macrophages. Key events underlying toxin entry were assessed through cell-based viability assays and western blots to determine the stage of intoxication blocked by RC1. RC1 protects host cells from LT when added up to 30 minutes post-intoxication and from various other bacterial toxins that exploit similar intracellular trafficking processes. Additionally, RC1 acts downstream of toxin pore formation but prior to toxin activity in the cytosol. Based on these data, we hypothesize the molecular target of RC1 is a host factor necessary for the translocation of LF from the lumen of the endosome to the cytosol. Identifying the molecular target of RC1 will further our understanding of anthrax pathogenesis and similar toxin-mediated diseases, which may lead to new therapeutics.

**SAT-1131****THE EFFECTS OF VIRAL DOSE ON THE KINETICS OF ADAPTIVE AND INNATE IMMUNE RESPONSE DURING INTRAVAGINAL INFECTION**

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Innate and adaptive immunity defends against viral infections in mammals. CD8 T-cells, an essential component of adaptive immunity, must expand in number quickly enough to successfully suppress viral load. In the study of HIV, it is believed that during mucosal infection, CD8 T-cell response is delayed and dampened compared with systemic infection. Using lymphocytic choriomeningitis virus (LCMV), the Sanjabi lab has evidence that a sub-optimal innate immune activation is responsible for this defect in CD8 T-cell response after vaginal viral infection. This may be due either to the tolerogenic mucosal environment that inhibits increased innate immune activation, or due to inefficiency in viral transmission across the mucosal barrier. However, it is still unknown why a mucosal infection elicits a delayed and diminished immune response. To address these possibilities, we vaginally infected three cohorts of mice with different doses of LCMV (1x, 2x, or 4x viral load per mouse, respectively), and monitored each cohort's innate and adaptive immune activation in the female reproductive tract (FRT), draining lymph nodes, spleen, and peripheral blood lymphocytes. We have found

that, during the period from 3 to 5 days after infection, the lower FRT experiences an increase in viral load while the iliac lymph node begins to clear the virus. Furthermore, increasing viral doses leads to more robust and faster CD8 T-cell responses. These results further confirm that the FRT environment inhibits efficient immune response and that increasing viral titrations alters CD8 T-cell kinetics.

#### **SAT-1126**

##### **STUDYING MYCOBACTERIOPHAGE GENOME SEQUENCES TO UNDERSTAND RELATIONSHIPS BETWEEN MYCOBACTERIOPHAGES**

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Bacteriophages comprise the largest biomass on Earth, with an estimated total of  $10^{31}$  phages in the biosphere; however, little is known about their diversity. Mycobacteriophages are viruses that infect mycobacterial species such as *M. tuberculosis* and *M. leprae*. We use *M. smegmatis* as a model because it is non-pathogenic and shares some traits with *M. tuberculosis*. Studying phages that infect *M. smegmatis* may improve our knowledge about the genetics of other mycobacteria. To date, 3,600 mycobacteriophages have been isolated, but only 530 have been sequenced. To gain insight into mycobacteriophage genetics, phages have been sequenced in order to find genome sequence similarities and cluster them. Relationships among phages are typically analyzed by comparing whole genomes. Currently, 21 clusters have been established, but particular clusters are highly represented among sequenced phages, while other clusters have few members. Sequencing novel phages or phages belonging to rarely sequenced clusters will expand our understanding of mycobacteriophage diversity. The goal of this project is to develop a simple and effective protocol for preliminary cluster determination by cloning and sequencing small fragments of phage genomes. This will serve as a base for a more informed selection of phages for whole genome sequencing, resulting in a broader picture of mycobacteriophage biology.

#### **FRI-1118**

##### **COMPARING THE DIVERSITY PRESENT IN SOIL METAGENOMIC LIBRARIES AND THE SOIL SOURCES USING DENATURING GRADIENT GEL ELECTROPHORESIS**

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Metagenomics is a tool to evaluate genomes in an environment, unraveling novel activities and microbial diversity using culture-independent approaches. Our laboratory generated metagenomic libraries (MgL) from Ventana Cave (VC) and Sierra Bermeja (SB) soils. While functional analysis has been done on these libraries, how representative the diversity found in the MgL related to its soil sample is unknown. The goal of this research is to compare the microbial diversity present in the MgL with the diversity in its soil source using denaturing gradient gel electrophoresis (DGGE). Fosmid DNA from induced MgL was extracted, and a direct DNA extraction from the soil samples was made. Fosmids were run throughout an agarose gel, and 2 defined bands were observed for each MgL, indicating different conformations. Bands

were excised and purified. Universal 16S-rDNA PCR was performed. A reamplification was done using DGGE primers. The amplicons were run through DGGE with gradients that ranged from 40 - 60%, 35 - 75%, and 45 - 70%. Band numbers were quantified and patterns were compared. The soil band patterns obtained from VC were a subset of the fosmid bands which suggests PCR bias, contrary to SB in which 29% of the MgL bands were present in the soil sample. Each conformation amplicon of VC showed different band patterns when compared to each other, in contrast to SB MgL in which both conformations showed the same band pattern. DGGE demonstrated that the MgL partially represents the diversity present in the soil source. However *in silico* analysis comparison is needed to assign an identity to band patterns.

#### **SAT-1130**

##### **ANALYSIS OF ANTIBIOTIC RESISTANCE GENES, *BLAZ/I* AND *MECA*, IN NON-CLINICAL SAMPLES OF *STAPHYLOCOCCUS***

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Emerging antibiotic resistance is a serious problem for public health. Beta-lactams are the most used antibiotics, prescribed in 60% of cases. As a result of this extensive use, *Staphylococci* have developed 2 major forms of resistance. One mechanism of resistance relies on *blaZ*, which encodes a beta-lactamase destroying penicillin. The second mechanism comes from *mecA* encoding altered penicillin-binding protein and causing broad resistance. The aim of this study is to determine antibiotic resistance profiles, examine the occurrence and genetic diversity of both genes, determine the extent of exchange of these genes, and relate antibiotic resistance profiles to gene presence. The 94 isolates were obtained from beaches in Southern California and from healthy humans. Bacteria were isolated using filtering and selective media and identified with MALDI-TOF mass spectrometry. Antibiotic resistance profiles were determined from disk diffusion tests according to the Clinical and Laboratory Standards Institute guidelines. Antibiotic resistance genes were PCR amplified and sequenced. According to the disk diffusion test, 60% of isolates were resistant to penicillin, 52% were resistant to ampicillin, and 4% were resistant to cefoxitin. Also, 78% of isolates contained *blaZ* and 13% had *mecA*. The prevalence of *blaZ* and *mecA* genes on beaches of Southern California demonstrates that natural environments may harbor extensive antibiotic resistance genes. Continuous monitoring of natural habitats is necessary for a fuller understanding of the dynamics and generation of antibiotic resistance.

#### **SAT-1118**

##### **SYSTEM FOR CONTINUOUS EVOLUTION OF A TARGET GENE**

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We present an improved method for generating random mutant libraries of a plasmid-borne target gene in culture. The original system includes two components: an error-prone version of DNA polymerase I (low fidelity (LF Pol I)), and the second one bearing the gene of interest. LF Pol I contains 3 point mutations altering key Pol I residues for replication fidelity. Here we



describe a fourth mutation (K54E) affecting the 5'-3' exodomain of *Pol I* which mediates processing of Okazaki fragments during lagging-strand replication. We demonstrate that this mutation increases the fidelity of the polymerase *in vivo*. However, in cells expressing *K54E-LF Pol I*, we observed cumulative mutagenesis with serial passage, allowing us to raise the mutation frequency and control it. Further, we provide evidence suggesting that this cumulative mutagenesis is likely linked to the higher plasmid replication fidelity of the plasmid replication mentioned above. The continuous system for mutagenesis we describe here eliminates the need for multiple rounds of mutagenesis in order to achieve the desired mutation load. More importantly, this system allows evolution in real time, i.e., the implementation of a selection at the same time as mutations are generated. Our new system should facilitate the study of enzymatic evolution and explore different forms for generating mutations by modulating both the polymerase and host strain.

#### **FRI-1126**

##### **USE OF SYNTHETIC NEOGLYCOPROTEINS OF THE PARASITE *TRYPANOSOMA CRUZI* FOR THE DIAGNOSIS AND CHEMOTHERAPY FOLLOW-UP OF CHAGAS DISEASE**

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Chagas disease is spread by the triatomine bugs, or “kissing bugs,” which are vectors of the protozoan parasite, *Trypanosoma cruzi*. Chagas disease affects 8 - 10 million people in Latin America, resulting in approximately 10,000 - 12,000 deaths every year. Lately, it has also become a public health concern for non-endemic countries like the United States, Spain, Japan, and Australia. In the U.S., it is one of the top 5 neglected parasitic infections with an estimated 300,000 chronically infected, asymptomatic individuals. The available drugs are only partially effective and toxic, and there are no current vaccines to prevent or treat this emerging disease. In the present study, we use chemiluminescent enzyme-linked immunosorbent assays (CL-ELISA) to detect the reactivity of individual Chagasic sera (ChS) and normal human sera (NHS), obtained from patients from Brazil and Barcelona, to several synthetic neoglycoproteins (NGPs). These proteins contained non-reducing end terminal Gal $\alpha$ (1,2)Gal $\beta$  and/or Gal $\alpha$ (1,3)Gal $\beta$  epitopes covalently attached to bovine serum albumin (BSA). By using these different neoglycoproteins, we were able to determine that the greatest reactivity differential between ChS and NHS was observed when the Gal $\alpha$ (1,3)Gal $\beta$ -BSA was employed. These findings may eventually lead to the development of synthetic glycoconjugate as reliable diagnostic and prognostic tools for Chagas disease.

**SAT-1140****ANTIMICROBIAL PROPERTIES OF A TRADITIONAL MEDICINAL PLANT, *LUPINUS VARIICOLOR***

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Overuse of antibiotics has selected new strains of bacterial pathogens that are resistant to the antibiotics used to combat them. Many plants have been used for centuries by traditional healers and may have antibacterial properties. Native Americans used *Lupinus* spp. for disinfection and treatment of bladder infections. Our hypothesis is that extracts of parts of *Lupinus variicolor* will inhibit bacterial growth. We screened plant parts for their antimicrobial activity using well-diffusion assays. Leaf, flower, stem, and root extracts (1.0 g/mL) were prepared in methanol, ethanol, and acetone, and were tested against Gram-positive *Staphylococcus aureus*, Gram-negative *Escherichia coli*, *Pseudomonas aeruginosa*, *Penicillium* sp., and *Candida tropicalis* fungi. The alcoholic extracts inhibited the Gram-negative bacteria. The methanolic stem extract is most effective against *E. coli*. The methanolic stem extract inhibition zone is less than that of commercial ceftazidime disks. The minimum inhibitory concentration is 83 mg/mL, and the minimum bactericidal concentration is 330 mg/mL. We are currently expanding these results to characterize the antimicrobial chemicals. This plant may provide a source of a new antibacterial agents against antibiotic-resistant bacteria.

**SAT-1129****USE OF SERUM PROCALCITONIN TO DISTINGUISH VIRAL FROM BACTERIAL PNEUMONIA IN PEDIATRIC PATIENTS**

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Procalcitonin (PCT) is a biomarker used for the diagnosis of bacterial sepsis and systemic inflammation. PCT levels in healthy adults are < 0.5 ng/mL; PCT concentrations > 2.0 ng/mL are associated with bacterial sepsis. PCT has been used to differentiate viral from bacterial pneumonia in adults; however, the utility of this assay in pediatrics is uncertain. Our study sought to measure serum PCT levels in children with pneumonia of known etiology to determine if PCT levels correlate with a bacterial vs. non-bacterial origin. This study was approved by the Institutional Review Boards of the University of Utah and Primary Children's Hospital (PCH). Acute sera were obtained from pediatric patients admitted to PCH with pneumonia. Etiologies included bacterial, viral, combined bacterial and viral, or no pathogen detected (unknown). PCT levels were measured retrospectively using the VIDAS BRAHMS Procalcitonin<sup>®</sup> assay for all patients. Children (n = 90, age range 1 to 193 months) were evaluated: 27 with bacteria (including 8 with a virus detected), 47 with viruses alone, and 16 without an etiology. Excluding mycoplasma, the median PCT level for bacterial pneumonia was 3.93 (IQR 0.93 to 8.89) and for viral or unknown pneumonia was 0.50 (IQR 0.14 to 1.22). While the difference in median values between bacterial vs. non-bacterial pneumonia was not statistically significant, there was a trend. PCT levels show promise as a marker of bacterial vs. non-bacterial pneumonia in pediatrics. Further studies are warranted to better define PCT thresholds that may be used to differentiate bacterial and viral etiologies.

**SAT-1122****TAXONOMIC COMPOSITION OF CYANOBACTERIA IN THE GUT ECOSYSTEM OF MALARIA MOSQUITO *ANOPHELES GAMBIAE***

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Previously we have reported that the cyanobacteria were one of prominent inhabitants in the microbial community in the mosquito gut during the larval stage. Here, we further characterize the taxonomic composition of these cyanobacteria. The programs used were RDP Classifier, mothur, SeqMan, NCBI database, and MEGA6. The sequencing reads of bacterial 16S ribosomal gene fragments were classified by RDP classifier. The resulting cyanobacteria reads were separated into the subgroups cyanobacteria and chloroplast. The reads in these two subgroups were clustered using alignment program SeqMan with 97% similarity as the cutoff. The resulting contigs were used to make a phylogenetic tree using the MEGA6 program. Three clades were identified: Cyanobacteria, Bacillariophyta, and Chlorophyta. The Cyanobacteria clade included five taxa: *Nostoc*, *Microcoleus* sp., *Cyanobium* sp., *Geitlerinema* sp., and *Leptolyngbya boryana*. The second clade belongs to Bacillariophyta: *Durinskia baltica*, *Fistulifera* sp., and *Cymatopleura solea*. The third clade consisted of five taxa related to Chlorophyta: *Oocystis*, *Chlorella*, *Scenedesmus*, *Chlamydomonas*, and *Dunaliella*. The results support the evolutionary theory that chloroplasts evolved from cyanobacteria since the two clades containing the chloroplasts have been grouped together with a high level of certainty. However, the algae community in the larval mosquito gut may be much more diverse than this study suggests. The data implies that cyanobacteria and algae are a possible food source for the mosquito larvae. Our goal in identifying these cyanobacteria is to determine species that could be used as a potential larvicide against mosquito larvae.

**FRI-1123****SEASONAL VARIATIONS OF CYANOBACTERIAL DIVERSITY AND BIOGEOCHEMISTRY IN YOUNG AND MATURE HYPERSALINE MATS**

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We have combined microscopic, molecular phylogenic (i.e., genomic libraries and FAME analysis), and biogeochemical approaches to study the differences between the cyanobacterial communities present in two tropical hypersaline microbial mats that are in different developmental stages but exposed to similar climatological conditions and seasonal variations. One mat is ephemeral and is named Fraternidad, while the Candelaria mat is more developed. The diversity of Cyanobacteria found in this study was low, as demonstrated by the Chao 1 estimator, with a maximum of 18 and 60 species for Fraternidad and Candelaria mats, respectively. The rarefaction curve and Shannon-Weaver diversity index suggests that microbial mats from Candelaria are more diverse; however, cyanobacterial communities did reflect major changes among seasons. Our genomic libraries reported filamentous cyanos such as *Microcoleus* sp., *Phormidium* sp., and *Lyngbya* sp. as numerous in the mature mats while

unicellular forms such as *Eubacterium* sp. dominate in the Fraternidad system. To complement this phylogenetic information, we analyzed the total FAME extracted from each mat sample during seasons. Again we reported differences in the cyanobacterial communities present in each mat but not seasonal segregations. We also found a correlation between the main fatty acids extracted from the mats and those reported from pure cultures of the same cyanobacteria grown under axenic conditions. In conclusion, this work demonstrates spatial but not temporal molecular diversity between two types of tropical hypersaline microbial mats, one of them being less developed than the other.

#### **FRI-1125**

##### ***PSEUDOMONAS AERUGINOSA* QUORUM SENSING IN CHRONIC WOUND INFECTIONS**

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*Pseudomonas aeruginosa* is one of the most frequent causes of chronic wound infections. The production of the most virulence factors that contribute to the pathogenesis of *P. aeruginosa* is regulated by quorum sensing (QS). QS in *P. aeruginosa* involves three distinct regulatory systems which alter gene expression in response to the amount of specific chemical signals within an environment. We have previously demonstrated that QS is essential to the pathogenesis of *P. aeruginosa* in burn wound infections and in ischemic wounds; however, little has been elucidated about the role of QS in the chronic wound environment. To determine the extent of QS activity in *P. aeruginosa*-infected chronic wounds, we used LCMS to detect QS signals in murine chronic wound tissue, used fluorescent QS reporter strains and confocal microscopy to indirectly visualize the expression of *P. aeruginosa* QS genes *in situ*; analyzed the global expression of *P. aeruginosa* *in vivo* with RNAseq technology, and compared the infection sequela of wild-type *P. aeruginosa* versus a QS mutant in mouse chronic wounds. Our data indicate that QS is active early in murine chronic wound infections but quickly tapers off. We also observed that a QS mutant strain of *P. aeruginosa* was significantly less tolerant to gentamicin treatment *in situ* compared to a wild-type strain and that the tolerance of the wt was reduced after early treatment with a QS inhibitor. Taken together, our data indicate that QS may be important in the formation of biofilms early in chronic wound infections, resulting in increased antibiotic tolerance

**SAT-1124****INHIBITION STUDIES USING SAFFRON EXTRACT AGAINST *STREPTOCOCCUS MUTANS***

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The oral cavity is prone to dental and periodontal diseases caused by various bacteria residing in the mouth. One of the most common bacteria associated with dental plaque and tooth decay is *Streptococcus mutans*. This bacterium resides in organic biofilms and is the main causative agent of dental caries. Biofilms are communities of microbes attached to moist surfaces, such as teeth and gums, using extrapolymeric substances (EPS) that they synthesize. In previous studies, we have shown that mouthwashes containing cetylpyridinium chloride (CPC) as their active agent are best able to kill *S. mutans* within biofilms. However, using natural inhibitors rather than harsh chemicals would be less harmful to the patient. Recently, we have shown that garlic, turmeric, and saffron extracts successfully inhibit *Streptococcus mutans* in biofilms. Saffron has shown a percent inhibition of up to 85 % and is the compound of interest in this study. The minimum bactericidal concentration (MBC) of the saffron extract required for killing *S. mutans* as well as its target and mechanism of action are being investigated.

**SAT-1128****IMMUNOMODULATORY MECHANISMS OF THE DIETARY FLAVONOID APIGENIN**

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Sepsis is a deadly inflammatory disease. Despite advances in treatments, the mortality rate among patients with sepsis remains high. Current treatments accompany adverse effects, prompting the need for alternative therapeutic approaches. Flavonoids are dietary compounds with anti-inflammatory characteristics. Apigenin, an abundant flavonoid found in celery and parsley, prevents LPS-induced lethality *in vivo* and inhibits the LPS-induced IKKb/NF- $\kappa$ B activity. Previous studies using the cecal ligation and puncture (CLP) mouse model of sepsis showed that apigenin reduces CLP-induced mortality and increases microbial clearance in liver and blood. Yet, the mechanisms of how apigenin provides anti-inflammatory activity remain unclear. We hypothesized that apigenin increases bacterial clearance and survival by modulating the activity of the IKKb/NF- $\kappa$ B-pathway. Preliminary results showed that apigenin increases bacteria clearance by whole blood leukocytes incubated with mice gut microbiota. Using conditioned media from whole blood treated with LPS or LPS and apigenin showed that apigenin does not induce the release of anti-microbial agents, suggesting an improvement in the phagocytic activity of leukocytes by apigenin. Studies using bone marrow macrophages (wildtype and IKKb<sup>KO</sup> knockout) transfected with constitutive active IKKb revealed that apigenin reduces LPS-induced expression of TNFa (pro-inflammatory cytokine) in an IKKb dependent pathway while reducing expression of IL-10 (anti-inflammatory cytokine) independently of IKKb. Supporting our study, others have shown that knockout of IL-10 along with TNFa inhibition improves bacteria clearance and promotes survival in septic mice. Altogether, these results indicate that

apigenin promotes survival in septic mice by restoring normal immune function suggesting an alternative approach for the treatment of sepsis.

#### **FRI-1136**

##### **NON APOPTOIC PS REDISTRIBUTION IN ACTIVATING MAST CELLS**

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Mast cells drive inflammation in atopic disorders. Massive membrane rearrangement in the form of acquired phospholipid asymmetry, exosome formation, vesicularization, and degranulation of secretory granules follows antigenic ligation of the high affinity receptor for IgE, FcεRI. During activation, mast cells manifest these changes and then recover without loss of membrane integrity and are able to complete numerous activation-recovery cycles throughout their lifetimes. We hypothesize that controlled, non-apoptotic phosphatidylserine (PS) redistribution between the cytoplasmic and extracellular leaflets of the plasma membrane (PM) is a common requisite for the membrane proximal signaling events, the dynamic formation of exosomes and degranulation, and mast cell pro-inflammatory responses. Scramblases are lipid transporters that can bi-directionally shuttle lipids between the leaflets of the PM and can be activated by divalent cations. Phospholipid scramblase 1 (PLSCR1) and anoctamin 6 (TMEM16F) are two molecules that may mediate non-apoptotic PS flipping during mast cell activation. Confocal microscopy was used to characterize the kinetics and localization of external leaflet (exofacial) PS exposure in response to IgE/antigen and calcium ionophore. Additional histochemistry and microscopy assessed localization of PLSCR1 and TMEM16F. Presence and phosphorylation of PLSCR1 and TMEM16F were characterized by western blot. PS exposure in mast cells is calcium dependent, and ionophoric and antigen-driven calcium signals result in PS exposure. PLSCR1 and TMEM16F are present in the model mast cell line RBL2H3 but are differentially localized within the cell. Regulated exposure of anionic PS on the exofacial surface may contribute to mast cell activation in the absence of apoptosis.

#### **SAT-1136**

##### **QUANTIFYING PROTEIN SECRETION BY ASSAYING A TYPE III SECRETION SYSTEM IN *SALMONELLA***

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Overproducing heterologous proteins in bacteria often results in cell toxicity and aggregation of proteins in the cytoplasm. Additionally, current procedures for purification and isolation of these cytoplasmic aggregates, or inclusion bodies, are complicated because they require refolding the protein into its native fold. Protein secretion into the extracellular space may improve the yield of native protein. We have engineered a type III secretion system (T3SS) of *Salmonella* by site-specific mutagenesis of the *prgI* gene, which encodes the needle component required for secretion, and isolated mutations that led to higher protein titer in the culture supernatant. However, conventional western blotting techniques require a large amount of time to screen each mutant. Instead, we determined a more robust analysis of secreted enzyme

by calculating  $V_{\max}$ , the maximum reaction rate, and  $k_{\text{cat}}$ , which represents the turnover rate of a single enzyme. We secreted the enzyme beta-lactamase and observed that the activity of the secreted protein correlated with the amount of secreted protein titer. Through application of the rate equation, we show that a high reaction rate indicates a high concentration of protein, and a low reaction rate indicates a low concentration of protein. This enzyme assay is a more sensitive and higher-throughput method for calculating the total concentration of enzyme secreted by the *prgI* mutants as it requires smaller quantities and is faster than quantitative western blotting.

#### **FRI-1142**

##### **THE EFFECTS OF ELECTRIC AND MAGNETIC FIELDS ON THE BIOHYDROGEN PRODUCING CYANOBACTERIA *ANABAENA VARIABILIS***

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The aim of this research is to study the effects of electric and magnetic fields on the growth and metabolic behavior of the nitrogen fixing cyanobacteria *Anabaena variabilis*. The study will provide scientific knowledge into the usage of *A. variabilis* for biofuel applications. Since there is an all-time high of carbon dioxide concentrations in recent decades, there is strong push toward developing and innovating technologies to reduce rising temperatures. This species when grown in the right conditions is capable of producing biohydrogen that could be captured and used as a clean alternative fuel. In this study, *A. variabilis* will be subjected to various magnitudes of electric and magnetic fields to determine a possible optimum threshold that increases growth rate and biohydrogen production. The metabolic behavior will be quantified by recording changes in protein using the standard Bradford assay and the phenol-sulfuric acid method for carbohydrate production along with recording any fluctuations in the hydrogenase enzyme using western blot analysis. The species will be exposed to external electric and magnetic fields of 10kV/cm-40kV/cm and 10 mT-100 mT, respectively. It is anticipated that results will enhance growth rate and inflate biohydrogen production. This research will further strengthen the usage of *A. variabilis* in clean alternative energy technologies to help suppress carbon dioxide concentration.

#### **NEUROSCIENCE**

#### **SAT-1164**

##### **ACUTE DOPAMINE TRANSPORTER INHIBITION ENHANCES PROBABILISTIC LEARNING PERFORMANCE IN MICE**

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Bipolar disorder (BD) is a chronic disorder with no cure. Therapeutics have been limited to compounds with serendipitous origins and unknown mechanisms; therefore, there is a call for a better understanding. Lithium is primarily used to treat BD but has been called into question for decades due to its strenuous, inconsistent, and detrimental side effects. Using pharmacological

means (GBR 12909), the manic abnormalities of BD were modeled in mice, and lithium was used to treat the abnormalities in the probabilistic learning task (PLT) and progressive ratio breakpoint test (PRBT). We hypothesized that GBR 12909 would impair learning and increase motivation-like behaviors, while lithium would moderate the effects of GBR 12909 and also impair learning in relation to cognitive effects. In contrast to what was expected, GBR 12909 improved performance in both paradigms. Lithium at low doses attenuated the effects of GBR 12909 and at high doses impaired cognition.

#### **SAT-1161**

#### **GABAergic interneuron deficits in a mouse model of Cornelia de Lange syndrome**

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Cornelia de Lange syndrome (CdLS) is a multi-system birth defects disorder, caused in the majority of cases by mutation in one allele of the *NIPBL* gene. In addition, individuals with CdLS exhibit a number of neurological disorders including microcephaly, propensity to seizures, repetitive behaviors, mental retardation, loss of hearing, and behaviors that fall within the autism spectrum. However the cellular and molecular etiology of these deficits is largely unknown. Recently, we have developed a mouse model of CdLS (*Nipbl*<sup>+/-</sup> mice) that exhibits many of the neurological and behavioral deficits associated with the human disorder, and preliminary data suggest that the number of GABAergic inhibitory interneurons is decreased in the brains of these mice. There are several subtypes of GABAergic inhibitory interneurons that play a role in these various processes; they can be distinguished by co-expression of GABA-synthetic enzymes and neuropeptides such as parvalbumin and somatostatin. Since our *Nipbl*<sup>+/-</sup> mouse shows a high frequency of seizure upon exposure to anesthetic agents, we hypothesize that the distribution and/or number of the different subtypes of GABAergic interneurons may be altered in different brain regions of these mice. We will test this hypothesis using a combination of methods including immunohistochemistry, *in situ* hybridization, and a Gad67-GFP transgenic reporter and quantify each sub-type of these neurons to identify specifically the affected region in the *Nipbl*<sup>+/-</sup> brain. The results of this research may lead to a better understanding of interneuron contribution to the neurological and behavioral deficits associated with CdLS and, thus, to more directed therapies for these problems.



**FRI-1152****PRENATAL EXPOSURE TO VPA CAUSES INCREASED EXPRESSION OF SYNAPTIC CELL ADHESION MOLECULES**

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Autism spectrum disorders are the most common neurodevelopmental disorders affecting children. Autism is a neurological disorder that affects the brain's normal development and impairs social and communication skills. Prenatal exposure to valproic acid (VPA), a commonly-prescribed anticonvulsant medication, has been shown to greatly increase the risk of autism and other neurodevelopmental disorders (NDDs). Previous research using rodent models, as well as human fMRI studies, suggest that various NDD models and diagnosed humans have significant changes in network connectivity and excitability. Moreover, genetic screens of both rodent models and humans with NDD are often marked by misexpression of synaptic cell adhesion molecules (CAMs), cell surface proteins that function to stabilize and maintain synapses. Neuroligin-1 (NL-1) is a postsynaptic CAM expressed at excitatory synapses. Exposing cultured neurons to VPA causes increased expression of the cell adhesion molecule NL-1. This suggests NL-1 and perhaps its counterpart neurexin (NRX), a presynaptic CAM that interacts with NL1, may play a role in the onset of VPA-induced neurodevelopmental disorders. Recently, our lab developed a *Xenopus* tadpole model to study VPA-induced neurodevelopmental disorders. We hypothesize that exposing developing tadpoles to VPA during a similar gestational period will cause increased expression of NL-1 *in vivo* in the intact brain. To test this hypothesis, we conduct western blot analyses to measure levels of NL-1 and NRX. If NL-1 expression is increased, this will be the first study to demonstrate that VPA causes increased expression of NL-1 *in-vivo* and could suggest a significant role of NL-1 in the onset of NDD.

**SAT-902****EFFECTS OF GLUTAMATE ON EXTRACELLULAR H<sup>+</sup> FLUXES OF HORIZONTAL CELLS ISOLATED FROM THE RETINA OF THE SHARK (*MUSTELUS CANIS*)**

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There is considerable current evidence to suggest that alterations in the concentration of extracellular protons (H<sup>+</sup>) may mediate feedback inhibition from retinal horizontal cells onto vertebrate photoreceptors, creating the classic surround portion of the receptive fields of retinal bipolar cells. If this hypothesis is correct, then depolarization of horizontal cells should induce an extracellular acidification of the environment directly adjacent to the cell membrane. We sought to test this hypothesis by examining proton fluxes from horizontal cells isolated from the retina of the smooth dogfish (*Mustelus canis*). Ultra-sensitive, self-referencing H<sup>+</sup>-selective microelectrodes were used to monitor extracellular H<sup>+</sup> fluxes from horizontal cells isolated using a papain dissociation protocol. We found that unstimulated cells typically displayed a standing proton flux indicating a higher standing concentration of protons adjacent to the membrane as compared to the point 30  $\mu$ m distant in the surrounding solution. Stimulation of horizontal cells with 1 mM glutamate induced a decrease in proton flux, lowering

the concentration of free hydrogen ions around the cell. These data suggest that shark horizontal cells respond to the presumed photoreceptor neurotransmitter glutamate by reducing the overall level of protons at the external face of the cells, precisely opposite to the prediction of the H<sup>+</sup> hypothesis for lateral inhibition. These data are also consistent with data from several other species (catfish, goldfish, and skate), for which horizontal cells also show an extracellular alkalinization upon stimulation with glutamate.

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#### **FRI-1147**

##### **A COMPARISON OF LOCOMOTOR BEHAVIOR BETWEEN NORTH AMERICAN (*PERIPLANETA AMERICANA*) AND SOUTH AMERICAN (*BLAPTICA DUBIA*) COCKROACHES**

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Octopamine (OCT) belongs to a group of compounds known as biogenic amines. OCT is found in both vertebrate and invertebrate nervous systems and acts as a neurotransmitter and a neurohormone. OCT is essential for the regulation of goal-objective behaviors as well as learning and memory. The purpose of this research is to identify differences in locomotor behavior between two species of cockroaches, the North American (NA) and the South American (SA). We hypothesized that the NA cockroaches are faster than the SA cockroaches. We utilized an open chamber (51cm x 16cm x 31cm), and narrowed a track (51cm x 8cm x 9cm). Using 5 male and 5 female cockroaches from each species, we placed a cockroach into the chamber and ran 60-second trials. By placing blank poster sheets adjacent to the tank, we traced their path. We measured time in motion and time stopped using a stopwatch. From the traced paths, we measured distance traveled in cm using a seamstress tape. Overall, we calculated velocity (60 seconds - time stopped = time in motion / distance traveled). The data analyses suggest both male and female NA cockroaches are faster than SA cockroaches. NA cockroaches spend less time in motion, stop more frequently than SA cockroaches, and there is a significant variability in locomotor behavior from males to females within the NA cockroaches compared to the SA cockroaches. In conclusion, the NA cockroaches are faster than SA cockroaches. Our research is ongoing, and we expect to prove a correlation between octopamine and cockroach locomotor behavior.

#### **SAT-904**

##### **USING FUNCTIONAL MAGNETIC NEUROIMAGING BIOFEEDBACK TO TREAT AUDITORY HALLUCINATIONS IN SCHIZOPHRENIC POPULATIONS**

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Functional magnetic resonance imaging (fMRI) biofeedback allows for direct control of specific regional brain activation via modulation of blood oxygen level dependent responses, offering a promising approach to non-invasive, therapeutic interventions. About 75% of schizophrenia

patients experience auditory hallucinations, and a third of those report that these hallucinations cannot be well controlled by medication. fMRI biofeedback may offer a promising treatment option for these patients. This research seeks 1) to confirm the hypothesis that the superior temporal gyrus (STG) may be overactive in schizophrenics who experience auditory hallucinations, and 2) to pilot the use fMRI biofeedback as a tool for reducing temporal lobe activation in this patient population. In this study, participants underwent an initial scan which introduced a self-other task consisting of self and others' voices speaking semantically and emotionally neutral sentences during scan acquisition. This was followed by a second scan where participants underwent biofeedback training of the STG. Our initial pilot study has revealed consistent activation in the STG and inferior frontal gyrus in the self > other contrast in at least 3 of 4 patient participants ( $p = .05$ ). Early findings also suggest that schizophrenic participants are more likely to have lateralized auditory activation in the left temporal lobe than controls for both self and other sentences. As the first study to use fMRI biofeedback to attenuate auditory hallucinations, this work acts both as a proof of concept and also as a neuroscience tool to investigate the brain regions involved in auditory hallucinations.

### **SAT-1153**

#### **IDENTIFYING UFL1 SUBSTRATES THAT MAY BE IMPLICATED IN SCHIZOPHRENIA**

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Many seemingly unrelated genes have been associated with schizophrenia (Scz). A major goal is to understand how these genes function in common biochemical pathways. Among the Scz (and also autism (ASD))-implicated genes are certain E3 ligase components. E3 ligases are enzyme complexes that regulate the stability or function of target proteins by catalyzing the transfer of ubiquitin or ubiquitin-like molecules to them. To identify other biochemical connections that bind some of the Scz and ASD associated genes into pathways, we hypothesized that this set of Scz- and ASD-associated E3 ligases target a set of proteins in neurons, some of which are products of other genes implicated in schizophrenia. We are developing biochemical methods that utilize enzymatic tagging in cells to identify substrates and binding partners of the E3 ligase, UFL1, involved in the ufmylation of substrates. UFM1 is a ubiquitin-like protein of unknown function. To identify UFL1 substrates, we used Avitag technology involving the biotinylation of AviTagged UFM1 to capture UFM1-tagged proteins. We are working to isolate and identify UFM1-tagged substrates and compare them to the set of Scz GWAS genes to see if there is an overlap. If we find an overlap with any substrates, it could indicate that ufmylation of these substrates is an important pathway implicated in schizophrenia. Further study of this pathway may provide us with a better mechanistic understanding of these disorders and a possible target for treatment.

**SAT-1152****REGULATION OF ADULT HIPPOCAMPAL NEUROGENESIS BY HYPOXIA INDUCIBLE FACTOR 1-ALPHA (HIF1- $\alpha$ )**

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Adult hippocampal neurogenesis from neural stem and progenitor cells (NSPCs) is a unique form of adult brain plasticity linked to learning and memory. Previous studies by our lab have demonstrated constitutive expression of stabilized HIF1- $\alpha$  within NSPCs of the hippocampal subgranular zone (SGZ) of adult mice. Here, we investigated the hypothesis that HIF1- $\alpha$  performs a vital role in neurogenesis and performance on a neurogenesis-dependent learning task. We utilized a tamoxifen-inducible Cre-loxP approach to selectively delete exon 1 of the *Hif1 $\alpha$*  gene within NSPCs from nestin-CreER<sup>T2</sup>/R26R-YFP/ Hif1 $\alpha$ <sup>fl/fl</sup> triple transgenic mice. The inactivation of HIF1- $\alpha$  within NSPCs resulted in a 70% reduction in the number of YFP+ dentate granule cells (DGCs) compared to control nestin-CreER<sup>T2</sup>/R26R-YFP/ Hif1 $\alpha$ <sup>wt/wt</sup> mice ( $p < 0.05$ ,  $n = 5$  mice/group) by 45 days following tamoxifen administration. To determine whether the impaired neurogenesis following *Hif1 $\alpha$*  gene deletion is associated with impaired performance on a neurogenesis-dependent learning task, we tested mice on an A-B context discrimination fear conditioning learning paradigm. This task requires the formation of associations between distinct environmental contexts and an aversive stimulus. Our preliminary experiments demonstrated a significant impairment of learning in nestin-CreER<sup>T2</sup>/R26R-YFP/ Hif1 $\alpha$ <sup>fl/fl</sup> compared to nestin-CreER<sup>T2</sup>/R26R-YFP/ Hif1 $\alpha$ <sup>wt/wt</sup> mice at 45 days post tamoxifen exposure ( $p < 0.025$  at days 4 and 5 of training,  $n = 3$  to 7 per group). Currently, we are conducting fate map analysis of YFP+ cells to determine the stage of neurogenesis that is most vulnerable to *Hif1 $\alpha$*  gene deletion.

**SAT-1148****THE DESIGN AND EVALUATION OF CGRP8-37 RECOMBINANT PEPTIDE CONSTRUCT IN A MODEL OF NERVE INJURY-INDUCED PAIN IN RATS**

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Neuropathic pain induced by spinal cord injury insufficiently responds to current pharmacological treatment. New therapeutic approaches are needed. Calcitonin gene-related peptide (CGRP) is produced by neurons in the DRG and thought to play a key role in nociceptive neurotransmission. Hypersensitivity to CGRP in response to injury may contribute to persistent neuropathic pain. Truncated CGRP, CGRP8-37, a CGRP antagonist, can reverse symptoms of neuropathic pain. Using the chronic constriction injury model (CCI), intrathecally injected CGRP8-37 was found to reduce neuropathic pain in a dose-related fashion in rats. Therefore, CGRP8-37 may be suitable for gene therapy of chronic pain. The aim of this study was to design a cDNA clone of CGRP8-37 and to evaluate its effects in neuropathic pain models. To accomplish this, the CGRP8-37 sequence from human CGRP cDNA was amplified. CGRP8-37 was ligated to pGEMT-EZ cloning vector, and the sequence was confirmed. The CGRP8-37 fragment

was subcloned downstream of ssPAM/pGEMT, and the entire ssPAM-CGRP8-37 sequence was subcloned to AAV2/8 transfer plasmid. Plasmids encoding CGRP8-37 were used to transduce HEK cells. *In vitro* immunocytochemistry confirmed production of recombinant CGRP8-37 in transduced HEK cells. For screening of the antinociceptive activity of the secreted peptide, supernatant was collected and injected intrathecally in rats with CCI. Intrathecal delivery of supernatant dose dependently reduced neuropathic pain. The antinociceptive effect of the concentrated supernatant was comparable to that of the authentic CGRP8-37 peptide injected intrathecally in CCI animals. These results suggest that recombinantly derived CGRP8-37 retains antinociceptive activity and may be a strategy for gene therapy in pain models.

#### **SAT-1147**

##### **TOP SCORING PAIR IDENTIFICATION OF STRESS HISTORY BIOMARKERS IN MOUSE HIPPOCAMPUS**

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We undertake the problem of identifying biomarkers for stress history in mice, using microarray data sets from a variety of stress and control conditions. The approach seeks to identify gene pairs through statistical analysis and ranking order, using the algorithm top scoring pair (TSP) in R, which allows us to identify lasting, quantifiable changes in hippocampal RNA expression resulting from stress. The TSP method of measuring gene expression patterns has been carried out by others by analyzing microarray data and focusing on pairwise comparisons of genes for a number of disorders and organisms. This focused approach allows for the comparison of single pairs of genes that change their expression levels from one value to another, in essence, inverting their expression levels. This approach has the advantage of being done *in silico* with the ability to examine microarray data via the TSP rank-based system. Further, the results can be used to query other data sets, including both array and sequence data. The rank-based analysis of microarray data to measure gene expression profiles of stressed vs. non-stressed mice may provide insight into specific genes that influence their stress response, which would allow for these biomarkers to be identified and tested for using a simple RT-PCR assay. The present work will identify candidate pairs and validate them, both *in silico* and *in vivo*.

#### **FRI-1146**

##### **PREDICTORS OF LONGITUDINAL CHANGE IN WHITE MATTER HYPERINTENSITIES**

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White matter (WM) integrity has been shown to be important both in speed of processing and in cognitively complex domains such as executive functioning. White matter hyperintensities (WMH), as an indicator of WM integrity, have also been related to vascular risk and its impact on cognitive functioning. While concurrent associations between WMH volume, cognition, and vascular risk have been studied, there is relatively limited examination of factors associated with short-term longitudinal change in WMH volume in cognitively healthy subjects. We

hypothesize steeper increase in WMH with age and for  $\epsilon 4$  carriers. In this study, we examine 4 occasions of change in WMH volume over a 6-year interval in 87 cognitively normal adults in a MANCOVA design. Approximately half the sample had been diagnosed with hypertension, although  $\epsilon 4$  carriers did not differ in percent with hypertension. Predictor variables included age (midlife/old age) and APOE  $\epsilon 4$  status with education as a covariate. Mean WMH volume doubled over the 4 occasions of measurement with older subjects having significantly higher WMH volume across occasions. Older subjects showed a steeper rate of increase across time, with older  $\epsilon 4$  carriers showing the steepest increase in WMH volume, compared to  $\epsilon 4$  noncarriers. Carriers and noncarriers did not differ at baseline. This study extends prior findings in examining rate of increase in WMH volume over 4 occasions in healthy, cognitively normal adults, examining change in midlife versus old age. Both age and APOE  $\epsilon 4$  status were shown to contribute to rate of increase in WMH volume over time.

## **FRI-902**

### **MAPPING THE NEURAL CIRCUITRY OF THE VENTRAL PALLIDUM**

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Neuropsychiatric disorders in the United States are estimated to cost over \$300 billion annually. Despite their cost and prevalence, there are significant gaps in our knowledge about the neural mechanisms that lead to these disorders. There are specialized neural circuits in the brain that underlie rewarding and aversive behavior. Changes to these systems may lead to neuropsychiatric illnesses, such as depression or addiction. In this study, we examine the neural circuitry of the ventral pallidum (VP), a region that anatomical and behavioral studies suggest is important in mood disorders, yet remains under studied. We approached this problem in multiple ways. First, we used retrograde tracing on wild-type mice to examine VP connections. Next, we used genetically modified mice to determine the inputs and outputs of 2 prominent neuronal VP subtypes: the parvalbumin (PV) expressing neurons and the choline acetyltransferase (ChAT) expressing neurons. Different connectivity of these distinct populations may suggest differential roles of the 2 types of cells in neuropsychiatric illness. Our results indicate that PV-expressing neurons project onto regions such as the ventral tegmental area, the lateral habenula, the lateral hypothalamus, and the mediodorsal nucleus of thalamus. The ChAT-expressing neurons, however, only have strong projections to the basolateral amygdala and central amygdala. Many of these locations receiving inputs from the VP also send reciprocal projections back to the VP. Determining these neural systems of reward represent early steps in discovering the mechanisms of neuropsychiatric disorders, providing the foundation for future studies to develop more effective treatments and better prevention strategies for mood disorders.

**FRI-901****NMDAR SUBUNIT EXPRESSION IN THE HIPPOCAMPUS OF RATS WITH FREE ACCESS TO RUNNING WHEELS**

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Exercise enhances the rate of neurogenesis in the mammalian hippocampus; what is less well understood is the potential mechanism by which this occurs. There is evidence to suggest that voluntary exercise (VEx) can enhance glutamatergic transmission and LTP in the hippocampus, suggesting a possible role for the N-methyl-d-aspartate receptor (NMDAR) in the increased neurogenesis subsequent to wheel running observed in rodents. Additionally, NMDARs have been implicated in regulating neurogenic properties of dentate gyrus granule cells in adult animals, further implicating a potential role in the exercise/neurogenesis relationship. Further, it is not well understood if the effects of exercise are regionally specific to the dorsal dentate gyrus, which exhibits a higher rate of neurogenesis than the ventral region. In the present study, we evaluated the biochemical expression of NMDAR subunits 2A, 2B, and pTyr1472-2B, all of which convey critical implications for receptor functionality. This evaluation was done in both the dorsal and ventral hippocampus in sedentary (Sed) and VEx rats to test the hypothesis that changes in the NMDAR system underlie the observed, enhanced neurogenesis in the hippocampus. Adult rats in the VEx group were housed with free access to monitored running wheels and then sacrificed after 6 weeks, or age-matched for animals in the Sed group. Protein samples were processed for western blot analysis and probed with primary antibodies for the NMDAR subunits previously mentioned. Preliminary evidence demonstrates downregulation of the pNR2B subunit, implying enhanced function of the NMDAR system, which could be potentially contributing to the exercise related neurogenic promoting effects in the hippocampus .

**FRI-1144****PROTEIN AGGREGATION INHIBITORS DECREASE NEURAL CELL DEATH IN THE SPINAL CORD OF DIETHYLMALEATE-TREATED MICE**

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Reduced levels of the antioxidant glutathione and increased protein oxidation are observed in several neuroinflammatory and neurodegenerative disorders. Protein oxidation triggers the formation of large, protease-resistant aggregates that are believed to be cytotoxic. Indeed, we have previously shown that the protein aggregation inhibitors congo red (CR) and 2-hydroxypropyl  $\beta$ -cyclodextrin (HPCD) significantly reduce cell death in glutathione-depleted neuron-like PC12 cells. In this study, we investigate whether CR and HPCD also prevent neural cell death *in vivo*. Ten week-old C57BL/6 mice were given an intraperitoneal (ip) injection of diethylmaleate (DEM) (6.0 mmol/kg), a treatment that reduces glutathione levels in the spinal

cord by 70-80%. Some DEM-treated animals also received an ip injection of either CR (40 nmol/kg) or HPCD (20 nmol/kg). After 12 hours, mice were euthanized and the spinal cord was rapidly removed and processed for immunohistochemical analysis. Apoptotic cell death in the lumbar spinal cord was determined by TUNEL staining, and neurons, oligodendrocytes, and astrocytes were identified using antibodies against NeuN, CAII and GFAP, respectively. We found that DEM treatment increases the number of apoptotic cells by 10-fold and that both protein aggregation inhibitors decrease cell death by 50%. TUNEL-positive cells in glutathione-depleted mice were identified as neurons (51%), oligodendrocytes (9%) and astrocytes (20%), and both CR and HPCD reduced apoptosis of all these cell types. Our results not only demonstrate the cytotoxic role of protein aggregation *in vivo* but also validate the therapeutic potential of these agents. (Supported by National Institutes of Health grants NS057755 and NS084042, and by the IMSD program.)

#### **FRI-1161**

#### **EFFECTS OF TGF- $\beta$ SIGNALING IN ASTROCYTIC PROLIFERATION IN MOUSE HIPPOCAMPUS DURING POST TRAUMATIC EPILEPSY**

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The blood brain barrier (BBB) is required for maintaining the privileged environment necessary for proper CNS function. Traumatic brain injury (TBI) disrupts the BBB and causes extravasation of serum albumin into the brain parenchyma, resulting in inflammation and the delayed onset of chronic seizures and epilepsy. Although post-traumatic epilepsy (PTE) affects millions of people worldwide, no effective anti-epileptic treatment currently exists. Our lab has previously shown that albumin activates the pro-inflammatory transforming growth factor-beta (TGF- $\beta$ ) signaling cascade, specifically in astrocytes, and that this initial injury response is a key early event in epileptogenesis. However, the specific response of hippocampal astrocytes to albumin remains insufficiently characterized. We hypothesize that albumin exposure will cause increased reactive astrogliosis, and that the pharmacological blockade of TGF- $\beta$  signaling will reduce astrocyte activation and proliferation. Using specific transgenic approaches to analyze the spatio-temporal patterns of reactive astrogliosis, as well as blocking astrocytic TGF- $\beta$  signaling *in vivo*, we assessed the effects of both albumin and astrocytic signaling on reactive astrogliosis in the adult mouse hippocampus. Additionally, we used an *in vitro* approach to explore the effects of serum albumin on astrocyte calcium signaling. These experiments will further our understanding of the astrocyte injury response and explore the potential for preventive treatments targeted at astrocyte reactivity before the onset of epilepsy.



**SAT-1157****NMDAR ANTAGONISM CAUSES DIFFERENTIAL SYNAPTIC PROTEIN EXPRESSION IN A SCHIZOPHRENIC MOUSE MODEL**

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Schizophrenia is a severe brain mental disorder that appears in late adolescence or early adulthood and affects millions of people. It has been previously shown that exposure to the N-methyl-D-aspartate receptor (NMDAR) antagonist, ketamine, at a critical developmental period can lead to loss of parvalbumin expressing (PV+) interneurons and changes in electrophysiological properties in the mouse prefrontal cortex (PFC), as seen similarly in human schizophrenia postmortem samples. Therefore, our hypothesis is that NMDAR antagonism at postnatal week 2, which is the onset of synaptogenesis and PV+ maturation, can alter the maturation program of the PFC; this in turn, could be behind the alterations observed in PV+ interneurons. High-throughput sequencing of mRNA in the PFC tissue from 2, 4, 6, and 10 weeks of developmental age in ketamine-treated mice showed significant alterations in the transcriptional profile of neurodevelopmental and synaptic genes compared to saline treated. Currently, we are validating the differential protein expression of synaptic genes such as *Citron*, *ErbB4*, *Shank1*, *Cacna1e*, *Grin 2A*, and *Grin 2B* using immunofluorescence to see changes at specific neurons and western blot of the PFC at different developmental ages of ketamine and saline treated animals. In conclusion, the NMDAR hypofunction mouse model will enable us to understand the altered maturation of cortical neurons at the critical developmental period through their transcriptional and proteome profile. This can lead to a better understanding of human schizophrenia.

**FRI-1157****A NEW DATA-DRIVEN APPROACH TO DEFINE FUNCTIONAL CIRCUITRY FROM TRACT-TRACING BY MANGANESE ENHANCED MAGNETIC RESONANCE IMAGING (MEMRI)**

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The mesolimbic cortical circuitry plays a major role in decision-making and emotional responses. This circuitry depends on connections between the medial prefrontal cortex (mPFC) and deeper structures throughout the brain. Here, we report a novel computational method to investigate functional connections emanating from the mPFC. Mn<sup>2+</sup>, a paramagnetic ion that traces active circuits, was injected into the mPFC of living wild-type mice (n = 20) and 3D whole brain images at 90  $\mu\text{m}^3$  resolution captured before and at various time points later by high-field T<sub>1</sub>-weighted magnetic resonance imaging. After skull-stripping and nonlinear alignment, datasets were analyzed using independent component analysis (ICA), a data-driven approach that does not assume a specific time-course shape. Results revealed multiple components with connections to the mPFC, including thalamus, amygdala, ventral tegmental area, and other

limbic-system nuclei, each with a different connectivity time dependence. Functional network connectivity (cross-correlation among ICA timecourses) was used to evaluate the inter-relationship among these components in time. We are in process of performing similar analyses on littermates knocked-out for each of the 3 monoamine transporters, SERT, DAT and NET, major contributors to the mesolimbic circuit. This research is on the frontier of work identifying monoamine transporter networks, which are difficult to identify by other tracing or tractography approaches. A comparison of components from wild-type dataset and knockout mice will aid in localization of individual transport networks. (Supported by RO1 MH096093 (ELB) and P20GM103472 (VDC).)

#### **FRI-1163**

##### **ANALYSIS OF THREE-DIMENSIONAL BEHAVIOR OF *C. ELEGANS* STIMULATED BY BLUE LIGHT**

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The nematode *Caenorhabditis elegans* is widely used as a model organism for its simple neural network and wide range of response to physical stimuli. These responses to physical stimulations have been widely studied in a two-dimensional environment. However these observations are not optimal since they do not reflect the three-dimensional space in which *C. elegans* naturally exist. Not much is known about the behavior of *C. elegans* after physical stimulation in three-dimensional environments. In order to explore this behavior, *C. elegans* placed within a cuvette were stimulated by blue light. This was done under different gelatin concentrations. The differing concentrations of gelatin varied the ability of *C. elegans* to move about freely. A three-dimensional worm tracking program using MATLAB software was used to track *C. elegans* and analyze its behavior in three dimensions under the different gelatin concentrations. The blue light triggered avoidance behavior in the worm that followed with varying movement dependent on the concentration of the gelatin. The analysis of *C. elegans* in a three-dimensional environment provides insight into their natural locomotion, and supports better understanding of its behavior in response to other physical stimulations.

#### **SAT-1151**

##### **THE ROLE OF AUTOPHAGY PROTEINS IN *C. ELEGANS* PRESYNAPTIC ASSEMBLY**

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Autophagy is an evolutionarily conserved cellular process through which proteins and damaged organelles are degraded via a lysosomal pathway. Autophagy is especially required in post-mitotic cells, such as neurons, for degradation of damaged proteins and organelles for cell maintenance. It has been shown that autophagy plays an important role in processes such as neurodegeneration and synaptic plasticity. These findings prompted us to question whether autophagy is required for the formation or maintenance of synapses. For our studies, we examined a neuron in the nerve ring of the nematode *C. elegans* and fluorescently labeled synaptic vesicle proteins RAB-3 and SNB-1. RAB-3 is a small GTPase that associates with

synaptic vesicles, and SNB-1 is a component of the SNARE complex required for synaptic vesicle fusion. With these markers, we examined synaptic vesicle localization in autophagy pathway mutants. We identify 13 autophagy pathway components that are required for presynaptic assembly. We also showed that ATG-9, a component of the autophagy pathway, co-localizes with RAB-3 in presynaptic regions and that ATG-9 presynaptic localization is dependent on the synaptic-vesicle-specific kinesin, UNC-104. To further determine the role of autophagy in presynaptic assembly, we generated a lysosomal marker using GFP-tagged LAAT-1. We used this marker to visualize the subcellular localization pattern of lysosomes and to determine whether lysosomal localization changes in autophagy pathway component mutants. For future directions, we are also performing a forward genetic suppressor screen in one of the autophagy mutant backgrounds to determine other genes acting in this pathway to instruct presynaptic assembly.

### **SAT-903**

#### **LIGHT AVERSION IN MICE AS A MODEL OF PHOTOPHOBIA**

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Migraine is a chronic neurological disorder that affects approximately 12% of the world's population. Some patients who experience migraines show photophobia, which is the aversion to light. It is considered a relevant phenotype that is seen in the majority of migraine patients. In this study, we used animal models to elucidate the mechanism of migraines and various phenotypes affiliated with migraine. This project used a modified elevated plus maze (EPM) where the closed arms of the maze were illuminated with bright lights. Nitroglycerin (NTG) is shown to lower pain thresholds and increase light-aversive behaviors in mice. While EPM usually measures anxiety, by modifying the maze and combining with NTG, we could measure whether the animal avoided the brightly lit, closed arms. We expected the mice injected with NTG to spend more time exploring the dark, open arms and avoiding the lit, closed arms. This experiment focused on light-aversive behaviors in cluster differentiation 1 (CD 1), both wild type and those with green fluorescent protein (GFP) under a glutamate decarboxylase 67 promoter (GAD 67 GFP). Our results suggest that different genetic animal models seem to display different aversive behavioral phenotypes to light. Though much of the work is preliminary, it validates the use of a modified EPM to measure light-aversive behavior in mice and the development of animal models to test migraine related phenotypes.

### **FRI-1158**

#### **COMPLEMENT ACTIVATION AND NEURODEGENERATION IN PROGRANULIN-DEFICIENT MODELS OF FRONTOTEMPORAL DEMENTIA**

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Mutations in progranulin (PGRN) have been causally linked to frontotemporal dementia (FTD). Several recent studies have shown that PGRN deficiency leads to aberrant microglial activation and an increased neuroinflammatory response. However, the mechanism by which PGRN

mutations contribute to FTD remains unclear. Previous results showed that PGRN deficiency leads to a drastic, age-dependent upregulation of complement genes that correlates with the increased neuroinflammation. Given the well-documented role of the complement system in synaptic pruning in the developing visual system, we further hypothesized that over-activation of the complement system and the neuroinflammatory response in Grn-null mice could lead to neurodegeneration by excessive synaptic pruning. In support of this hypothesis, previous results showed that microglia from Grn-null mutants exhibited more aggressive synaptic pruning in microglia-neuron co-cultures and in the ventral thalamus of old Grn-null mutants. A model was proposed showing complement activation can also occur in the lysosomes of activated microglia cells via the proteolytic activity of lysosomal cathepsins. To further study intracellular complement activation, we determined the level of complement and lysosomal protease RNA expression through qRT-PCR in these cells to identify if lysosomal proteases were upregulated in Grn-deficient microglia. In addition, we performed TCA precipitation and western blots on the conditioned media obtained from primary microglia to determine if Grn-deficient microglia cells secrete more complement proteins and inflammatory factors. Judging from the overactive phenotype in Grn-deficient microglia, we expect to see an upregulation in lysosomal protease RNA, resulting in the increase of secreted complement proteins and cytokines.

#### **FRI-1150**

#### **BIOREPOSITORY TO ESTABLISH THE AETIOLOGY OF SINOVENOUS THROMBOSIS (BEAST): AN INTERNATIONAL COLLABORATION**

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Cerebral sinovenous thrombosis, CSVT, is a rare form of cerebrovascular disease that accounts for approximately 1% of all strokes and has a mortality rate of 10 - 13%. Known CSVT risk factors include oral contraceptive use, pregnancy, and meningitis. However, 15% of CSVT cases are reported without any risk factors, and 22% of CSVT cases have inherited thrombophilias. Our project collected DNA from CSVT patients seen at the University of Utah for contribution to the international DNA biorepository for exome genotype analysis. Participants were collected from retrospective chart reviews of CSVT patients. Data on age, gender, environmental risks, familial, social, and medical history, diagnostics, treatments, and outcomes were extracted from the medical record and via patient interviews. Controls are adults without a history of clotting disorders. Collected DNA samples from controls and CSVT participants will be analyzed for exome genotypes. Over the past 13 years (2000-2013), the hospital has seen 349 patients with CSVT; 205 (58.7%) are female. The age range at time of CSVT is 1 to 81 years old (mean 68.2, 138.3 SD). Risk factors include concurrent infection (19%) and smoking (21.4%). Ten CSVT patients and 3 controls have completed the blood draw and data collection. We will continue to contact patients for further enrollment. Identifying cerebral sinovenous thrombosis risk factors is important in order to understand how to prevent this severe disease.

**FRI-916****LEVELS AND ACTIVITY OF MITOCHONDRIAL LON PROTEASE IN EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS**

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Multiple sclerosis (MS) and other diseases of the central nervous system are characterized by an increase in the amount of oxidized proteins, which leads to the formation of cytotoxic aggregates. The build-up of these damaged proteins within cells may be caused not only by a rise in the rate of oxidation but also by a reduction in the activity of the proteases that remove them. The proteasome and the Lon protease are responsible for the removal of oxidized proteins in the cytoplasm and mitochondria, respectively. In preliminary studies, this laboratory has found that mitochondria from the brain of MS patients contain high levels of oxidized proteins. Based on this and several other observations, we hypothesize that the concentration and/or specific activity of the Lon protease is reduced in MS and its animal model, experimental autoimmune encephalomyelitis (EAE). To test this novel idea, we plan first to quantify the levels of this protease in the spinal cord of control and EAE mice by western blot analysis using a Lon specific antibody. The amount of mitochondria will be determined on the same blot using a VDAC/porin antibody. Second, we plan to measure the activity of Lon protease in isolated mitochondria using fluorescent peptide substrates. If these experiments are successful, we will correlate changes in the activity/levels of this protease with various histopathological markers during the course of the disease. Through these studies, we hope to gain insight into the role of Lon protease in demyelinating disorders.

**FRI-1162****INFLUENCE OF DIETARY CHOLESTEROL AND COPPER ON LONGEVITY, NEURODEGENERATION, LEARNING, AND MEMORY IN A *DROSOPHILA* MODEL OF ALZHEIMER'S DISEASE**

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With the global population increasing and living longer, age-related cognitive decline, dementia, is an increasing concern. In 2013, Alzheimer's disease (AD), the most common form of dementia, was the sixth-leading cause of death in the U.S.; 5.2 million Americans had AD as did 35 million individuals worldwide. Medical expenses related to AD are projected to surge from \$203 billion in 2013 to \$1.2 trillion per year by 2050. With no effective treatments, there is a great need to understand this disease, improve therapies, and develop preventive treatments. While epidemiological studies have found correlations between AD and dietary cholesterol and copper, there are few studies that address the causal relationship between AD and high cholesterol and/or copper. Using a *Drosophila* model of AD, this study investigates the effects of dietary cholesterol, copper, and their interaction on AD pathology. Like mouse AD models, the *Drosophila* AD model exhibits decreased activity, decreased longevity, altered learning and memory, and neuronal accumulation of A-beta (A $\beta$ ), the key peptide involved in AD. We are feeding *Drosophila* AD models diets with differing levels of cholesterol and/or copper and observing the effects on A $\beta$  accumulation, longevity, activity level, neural

degeneration, learning, and memory. We hypothesize that high levels of cholesterol and copper will exacerbate AD-like pathology in *Drosophila* and will synergistically increase neurodegeneration and other aspects of AD-like pathology. If this hypothesis is supported, this study will provide an impetus for similar studies in the human population.

#### **SAT-901**

##### **INVESTIGATION OF OPC DEVELOPMENT IN TRANSGENIC SUFU KNOCKOUT MICE**

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In the developing forebrain, oligodendrocyte precursor cells (OPCs) differentiate into oligodendrocytes that are responsible for the structure and myelination of neuronal axons. Understanding the mechanisms that control OPC development is of interest because of its implications in a number of dysmyelinating syndromes, multiple sclerosis, and tumors such as gliomagenesis. To this end, we are examining the role of suppressor of fused (Sufu), a cytoplasmic protein with important roles in signaling pathways that function in neural progenitors. Our lab has previously showed that heterozygous Sufu knock-out mice exhibit enhanced production of OPCs at embryonic (E) stage 15.5 and postnatal day (P) 2 in the forebrain. To specifically explore the function of Sufu in neural progenitors, we used the Cre-LoxP transgenic system to conditionally delete Sufu in neural progenitors in the developing cortex at E13.5 prior to the onset of gliogenesis, when OPCs and oligodendrocytes are generated. We performed a series of immunofluorescence experiments using specific antibodies to assay for proliferating OPCs and mature oligodendrocytes at E16, E18, P1, and P7. These experiments are in progress, and the results will be presented at the conference. These studies will allow us to determine whether the deletion of Sufu, specifically in cortical progenitors, alters their ability to generate OPCs that eventually differentiate into oligodendrocytes.

#### **FRI-1148**

##### **CHARACTERIZATION OF MYELIN P2 AND SLITRK ECHINODERM GENES AND THEIR EXPRESSION DURING INTESTINAL REGENERATION**

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Organ and tissue regeneration is a complex cellular process in which, after an injury, an organism can form new tissues that are very similar in structure and function to those before the lesion. Unfortunately, many of the molecular events that occur during organ regeneration are still unknown. To address this, our laboratory uses the sea cucumber, *Holothuria glaberrima*, as a model organism due to its ability to regenerate its intestine. Using a database generated by next generation sequencing (NGS), we identified two genes that might be associated with regeneration: *Slitrk* and the gene that encodes Myelin P2 protein. We then analyzed these transcripts using various bioinformatic tools. The expression of these genes in the organism was demonstrated using sqPCR and a gene expression profile of various tissues. Also, an expression profile was established at different stages of intestinal regeneration. To

view the spatial localization of Myelin P2 protein, we developed an antibody and localized its expression to the coelomic epithelium. Though further experiments are necessary, our findings show that, in the sea cucumber, these genes are expressed during specific stages of the intestinal regenerative process. We believe that understanding the role of these genes may aid in the elucidation of possible patterns of organ regeneration of *H. glaberrima*.

#### **FRI-1164**

##### **THE STUDY OF PERSONALITY TRAITS IN RELATION TO THE ACUTE SUBJECTIVE EFFECTS OF AMPHETAMINE IN HEALTHY PARTICIPANTS**

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Individual differences in relation to d-amphetamine (AMPH) effects on measures of personality traits have been reported. Although the causes of such differences between subjects is not clear, behavioral tests show an association between the neurochemical mechanism of direct drug effects and the actual neurobiological basis of personality traits. These findings suggest that individual differences in responses to stimulant drugs may be directly influenced by individual differences in personality among additional factors. Our goal is to further investigate the specific personality correlates of d-amphetamine effects related to subjective feelings using non-overlapping measures of the personality traits related to reward sensitivity and impulsivity in healthy participants. We hypothesize that individuals with high reward sensitivity will have a greater positive activation response to moderate dose d-amphetamine, showing greater feelings of euphoria, elevated mood, and stimulation as opposed to individuals with low reward sensitivity who will have a lower positive activation response to low and high doses of d-amphetamine. We also hypothesize that individuals with low impulsivity will have lower positive subjective and mood effects from d-amphetamine as opposed to individuals with high impulsivity. Our lab will test these hypotheses using the subjective states assessments, Addiction Research Center Inventory, a visual analogue drug effects questionnaire, and an experimental version of the profile of mood states. To evaluate brain correlates of these traits and states, we will look at brain activation in the limbic system and prefrontal cortex to investigate the neural basis of personality and AMPH-related subjective responses.

#### **SAT-1145**

##### **SELECTIVE DEFICITS IN SOCIAL BEHAVIOR IN ADULT MICE AFTER TRAUMATIC BRAIN INJURY AT ADOLESCENCE**

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Traumatic brain injury (TBI) is a leading cause of death and disability in children worldwide. In spite of advances in research, we have yet to understand the full spectrum of behavioral deficits that persist into adulthood after injury to the developing brain. We have previously shown that TBI at post-natal day 21 (p21), results in marked long-term deficits in social interactions. Here we investigated the behavioral consequences of TBI at p35 (adolescent) in

male C57Bl/6J mice. Mice were subjected to either a focal TBI (n = 9) or sham surgical controls (n = 9). Mice were behaviorally tested starting at p70 (adulthood) by an investigator blinded to treatment (Sham or TBI). Assessments included performance in an open field and evaluation of behaviors associated with scent marking, resident intruder, buried food, and three-chamber tasks. We found a selective deficit in preference for social novelty using the three-chamber test, indicating impairment in social recognition and memory; however, mice expressed normal sociability, social investigation, and socio-sexual communication with normal olfactory function despite the injury. Histological analyses revealed a significant loss of white matter volume in brain-injured mice at adulthood, a finding that may in part contribute to social deficits. In conclusion, we demonstrate that TBI to the adolescent brain results in selective social deficits, a finding that contrasts the more profound social deficits seen in mice that are subjected to TBI at a younger age. Thus, the age at time of injury should be considered when developing therapies for brain-injured children.

#### **SAT-1156**

#### **VOCALIZATION DEVELOPMENT AND EXECUTIVE FUNCTIONING DEFICITS IN A MOUSE MODEL OF KLINEFELTER SYNDROME**

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Klinefelter syndrome (KS) is a genetic disorder caused by the karyotype XXY. Men with KS experience low testosterone levels, gynecomastia, infertility, abnormal speech development, social isolation, and problems with executive functioning. The cognitive defects found in men with KS have been studied using the XY\* mouse model. The XY\* model has a variant of the Y chromosome that produces mice with unusual complements of sex chromosomes including XXY\*, which is genetically similar to XXY. Previous work using the XY\* mouse model shows that XXY\* mice had similar social and cognitive phenotypes as men with KS, such as increased social isolation and different partner preferences. Using the XY\* model, we investigated delayed speech and language development and deficits in executive functioning. As an approach to understanding these phenomena, two behavioral phenotypes were measured: mouse pup vocalization development and adult reversal learning ability. Here the hypothesis was that XXY\* mice will have abnormalities in vocalizations during infancy and have impaired reversal learning ability as adults compared to XY\* mice. Ultrasonic pup-retrieval-call recordings were used to measure vocalization development, and an operant behavioral task for impaired inhibition was used for assessing reversal learning ability. If the XXY\* mice demonstrate abnormal or less complex vocalizations and impaired reversal learning ability compared to XY\* mice, it can be concluded that the XXY\* mice produce additional similar cognitive phenotypes as found in KS men. Further investigation will develop a better understanding of the molecular mechanisms of the cognitive phenotype in men affected by KS.



**SAT-1146****HIPPOCAMPAL KCND2 PROTEIN AND GENE EXPRESSION IN MCGILL-THY1-APP TRANSGENIC MICE**

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Alzheimer's disease (AD) is a devastating neurological disease culminating in permanent mental impairment. Neurofibrillary tangles of the amyloid-beta ( $A\beta$ ) protein lead to neurodegeneration and memory deficits in the CA1 and dentate gyrus of the hippocampus. In hippocampal neurons,  $A\beta$  has been associated with increases in expression of certain Kv channels, in particular, Kv3.4, Kv4.2, Kv4.4, and KCNE3, which may lead to apoptosis. When voltage-gated  $K^+$  (Kv) channels open, repolarization of neurons occurs via  $K^+$  efflux to bring the cell back to resting potential. Increased expression of Kv channels might allow for greater efflux of  $K^+$ , rendering the neuron hyperexcitable. In this study, we characterized the new animal model, Transgenic McGill-Thy1-APP mice, which display AD pathology due to the addition of the human amyloid precursor protein (APP) gene with the Swedish and Indiana mutations. This gene causes  $A\beta$  deposits and cognitive deficits in as little as four months after birth in transgenic mice. Protein and RNA expression of KCND2, a type of Kv channel, was examined in hippocampal tissue to provide evidence to the potential link between amount of KCND2 and AD pathology. Results show a peculiar correlation between RNA and protein expression in the transgenic model; namely, a drop in RNA expression at five months of age followed by a drop in protein expression at seven months of age in the transgenic model, adding evidence to support the involvement of Kv channels in AD and their potential as targets for therapeutic purposes.

**SAT-1162****CORTICO-HIPPOCAMPAL LOSS OF GLUN2B CONTAINING NMDAR AND ATTENTIONAL SET-SHIFTING IN THE MOUSE**

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Numerous disorders including schizophrenia, Parkinson's, and ADHD are accompanied by deficits in executive control, including impaired behavioral flexibility. Behavioral flexibility is thought to be mediated by circuits connecting the basal ganglia and the prefrontal cortex. In order to provide potential therapeutic targets for executive control deficits, we must first understand how these circuits behave optimally to mediate learning and behavioral flexibility. One potential molecular mechanism mediating these circuits is N-methyl-D-aspartate receptor (NMDAR). NMDAR are heterotetramers with specific subunits conferring physiological and molecular properties to individual receptors. The GluN2B subunit is expressed robustly in the prefrontal cortex and may be particularly involved in flexible behavior. We investigated whether genetic cortico-hippocampal loss of GluN2B would impair the formation of an attentional set and the ability to shift attention from one set to another. GluN2B knockout mice and controls were tested on an attentional set-shifting task using tactile and olfactory dimensions. Preliminary results suggest loss of GluN2B does not impair simple pair-wise

discrimination learning in either modality but may impair the ability to form an attentional set over the course of the task. The non-specific nature of the genetic knockout means that loss of GluN2B in specific cortical areas (and hippocampus) may be driving the impaired set-formation in this model. Planned experiments examining GluN2B in specific cortical areas will elucidate the nature of these deficits. The current results further support the role of GluN2B in learning and memory process and suggest that it may play a novel role in top-down control of attention.

#### **SAT-1144**

##### **NEURON-SPECIFIC PATHOLOGY IN A DOXYCYCLINE-INDUCIBLE MODEL OF FRAGILE X-ASSOCIATED TREMOR/ATAXIA SYNDROME (FXTAS)**

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Fragile X-associated tremor/ataxia syndrome (FXTAS) is a neurodegenerative disorder characterized by poor motor function including tremor/ataxia, increased anxiety, and cognitive impairments. Individuals with FXTAS possess a CGG trinucleotide repeat expansion between 55 and 200 repeats on the fragile X mental retardation 1 (*FMR1*) gene. This expansion, referred to as a premutation, results in an mRNA toxic gain of function that can damage the brain and affect an individual's motor function and cognitive ability. Both neurons and astrocytes are involved in FXTAS pathology. However, the relative contribution of neurons versus astrocytes to disease is unknown. In order to examine this issue, we have developed a new dox-inducible mouse model in which expression of a CGG98 trinucleotide repeat expansion is controlled by the neuron-specific promoter CaMKII $\alpha$ . When mice are given doxycycline in their drinking water, the CGG98 repeat is expressed in neurons throughout the forebrain, including the cortex, hippocampus, striatum, and amygdala. In addition, these mice develop intranuclear protein inclusions, the hallmark pathology seen in FXTAS. The neuron specific development and distribution of these intranuclear inclusions in the brain will be described. The mice are also undergoing behavioral testing to determine if their motor function, memory, anxiety, or locomotor activity are altered. The results of these studies will establish whether expression of a CGG98 repeat expansion in neurons is necessary and sufficient to reproduce the symptoms of FXTAS and will, therefore, contribute to our knowledge of the importance of pathology in neurons versus astrocytes to the full development of disease.

#### **SAT-1127**

##### **HUMAN NEURAL STEM CELL GRAFTS IN MONKEY SPINAL CORD INJURIES: TIMECOURSE OF MATURATION**

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Neural stem cells (NSCs) hold potential as therapy for spinal cord injuries (SCI). We recently reported that grafts of rat or human pluripotent NSCs in sites of severe SCI formed new neural relays and mediated functional recovery. In preliminary studies of a monkey model of SCI, we have replicated the anatomical component of our rodent study (graft survival, integration with

the host cord, and profuse, long-distance axon growth). We are now assessing the timecourse of graft maturation and differentiation. We hypothesize that human NSCs grafted onto an injured non-human primate spinal cord develop temporally and morphologically as they would during normal human development. We grafted GFP-expressing human NSCs (566RSC-UBQT, NeuralStem, Inc.) into 5 adult Rhesus macaques 2 weeks after C7 lateral hemisection lesions. Subjects were sacrificed 2 to 9 months after grafting, and tissue was immunolabeled for markers of mature and immature neurons and axons. Cell number, density, and size, which can reflect neuronal and circuit maturation, are currently being quantified in confocal image stacks using ImageJ software. Graft-derived axon number and caliber are being quantified using StereoInvestigator software. We predict that cell number, cell density, and axon count will decrease, and that cell size and axon caliber will increase as survival time after grafting increases and graft-derived circuitry matures. These analyses will help determine timepoints for behavioral analysis and optimal conditions for NSC grafting in future studies in non-human primates. Those future studies, in turn, will aid the translation of NSC therapy to human clinical trials.

#### **SAT-1149**

#### **ACCUMULATION OF PARIS IN A DOPAMINERGIC CELL LINE MODEL LEADS TO PROGRESSIVE IMPAIRMENT OF MITOCHONDRIAL FUNCTION**

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Parkinson's disease (PD) is a common neurodegenerative disease characterized by progressive motor impairment caused by the loss of dopaminergic (DA) neurons in the substantia nigra pars compacta (SNpc). Significant evidence points to mitochondrial impairment as a key pathogenic event in PD. Parkin interacting substrate (PARIS) is a transcriptional repressor of PGC-1 $\alpha$  that is accumulated in post-mortem PD brain samples and is a key mediator of dopaminergic cell death in models of parkin-linked PD. The impact of PARIS on mitochondrial function has not been described. Here we generated a PC-12 dopaminergic cell line model harboring a tet-promoter-driven PARIS transgene in order to investigate the impact of PARIS accumulation on mitochondrial function using microplate-based respirometry. Induction of the transgene by doxycycline removal induces robust PARIS overexpression and suppression of PGC-1 $\alpha$  levels. PC-12 cells overexpressing PARIS exhibit a 37.27 (+/- 6)% reduction in maximal (CCCP-induced) mitochondrial respiration and a 64.8 (+/- 3.2)% reduction in respiratory reserve capacity with no significant differences in basal respiration or proton leaks. Continued induction of PARIS leads to progressive basal respiration deficits and a reduction in mitochondrial protein markers. Our findings suggest that PARIS accumulation leads to progressive reductions in mitochondrial health which may underlie dopaminergic cell death in PD.

**FRI-905****INVESTIGATION OF THE ROLE OF PFN-1 IN NEURAL DEVELOPMENT**

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The human nervous system consists of 85 billion neurons. Correct wiring of the nervous system is crucial for behavior, thinking, and perception. During neural development, neurons migrate to appropriate areas, and neurites are guided to target regions. Once a neurite reaches its target region, it must identify its correct partner among many target neurites, a process called synaptic partner recognition (SPR). SPR is a fundamental process, yet it is poorly understood. Understanding the molecules that play roles in SPR will give us insight into neural circuit formation. To investigate SPR, we study synapses between sensory neurons and interneurons in the genetic model organism *C. elegans* to visualize these synapses *in vivo*. We introduced a fluorescent marker called neuroligin-1 GFP reconstitution across synaptic partners (NLG-1 GRASP), into wild-type and mutant animals. Studies in *Drosophila* indicate that an actin-binding protein, profilin-1 (PFN-1), is required for axon outgrowth and guidance. We hypothesize that the *C. elegans* homolog pfn-1 also plays a role in SPR. We predict that pfn-1 mutants will display reduced synapse formation relative to wild-type animals. To investigate this, we assayed NLG-1 GRASP fluorescence intensity as a measure of connectivity between the PHB sensory neurons and AVA interneurons. Our preliminary analysis suggests that there are no severe defects in SPR in pfn-1 mutants. However, our preliminary data suggests that PHB axon may slightly overextend in pfn-1 mutants suggesting that PFN-1 may play an inhibitory role in axon extension in *C. elegans*.

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**FRI-1145****DELIVERY OF A CONSTITUTIVELY ACTIVE MUTANT OF THE NETRIN-1 RECEPTOR, DELETED IN COLORECTAL CANCER (DCC) TO PROMOTE CORTICOSPINAL TRACT REGENERATION FOLLOWING SPINAL CORD INJURY**

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Millions of Americans live with spinal cord injury (SCI), resulting in permanent paralysis and sensory loss. One of the most important tracts affected by SCI is the corticospinal tract (CST), responsible for fine motor control. To date, attempts to enhance CST regeneration have met with very limited success. We have recently reported successful implementation of neural stem cell (NSC) transplantation for SCI. These grafts proliferate into mature neurons, sending long-distance axonal projections throughout the CNS. Importantly, NSC grafts form functional relays between supraspinal neurons and sites below the lesion. Moderate CST regeneration into this NSC graft has been demonstrated; however, no improvement in motor tasks was observed. Our ultimate goal is to combine NSC grafts with gene therapy to enhance the intrinsic regenerative capacity of CST neurons. DCC is a Netrin-1 receptor that enhances axon outgrowth upon homodimerization. We hypothesize that overexpressing a constitutively active form of DCC in CST neurons will enhance regeneration into NSC grafts following SCI. To test this, we have

generated novel AAV viral constructs and are currently validating their effect on neurite outgrowth *in vitro*. We will assess the effects of DCC overexpression on CST regeneration *in vivo* by transducing cortical motor neurons with AAV one week after SCI and NSC transplantation; 6 weeks later, growth of GFP+ axons into the graft will be assessed. Positive results will provide a novel and promising new strategy for CST regeneration and greater understanding of the intrinsic molecular mechanisms that can enhance regeneration of adult, injured CNS axons.

#### **FRI-903**

##### **NOVEL BEHAVIORAL PARADIGMS TO ASSAY NEURODEVELOPMENTAL DISORDERS IN THE *XENOPUS LAEVIS* TADPOLE**

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Experimental behavioral assays and animal models are essential to elucidate the mechanisms that underlie behavioral phenotypes associated with disorders such as autism. The *Xenopus laevis* tadpole has long been used as a model to study mechanisms that underlie developmental abnormalities. Many behaviors of the *Xenopus* tadpole have also been described, and its neural circuit development has been extensively studied and can be easily observed. As such, we aim to use the *X. laevis* tadpole as a model for neurodevelopmental disorders. In this study, we develop and validate a comprehensive set of methods and experimental approaches to quantify the behavior of *X. laevis* tadpoles and to test their neural development. The behavioral assays include visual avoidance behavior (a type of behavior in which the animal avoids objects engaging at a collision trajectory), acoustic startle reflex habituation (a form of non-associative memory that relies on the hindbrain circuitry), and pre-pulse inhibition (a type of hindbrain-mediated short-term sensory processing in which a weaker pre-stimulus inhibits the effects of a subsequent strong stimulus). This study provides the scientific community with a set of tools for experimentation on *X. laevis* tadpoles to uncover neural mechanisms for neurodevelopmental disorders.

#### **FRI-1153**

##### **STIMULATION AND VIRAL TRACING OF GLUCAGON NEURONS IN THE NUCLEUS OF THE SOLITARY TRACT**

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The pre-proglucagon (PPG)-derived glucagon-like-peptides (GLP-1/2) act centrally in hypothalamic nuclei to suppress food intake. It is hypothesized that this GLP-1/2 mediated satiety signaling originates from a population of PPG neurons in the medullary nucleus of the solitary tract (NTS). To investigate the behavioral effect and hodology of these neurons, the Knight lab created transgenic mice with Cre recombinase knocked into the start codon of PPG (PPG-Cre). Cre-recombinase expression closely resembled PPG expression in the NTS. Stereotaxic injection of viral vectors into the NTS of PPG-Cre mice transduced excitatory and inhibitory cre recombinase dependent DREADDs (designer receptors exclusively activated by designer drugs). To delineate the targets of PPG neuronal projections from the NTS, we

transduced fluorescently labeled Cre-dependent synaptophysin in the terminals of PPG neurons. Food intake was measured following administration of clozapine-N-oxide, a DREADD selective ligand, in both light and dark phase feeding as well as fasting-induced refeeding. The brains were imaged with confocal microscopy to identify the fluorescent synaptophysin-labeled targets of projections from PPG nerves and to confirm the fluorescence of DREADDs in PPG nerve cells. We anticipate the projections of PPG neurons to terminate in the arcuate, dorsomedial, and paraventricular nucleus of the hypothalamus and to suppress food intake when stimulated while increasing food intake when inhibited. These data implicate brainstem PPG neurons in GLP-regulated brain satiety signaling.

#### **FRI-1156**

##### **THE EFFECTS OF OBESITY ON MUSCLE SENSORY NEURONS**

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Obesity, or excessive accumulation of fat in the body, is a health problem that affects more than a third of United States citizens, according to the United States Centers for Disease Control and Prevention. Obesity and chronic musculoskeletal pain conditions often occur together, but the direct effect of obesity on the pain-sensing Group III/IV nociceptors is poorly understood. Obesity leads to a chronic inflammatory state and the release of factors, such as the increase of reactive oxygen species (ROS) induced by bradykinin (BK) that can alter the activity of Group III/IV nociceptors. We hypothesized that obesity can sensitize muscle nociceptors and make them more likely to respond to natural stimuli, like lactic acid. We will test this hypothesis with mice fed a high fat diet to induce obesity. We will use an isolated extensor digitorum longus (EDL) muscle-nerve preparation. With a suction electrode, we will record the reaction of the neurons from the obese mice compared with control mice. We will then expose the muscle to lactic acid at different pH levels and compare the response of the nociceptors. We expect a greater response to lactic acid in the obese animals, indicating that the neurons have been sensitized by obesity. A better understanding of the effects of obesity on muscle sensory afferents may help in the treatment of chronic musculoskeletal pain conditions in obesity. (This research was supported by NSF-REU Grant# DBI 1004350.)

#### **FRI-1155**

##### **STUDY OF SELECTIVE DEGENERATION OF DOPAMINE (DA) NEURONS IN GENETIC MODELS OF PARKINSON'S DISEASE USING *DROSOPHILA***

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Parkinson's disease (PD) is a neurodegenerative disorder characterized by the selective loss of DA neurons in the substantia nigra, a region of the mesencephalon that plays an important role in motor control and goal-directed behaviors. The molecular mechanisms underlying selective DA neuron degeneration in PD are still unknown. It is proposed that gradual accumulation of oxidants from increased levels of ex-vesicular DA molecules exacerbates the cytotoxicity induced by *parkin* and *pink1* mutations. We implement a loss and gain of function of VMAT in

order to genetically manipulate levels of dopamine in the PD brain and determine the physiological effects of ex-vesicular dopamine accumulation in *Drosophila*. The *vmat* gene codes for the vesicular monoamine transporter (VMAT) which functions as a uniporter to pack dopamine into synaptic vesicles. Our and another lab collaborated to generate a MIMIC-VMAT-e-GFP line (VMAT<sup>MIMIC-GFP</sup>) and a MIMIC-GAL4-VMAT fly to track the viability of dopamine neurons; and to selectively knock down *parkin* and *pink1* expression in the DA neurons of *vmat* mutant flies, respectively. It was found that crossing these flies with a hypomorphic *vmat* mutant allele disrupts the egg-laying phenotype mediated by VMAT function. We then used tyrosine hydroxylase antibody to quantify changes in the number of DA neurons in the adult brains of *vmat* mutants. It was found that adult brains were born with half the number of DA neurons as compared to the wild type. We are currently examining the additive effect of *parkin* and *pink1* mutations in the *vmat* mutant and wild-type background.

#### **FRI-1159**

#### **RUN OR REM: A COMPARATIVE ANALYSIS OF MEMORY CONSOLIDATION BETWEEN SLEEP AND EXERCISE CONDITIONS**

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The formation of memories depends on efficient encoding, consolidation, and retrieval. Memory consolidation has been shown to benefit from intervals of sleep and also acute exercise. Deeper levels of sleep actively contribute to the consolidation of declarative knowledge (e.g., learning new words), and bouts of acute exercise show similar increases to the consolidation of new memories. However, to date, these two activities have not been compared to test which is more beneficial for memory formation. To compare the effects of sleep and exercise on memory, 15 men and women, with ages ranging from 18 to 30 years, will be used. Participants will be given a memory task that involves learning 40 non-related word pairs. Within this task, subjects will matriculate through phases of encoding, immediate recall and delayed recall. One of the 3 conditions of sleep, exercise, or restful wake will occur between the immediate recall and delayed recall phases to test memory consolidation, which will be gauged by comparing the number of word pairs retained at immediate and delayed recall. We anticipate exercise will yield the highest rate of word pairs because of the increased cognitive and physical arousal. Given that both sleep efficiency and physical activity tend to decrease with age, comparing these 2 activities could lead to a deeper understanding of the processes influencing memory. Results from this study could also lead to a better understanding of memory decline and its progress across the lifespan.

**SAT-1163****THE ROLE OF THE CENTRAL COMPLEX IN VISUO-MOTOR CONTROL DURING OBSTACLE AVOIDANCE IN *DROSOPHILA MELANOGASTER***

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The central complex has been shown to represent visual information and be critical *in visuo-motor* integration. For functional analysis of the neural basis of the visuo-motor integration programs, *Drosophila melanogaster* offers sophisticated methods for genetic manipulation of a small subset of neurons. A behavioral assay has been developed to characterize the neural basis of visuo-motor control systems in *Drosophila melanogaster*. The paths of individual wild-type and mutant flies were recorded with a high-speed camera and tracked as they performed normal vertical walking, following a negative geotaxis (tap down) protocol. As flies performed their vertical walking, they encountered an obstacle with high visual contrast, which they are required to maneuver. Using the GAL4/UAS system, mutant lines were created by inserting TRPa1 channels into the ellipsoid body. TRPa1 is a heat and voltage gated channel activated at approximately 25 °C. In experiments, both mutant flies and wild-type flies walked at the same speed, even at temperatures necessary to activate the TRPa1 channels. However, channel activation in the ellipsoid body resulted in flies responding differentially to the visual obstacle. Flies initiated their turn much sooner (further away from the barrier) when compared to wild-type flies. The second mutant strains were generated by first crossing UAS-Kir2.1 flies with GAL80<sup>ts</sup>, which were crossed to ellipsoid body GAL4 driver lines. Using the GAL80<sup>ts</sup> in conjunction with UAS-Kir2.1 permits temperature controlled silencing of the GAL4 neurons. These experiments will provide insight into how visual information is transformed into motor programs.

**SAT-1150****SCHOOLING AS A NOVEL BEHAVIORAL ASSAY TO PROBE NEURODEVELOPMENTAL CHANGES FROM FMRP KNOCKDOWN AND VPA EXPOSURE IN THE *XENOPUS LAEVIS* MODEL FOR AUTISM**

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The development of novel animal models to study neurodevelopmental disorders such as autism is critical for understanding the basic biology underlying these disorders. The growing nervous system of *Xenopus laevis* tadpoles is an established animal model for neurodevelopment. Recent work in our laboratory, and in that of our collaborators, has explored two novel neurodevelopmental interventions resulting in abnormal formation of neural circuits in *Xenopus* tadpoles. Both exposure to valproate (VPA), a known teratogen associated with elevated incidence of autism following prenatal exposure, and knockdown of FMRP, a key protein in Fragile X Syndrome, a leading monogenetic cause of autism in humans, result in abnormally formed neural circuits in *Xenopus* tadpoles. One common feature of autism is the presence of sensory integration problems as well as deficits in social interaction. Here we show a novel test for assaying sensory integration and social interaction in *Xenopus* tadpoles,



by analyzing a multisensory aggregation behavior known as schooling, partially mediated by the optic tectum. We will assess the effects of VPA exposure and FMRP misexpression on this behavior. We hypothesize that VPA and FMRP misexpression will lead to abnormal schooling behavior in tadpoles. Our behavioral protocol analyzes inter-tadpole distances and co-orientation of nearby tadpoles to assess schooling. By studying an analogue of human social behavior in the *Xenopus laevis* model, we hope to provide a novel means of comparing human neuronal changes to an animal model and support further experiments using *Xenopus laevis* tadpoles.

#### **FRI-1160**

##### **DAYTIME COGNITIVE PERFORMANCE AND NIGHTTIME SLEEP PATTERNS IN RESPONSE TO SUNLIGHT OR FLUORESCENT LIGHT**

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Light is the primary synchronizer of the human circadian rhythm and also has acute alerting effects. This research will involve studying and comparing the participants in the NASA Ames Green building, which uses sunlight as its primary light source and in a traditional office building, which uses overhead florescent lighting and varying exposure to natural light. The purpose of this study is to determine whether the use of natural lighting as a primary light source improves daytime cognitive function and promotes nighttime sleep. Participants from the Green building and the Human Systems Integration building will be matched by gender, age, and sleep timing preferences and then studied throughout the same week. The subjects will wear actiwatches, complete PVT and DSST assessments three times per day, and keep daily sleep/work diaries. We hope that this study will provide data to support the idea that natural lighting and "green" architectural design are optimum to enhance healthy nighttime sleep patterns and daytime cognitive performance.

#### **SAT-1155**

##### **HUMAN RETINAL PROGENITOR CELLS AS A THERAPY FOR DEGENERATING PHOTORECEPTORS**

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Retinal photoreceptor cell degeneration is a common cause of blindness in diseases, such as retinitis pigmentosa, that currently have no cure. Our research involves analyzing the neuroprotective effects of a single intravitreal injection of human retinal progenitor cells (hRPC) into the RCS rat, an animal model of photoreceptor degeneration that has been well characterized. The photoreceptor cell death that occurs in this animal is due to a defect in the retinal pigment epithelium (RPE) that prevents the process of photoreceptor outer segment phagocytosis, eventually leading to photoreceptor cell death. This degeneration occurs on a highly predictable time scale, hence it is an excellent animal model to examine the protective effects of therapies such as hRPCs. To date, we have observed that the hRPCs remain viable in the vitreous for at least 2 months after injection and slows the loss of photoreceptor cells in the

outer nuclear layer (ONL). Immunohistochemical staining is used to monitor and detect the certain proteins that the progenitors are expressing. While the hRPCs do begin to express some adult proteins over time, this does not appear to interfere with the rescue effects nor have any adverse effects in the eye. We believe that the source of this rescue effect is from growth factors secreted by the hRPC. We further hypothesize that hRPC can serve as a continuous source of these growth factors that appear to preserve the photoreceptor cells in the ONL, thus preserving vision.

#### **SAT-905**

##### **EFFICACY OF THE P7C3-SERIES OF NEUROPROTECTIVE COMPOUNDS IN CELL CULTURE MODELS OF PARKINSON'S DISEASE**

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Parkinson's disease (PD) is one of the most common neurodegenerative disorders, with a prevalence of nearly 1% by age 65. Sadly, there is currently no medication to block the neurodegenerative process. Our lab, however, has reported previously that the P7C3-series of neuroprotective molecules protects dopaminergic neurons, the same neurons that die in patients with PD, in mouse, *Caenorhabditis elegans*, and rat models of PD. For example, P7C3 and its active analogs block death of dopaminergic neurons in the substantia nigra in mice exposed to 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP). P7C3-compounds also protect dopaminergic neurons in *C. elegans* from 1-methyl-4-phenylpyridinium (MPP+) toxicity, as well as dopaminergic neurons in rats from 6-hydroxydopamine (6-OHDA)-mediated toxicity. To facilitate investigation of the mechanism of P7C3-compounds, we are exploring their protective efficacy in isolated neuronal cultures. Specifically, we are testing whether P7C3 molecules block MPP+ or 6-OHDA-mediated toxicity in primary mouse cortical neurons. We use the 3-(4, 5-dimethylthiazolyl-2)-2, 5-diphenyltetrazolium bromide (MTT) assay, which quantifies the number of viable cells by spectrophotometrically measuring the amount of reduced MTT, an indicator of cell viability. We observe prominent primary neuronal cell death following exposure to MPP+ and 6-OHDA, and are now testing whether P7C3 molecules can block this cell death. Our hope is that this isolated culture system will enable us to rigorously investigate the mechanism of action of P7C3-molecules, and facilitate development of new approaches to treating patients with PD.

#### **SAT-1158**

##### **SUSCEPTIBILITY TO DOPAL TOXICITY IN A MOUSE MODEL OF ALPHA-SYNUCLEIN OVEREXPRESSION**

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Parkinson's disease (PD) is a neurodegenerative disorder characterized by the death of dopamine (DA) cells in the substantia nigra (SN) and aggregates of alpha-synuclein (aSyn) throughout the brain. Previous research suggests that mitochondrial dysfunction plays an important role in PD pathogenesis. Studies have shown that aSyn overexpression is toxic to DA

neurons making them more vulnerable to oxidative stress. In addition, 3,4-dihydroxyphenylacetaldehyde (DOPAL), a metabolite of DA, can induce aSyn aggregation, and damaged mitochondria are more susceptible to DOPAL toxicity. Under normal conditions, DOPAL is detoxified by aldehyde dehydrogenase (ALDH). The 2 main isoforms of ALDH, cytosolic ALDH1a1 and mitochondrial ALDH2, are expressed in a variety of brain regions, including the SN. We will use a transgenic PD mouse model overexpressing human, full-length wild-type aSyn under the Thy-1 promoter (Thy1-aSyn mice) to study the relationship between aSyn, ALDH, and DOPAL. We hypothesize that the aSyn overexpression and mitochondrial dysfunction observed in the Thy1-aSyn mice leads to an increased susceptibility of DA neurons to DOPAL toxicity. This sensitivity will trigger differential changes in ALDH1a1 and ALDH2 expression and DOPAL levels. To test our hypothesis, we will isolate tissue from the SN, striatum, and cortex of 6-month-old Thy1-aSyn mice and their wild-type littermates. These samples will then be used for an HPLC analysis of DOPAL levels, a western blotting analysis of ALDH protein expression, and an ELISA for ALDH2 activity. The results from this study may aid in the development of new therapeutic targets for treating PD.

#### **FRI-1151**

#### **POLO-LIKE KINASE INHIBITOR AS A THERAPEUTIC AGENT BY INDUCING MITOTIC ARREST IN GLIOBLASTOMA**

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The median survival for adult glioblastoma patients undergoing standard treatment is 2 to 3 years. Current therapeutic measures for glioblastoma (GBM) are broadly ineffective, therefore development of novel treatment options is of paramount importance. Polo-like kinase (PLK-4) is a centriole protein essential for regulating cell division. It has been established that PLK-4 is uniquely overexpressed in 80% of tumors which may contribute to genetic instability. Overexpression is not seen with normal non-dividing cells, making this protein an ideal and selective drug target. In this study, a PLK-4 inhibitor, developed previously by CIRM collaboration, was tested for its effect on GBM cells in culture. The mechanism of action of the PLK-4 inhibitor is to occlude mitotic division by allowing DNA replication to continue in the absence of cytokinesis, which inhibits proliferation and leads to cell death. We hypothesize that this PLK-4 inhibitor can be used as a therapeutic agent to treat glioblastoma by exploiting mitotic arrest to promote cell death. To address this hypothesis we tested the drug effect on different primary tumor cell lines in culture developed from patients with glioblastoma. We investigated the drug effect on cellular viability over time and its effect on DNA content. We fixed cells and stained them with Hoechst dye and used flow cytometry to identify cell viability and cell DNA content in 2n, 4n, and 8n populations. The evidence we obtained suggests that the specific PLK-4 inhibitor we are working with is a promising therapeutic agent that can effectively inhibit proliferation of glioblastoma.

**SAT-1160****REGIONAL RESPONSES TO TACTILE STIMULI BY A LEECH, *HELOBDELLA AUSTINENSIS***

Angela Hinton, William Kristan.

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In the investigation of how animals make choices based on internal and environmental factors, leeches have long been used as a model due to their simple, accessible nervous systems and their relatively small number of possible behavioral responses. Most leeches can be categorized according to their feeding habits as either carnivorous or sanguivorous, but some species can behave as both depending on their available food source. It has been shown that sanguivorous leeches prioritize feeding and do not readily respond to external stimuli during eating, while carnivorous leeches will abandon feeding in favor of motor response when physically stimulated. We hypothesized that the leech species *Helobdella austinensis*, which can behave both as a carnivore and as a sanguivore, would display diminished motor response to mechanical stimulation similar to that observed in a pure sanguivore. We mapped the locations of ganglia in *H. austinensis* to determine the parts of the leech's body to which each individual ganglion was directly linked. We then mechanically stimulated specimens at specific points using Von Frey hairs during active feeding in order to compare the frequencies of selected behaviors with those chosen by the leech during inactivity. We believe the results of this study will open a deeper understanding of multi-stimuli neuronal response, which ultimately contributes to our continued exploration of the nervous system.

**SAT-1154****DEEP BRAIN STIMULATION RESTORES COGNITIVE FUNCTION IN EPILEPTIC RATS**

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Epilepsy is a chronic neurological condition that affects approximately 1% of the population worldwide. The cost of diagnosing and treating intractable epilepsy in the U.S. alone is as high as \$4 billion annually. Patients with epilepsy and particularly temporal lobe epilepsy often report chronic learning and memory deficits. In a rodent model, pilocarpine-induced status epilepticus (SE) drives chronic epilepsy. Epileptic rats, similar to humans with temporal lobe epilepsy, have chronic abnormalities in hippocampal physiology that correlate with impaired cognition. We hypothesize that deep brain stimulation of the medial septum in the theta frequency range will drive hippocampal theta and improve cognitive function in pilocarpine-induced epileptic rats. Similar to previous studies, we found that epileptic rats had diminished theta oscillations, impaired spatial memory, and lower seizure thresholds. Stimulation of the medial septum (7.7 Hz, 80  $\mu$ A) significantly increased hippocampal theta oscillations, improved spatial learning, and increased seizure threshold, making it less likely that animals would seize. Deep brain stimulation, therefore, represents an exciting and novel way to improve the quality of life for millions of epileptic individuals suffering from seizures and chronic cognitive deficits.

**FRI-904****MODELING THE EFFECTS OF OXIDATIVE STRESS ON TDP-43 CELLULAR LOCALIZATION IN HUMAN-INDUCED PLURIPOTENT STEM CELLS DERIVED MOTOR NEURONS FROM ALS AND FTD PATIENTS**

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Excessive production of free radicals, also known as oxidative stress (OS), has been shown to contribute to neurodegeneration of motor neurons (MNs) in diseases such as amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD). OS can cause cellular dysfunction; however, it has not been shown to correlate with the transactive response DNA-binding protein (TDP-43), a prominent pathological feature in ALS and FTD. Here we use MNs derived from human induced pluripotent stem cells (iPSCs) in ALS and FTD versus controlled patients to investigate the effect of OS on TDP-43 cellular localization through treatment with hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>). This study addresses the hypothesis that H<sub>2</sub>O<sub>2</sub>-generated OS triggers the mislocalization of TDP-43 from the nucleus to the cytoplasm, a well-established disease phenotype, in iPSC lines with ALS- and FTD-associated mutations well before the onset of MN death, and mutation bearing lines will be sensitive to the H<sub>2</sub>O<sub>2</sub> insult before controls. We used a well-established 20-day protocol to derive motor neurons, and the quantity of motor neurons was validated at days 9 and 20. The differentiating cells were treated with H<sub>2</sub>O<sub>2</sub> for 48 hours at specific developmental time points and then assessed for markers of MN development and maturation, TDP-43 localization, as well as a marker of OS. Preliminary results show we are producing MN precursors at critical developmental time points and that initial treatment of the MNs does not cause precocious death. Successful completion of this study will help elucidate the role OS plays in the neurodegenerative process in ALS and FTD.

**FRI-1154****ETHANOL AND METHAMPHETAMINE INHIBIT NEURITE OUTGROWTH BY ALTERING G PROTEIN-CYTOSKELETAL INTERACTIONS**

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Neuronal structure and behavioral changes associated with drug abuse are thought to depend largely on alterations to G-protein coupled receptor (GPCR) signaling pathways. However, the molecular mechanisms that underlie the pathophysiological states resulting from drug abuse are not clearly understood. Previous studies showed that Gβγ, an important component of the GPCR pathway, interacts with microtubules (MTs) and actin filaments. This interaction induces neurite outgrowth of pheochromocytoma (PC12) cells and is inhibited by ethanol and methamphetamine. In the current study, we tested the hypothesis that ethanol and methamphetamine-induced inhibition of neurite outgrowth involves an altered relationship among Gβγ, MTs, and actin filaments. To test our hypothesis, we used PC12 cells as a model for neuronal differentiation. PC12 cells were allowed to differentiate in the presence of nerve growth factor (NGF) for 2 days followed by acute (1 hour) and chronic (2 days) treatment with

100 mM ethanol (EtOH) or 40  $\mu$ M of methamphetamine and subjected to whole cell lysis, subcellular fractionation, or confocal microscopy. We found that acute ethanol treatment reduced actin expression by 42% in NGF-differentiated PC12 cells, but tubulin expression remained unaltered in the presence of ethanol. The interactions among G $\beta$  $\gamma$ , tubulin, and actin were analyzed using co-immunoprecipitation. Results indicate that ethanol and methamphetamine significantly reduced tubulin-G $\beta$  $\gamma$  interactions in NGF-differentiated PC12 cells, while actin-G $\beta$  $\gamma$  interactions were increased in the presence of ethanol, suggesting a possible role of the drugs in altering MT-actin interaction. These findings provide insight into the mechanisms that alter the neuronal cytoskeleton during drug addiction.

#### **SAT-916**

##### **THE EFFECT OF CONTEXTUAL FEAR CONDITIONING ON THE DEVELOPMENT OF NEURAL STEM CELLS IN THE ADULT MOUSE HIPPOCAMPUS**

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The hippocampus is a structure within the mammalian brain implicated in memory formation. It is also one of 2 sites, the other being the subventricular zone that generates adult-born neurons from neural stem cells (NSCs). Emotional stimuli and, in particular, fear-conditioning stimuli (FCS) have been shown to affect the development of hippocampal NSCs in rodents. The development of NSCs into mature neurons progresses through various developmental stages that can be differentially regulated. Younger neurons (approximately 2 week-old NSCs) are pruned through a process of selective survival, while older neurons (approximately 5 week-old NSCs) may become tuned to specific cues and subsequently show preferential activation in response to those cues. Given the differential regulation of NSCs, we sought to investigate whether contextual fear conditioning at different times, specifically in 2.5- and 5-week-old new neurons, affects their development. We hypothesize that an FCS will increase the survival of 2.5-week-old neurons, and that a FCS given to 5-week-old neurons will increase their tuning to the fear-associated context. In both cases, we will also test whether the response of new neurons is long lasting by assessing the responsiveness of the new neurons to the fear-conditioned context several months after initial exposure. Together, these experiments seek to improve our understanding of the roles that new neurons play in the encoding of fearful memories in the hippocampus.

#### **SAT-1159**

##### **EXTREME BINOCULAR PLASTICITY AND DYNAMIC STRATEGY IMPLEMENTATION SUPPORTS VISION-DEPENDENT PREY CAPTURE IN CUTTLEFISH**

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Understanding how neurons cooperate to mediate and support goal-directed behaviors is an integral aspect of neuroscience. Cephalopod cuttlefish, highly visual creatures with a complex nervous system, are reported to undergo shifts in eye position during transition from prey to

predator. We quantitatively evaluated if ocular convergence occurs in cuttlefish in response to prey detection, asked whether such convergence is necessary for depth perception during prey-capture, and explored how cuttlefish adapt to conditions of altered stereopsis. Cuttlefish prey-capture behavior was filmed for eye movements and tentacle dynamics, which were analyzed by dual-angle, high-speed imaging. A semi-automated eye tracking software was used to generate 3D positional coordinates to calculate angle change between eyes throughout prey-capture. Stereopsis necessity for successful prey-capture was evaluated by filming hunting episodes and noting differences in prey-capture dynamics in animals that were temporarily blinded in one eye via sutures, and after recovery of vision to the deprived eye. Control cuttlefish displayed consistent patterns of tentacle dynamics alongside 100% prey-capture success, while blinded cuttlefish exhibited only 60% success. Miscalculation of tentacle line-up prior to ballistic strike and failing prey-capture were observed from unilateral lid suture, but were rescued by restoring sight in the deprived eye by suture removal. Thus, binocular convergence and stereopsis are necessary for cuttlefish prey-capture. Interestingly, novel head movements emerged during prey capture after unilateral lid suture, presumably sustaining motion parallax. These animals implement highly dynamic, rapidly adapted strategies for successful prey-capture. We are starting to investigate the underlying neural circuits that support this extreme plasticity.

## **NUTRITIONAL SCIENCES**

### **FRI-330**

#### **DIET AND METABOLIC SYNDROME AMONG OBESE YOUNG ADULTS**

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One in five U.S. adults have metabolic syndrome (MetS), defined as having 3 of the following criteria: large waist circumference (WC), high blood pressure, high fasting serum triglycerides and glucose, and low high density lipoprotein cholesterol (HDL-C). Most individuals with MetS are obese (BMI  $\geq 30$ ); however, little is known about why some individuals with obesity develop MetS and not others. A heart-healthy diet (rich in vegetables, legumes, milk, nuts, and whole grains) has been shown to treat MetS, but there is limited data about preventing MetS in obese adults. We hypothesized that obese young adults with a healthier diet will not have MetS. A total of 44 obese young adults aged 18 to 30 years in Salt Lake County, Utah, were enrolled. Weight, height, WC, blood pressure, fasting serum triglycerides, glucose, and HDL-C were measured. Participants also completed the National Institute of Health's "Vegetable and Fruit Screener" and "Multi-Food Screener" to obtain information on food consumption. Responses were converted to numerical scores for analysis. T-test and chi-square analyses were performed. Of the 38 participants included in the analyses (6 were excluded due to missing data), 13 (9 males) had MetS. There was no difference in dietary intake between those with and without MetS. Comparison of MetS criteria between the 2 groups revealed significant difference only in triglycerides ( $233.15 \pm 133.93$  vs.  $114.40 \pm 42.80$ ,  $p = 0.01$ ). In conclusion, diet is not associated with MetS, and triglycerides may be a defining criterion for developing MetS in this small cohort of obese young adults.

**FRI-332****CHANGES IN BODY WEIGHT AND HEALTH MARKERS FROM A SHORT-TERM VACATION**

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Creeping obesity is an important target for prevention of future weight gain. By evaluating short vacations (1 to 3 weeks), we can better assess how the accumulation of small body changes can lead to substantial body changes over a long period. The purpose of this study was to examine the effects of a short-term vacation on health measures in adults. Seventy-three subjects (31 males, 42 females, age =  $34 \pm 14$  years) completed 3 study visits. Visit 1 and visit 2 occurred within one week of departing and returning from the vacation, and visit 3 occurred five weeks after visit 2. During each visit, we measured the subjects' height, weight, waist to hip ratio, blood pressure, body composition, and stress levels. Body composition was measured using a Tanita bioelectrical impedance analysis (BIA) instrument. The significant differences from visit 1 to visit 2 included overall body weight ( $76.34 \pm 16.19$  kg vs.  $76.66 \pm 16.35$  kg), and females' body weight ( $68.83 \pm 13.62$  kg vs.  $69.18 \pm 13.88$  kg). Significant differences from visit 1 to visit 3 included overall stress score ( $18 \pm 5$  vs.  $16 \pm 6$ ), overall systolic blood pressure ( $119 \pm 14$  vs.  $117 \pm 12$ ), males' stress score ( $18 \pm 5$  vs.  $143 \pm 6$ ), and males waist to hip ratio ( $0.87 \pm 0.07$  vs.  $0.86 \pm 0.08$ ). There were no significant differences from visit 2 to visit 3. Subjects whose body weight showed a significant difference from visit 1 to visit 2, decreased at visit 3. Blood pressure, stress levels, and males' waist to hip ratio decreased from visit 1 to visit 3.

**SAT-331****CARDIOVASCULAR PROTECTIVE EFFECTS OF BLUEBERRY ANTHOCYANINS**

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Diabetes greatly increases the risk of cardiovascular diseases such as atherosclerosis. The vascular inflammation, resulting in the adhesion of monocytes to vascular endothelial cells (EC), is a key event in the pathogenesis of atherosclerosis in diabetes. High glucose and/or fat induces production of reactive oxygen species, which is associated with a defective nuclear factor- $\kappa$ B (NF $\kappa$ B) signaling and impaired endothelial nitric oxide synthase (eNOS)/nitric oxide (NO) signaling in EC. These signaling events induce inflammation by up regulating chemokines and adhesion molecules. Epidemiological and clinical studies support the beneficial vascular effects of anthocyanins, one class of flavonoids widely available in berry fruits. However, the effects of blueberry anthocyanins on diabetic vasculature and the underlying mechanisms are unknown. Human studies showed that anthocyanins such as cyanidin-3-glucoside (C3G) and malvidin-3-glucoside (M3G) appear in the serum following the consumption of blueberries. Our current project is aimed at determining whether these blueberry anthocyanins, at physiological concentration, reduce high-fat-induced endothelial inflammation in human aortic endothelial cells (HAEC) and to determine the signaling mechanisms involved. We will treat HAEC with C3G and M3G (30 nM) for 1 h followed by exposing HAEC to palmitate (500  $\mu$ M) for 5 h. We will assess EC-monocyte interaction using fluorescent-labeled THP-1 monocytes. The inflammatory chemokines (IL-8 and MCP-1) and adhesion molecules (ICAM-1, VCAM-1, and E-Selectin) will be measured by PCR. Western blot will



be used to measure eNOS phosphorylation and NFκB nuclear translocation. Our study will reveal the novel vascular beneficial effects of blueberry anthocyanins.

**SAT-918**

**MALE UNIVERSITY STUDENTS USE MORE NATURAL HEALTH PRODUCTS THAN FEMALES IN THE USA**

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Humans have used natural health products (NHP) such as aloe, mint, and lavender as a form of medicine due to easy accessibility, low cost, and desire for naturalness. Regrettably, much research has not been conducted on university students' NHP use, especially those of Middle Eastern (ME) descent. In this study, NHP are defined as vitamins, minerals, herbs, botanicals, and medicinal plants. Our hypotheses are: female university students use more NHP for health than male university students, ME students will use more NHP than non-ME students, and gender and ethnicity will be predictor variables for NHP use. An approved, cross-sectional study was conducted at Wayne State University in the winter semester of 2014. A 23-question survey was completed by 577 students including ME students. For data analyses, generalized linear model (GLM) and multiple logistic regression (MLR) were performed using SPSS, Version 22. The GLM found a significant difference in frequency of NHP use between genders and age ( $p = 0.030$  and  $p = 0.002$  respectively), not ethnicity ( $p = 0.617$ ). In MLR, the only factor predicting NHP use was age ( $p < 0.05$ ). An online survey of diverse university students was conducted to assess NHP use for well-being. We find gender differences in NHP use (males > females) unlike prior research. We also find frequency of use, not length of use, to be notable. Future research should assess males' use of NHP (frequency/age).

**FRI-918**

**DEVELOPMENT OF AN EXPERIMENTAL PROCEDURE FOR EXAMINING NUTRITIONAL REGULATION OF HEART RATE VARIABILITY**

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The foods we eat influence physical and mental health. However, these beneficial and detrimental nutritional effects of diets may depend on how physiological and metabolic systems throughout the body respond to the consumption of foods, nutrients, and diets. The autonomic nervous system (ANS) responds to food consumption and facilitates the digestion, delivery, and metabolism of food and nutrients throughout the body. The ability of this system to flexibly respond to and facilitate the body's response to the variety of nutrients entering the body differs from person to person and may, in part, determine the beneficial or detrimental effects of nutrition on health. In this study, we will test ANS responsiveness to mental and nutritional (food) stimuli by measuring changes in heart-rate variability (HRV). HRV is the fluctuation in the time interval between heart beats and is determined by activity in the ANS. HRV will be determined by examining the electrocardiograms (ECGs) derived from a small sensor worn by participants during the study. Changes in HRV will be measured while participants recall emotional events or think about and eat preferred and non-preferred

comfort foods. This work will help to establish an experimental model for testing the roles of key homeostatic systems in nutritional responsiveness and how variable responsiveness of these systems influences the effects of nutrition on mental and metabolic health.

#### **FRI-331**

##### **ALDEHYDE DEHYDROGENASE-1A2: A TARGET FOR MALE CONTRACEPTION**

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Unintended pregnancies continue to hamper population control. Moreover, these unplanned pregnancies are often associated with increased incidences of low birth weight, child abuse, and inadequate physical development. The introduction of bis-dichloroacetyl-diamines (BDADs) 50 years ago demonstrated that spermatogenesis in males could be reversibly inhibited. However, side effects resulting from inhibition of liver aldehyde dehydrogenase-2, the principal enzyme responsible for alcohol metabolism, prevented them from reaching consumer markets as commercial male contraceptives. Recently, aldehyde dehydrogenase-1A2 (ALDH1A2) was revealed as the target enzyme that the original BDAD derivatives inhibited. ALDH1A2 is an aldehyde dehydrogenase isoform localized to germ and Sertoli cells of the seminiferous tubules in mammalian testes. This enzyme catalyzes the production of retinoic acid from retinaldehyde. Inhibition of this isoform impedes retinoic acid production and its paracrine signaling function, which is critical to spermatogonia, subsequently curtailing spermatogenesis. We have synthesized compounds that demonstrate great specificity and affinity for ALDH1A2. We hypothesize these compounds will reduce ALDH1A2 activity and inhibit spermatogenesis *in vivo* without the side effects exhibited by the unsuccessful BDAD compounds. Multi-step organic synthesis, half maximal inhibitory concentration (IC<sub>50</sub>), and pharmacokinetic studies on mice are the principal methods we employed for synthesizing and determining the effectiveness of our compounds both *in vitro* and *in vivo*. In summary, ALDH1A2 offers an enticing target for male contraception. Further studies will be undertaken to assess the selectivity, clearance, and overall effectiveness of our compounds prior to prospective human clinical trials.

#### **FRI-917**

##### **ASSESSING DIFFERENCES IN SAUDI VS. U.S. COLLEGE STUDENTS' ACQUISITION OF NHP KNOWLEDGE**

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Complementary and alternative medicine (CAM) (e.g., traditional medicine) use may provide health benefits. Recently we showed that Aboriginal/Native students use elders as a significant information source to learn about natural health products (NHPs), as compared to non-native students. Little is known about Saudi vs. U.S. students' NHP knowledge sources. What NHPs do Saudi vs. U.S. college students use, and where do they acquire information about NHPs? We hypothesize a greater use and knowledge acquisition of NHPs by Saudi students due to a Saudi culture of traditional medicine. A cross-sectional study is underway at Wayne State University (U.S.A.) and King Saud University (KSA). There will be (n = 750) student participants from each

university. The online survey includes questions regarding NHPs used and learning sources (e.g., traditional elders, print media. etc.). Data will be analyzed with a chi square, fisher test, and regression analysis. Alpha level is set to 0.05 to highlight data that are statistically significant through SPSS software. Preliminary findings show that Saudi students use NHP more than non-Saudi U.S. students ( $p \leq 0.05$ ). Analyses are underway to assess sources of knowledge about NHPs used by students. We anticipate our final analyses and interpretations may impact greatly on future CAM healthcare and traditional medicine use in the U.S. and Saudi Arabia.

### **SAT-332**

#### **LEDs PHASING OUT HPS LIGHTING AS THE FUTURE'S GREEN ENERGY FOR INDOOR AGRICULTURAL PRODUCTION**

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Light emitting diodes (LEDs) are modern, solid-state lights having a 50,000+ hour lifespan while utilizing small amounts of energy. They need no special disposal and effectively convert electrical energy with little heat loss to their environment unlike high pressure sodium (HPS) lights. Presently, data is limited, and few studies have examined which light source is more efficient in output, energy efficiency, and as a supplemental light source for plants. This is the focus of this study. *Lactuca sativa* varieties were grown hydroponically from seed in a controlled greenhouse. They were provided nourishment by administration of a nutrient solution via an attached reservoir. Each experimental group was planted in 3 evenly spaced rows of 4 and provided supplemental lighting 12" to 13" above the canopy for 16 hours of daily light. A control was used to establish the standard for comparison. After approximately 28 days, each trial was harvested, samples dried at 60 °C for 72 hours, and dry weight obtained for lettuce to analyze and determine influence on growth. Experimental groups exhibited denser foliage than the control group as reflected by dry weight measured in grams. The LED group was found to have a significantly higher weight: almost twice that of the HPS group. In addition, LEDs were found to be more energy efficient in energy output ( $W/m^2$ ) and light efficiency (Lumens/W). Even though significant differences were found between the experimental groups and control, the LED group exhibited the most significant influence on plant growth, energy, and light efficiency suggesting they are the better alternative for indoor production.

### **FRI-917**

#### **VALIDATION STUDY OF A LASER AS A NEW TOOL FOR HEIGHT MEASUREMENT**

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Height is an essential measure for the evaluation of an adult's health, and especially important for the evaluation of children's health. Lasers have been popularly used in many areas such as construction, engineering, and in the government for defense purposes. Lasers are known for their accuracy, reliability, and ease of use. It can be reasoned then that lasers should be an accurate, reliable way of measuring height. Currently, stadiometers are the standard way of measuring height. For this study, a laser tool was created to measure volunteers' heights.

Volunteers were recruited from a total of 4 various public sites and were categorized into 3 groups: children (ages 2 - 12), adolescents (13 - 18), and adults (19+). A total of 128 participants were measured, with at least 30 in each group. Each participant was measured three times with the stadiometer and three times with the laser, and averages of both were calculated and compared. Results showed an overall strong positive correlation between measurements of the stadiometer and laser and showed that a laser may be a validated tool to use for height measurement. There is no significant difference between gender and ages, though a stronger positive correlation can be seen for adolescents. Location (indoor vs. outdoor) did show a significant difference, with indoor heights being more comparable between the laser and stadiometer than heights measured outdoors. Studies can now be performed to measure adaptability of lasers to the clinical setting for use in height measurements.

## **OTHER AGRICULTURAL SCIENCES**

### **FRI-735**

#### **WHERE HEALTH AND HORTICULTURE INTERSECT: A NAVAJO WELLNESS COLLABORATION – PRELIMINARY SHIPROCK, NM RESULTS**

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Benefits of gardening include access to healthy fruits and vegetables as well as exercise, which can reduce many health risks including diabetes and cancer. Our objectives were to understand perceived gardening barriers in the Shiprock community and track water usage to find out the cost of watering a garden in order to link perceived economic barriers with actual water usage data. After receiving Navajo Nation Human Research Review Board approval, we conducted survey sampling on June 03, 05, and 09, 2014, regarding resource options, financial barriers, and general barriers for gardening. The interview team consisted of 4 individuals, and each interviewer-assisted survey lasted approximately 30 minutes per participant. Sixty participants were interviewed. We also monitored the Shiprock community garden to track water meter usage for a period of 21 days and had 2 different individuals turning off and on the water. In setting up the garden, we used a garden water meter, filter, back flow preventer, ½ to 1-inch hose, and drip irrigation emitters. Results from the survey interviews showed that participants perceived that animals (31%) and insects and pests (23%) were the biggest barriers to gardening and that inputs like water were cost prohibitive. The Shiprock garden was, in fact, browsed by prairie dogs. Over the 21-day tracking period, however, 816.5 gallons of water were applied to the garden equaling \$2.45. This finding shows that, while survey respondents perceive water as a financial barrier to gardening, the actual cost of watering a small garden in Shiprock using tap water is relatively low.

## **SAT-736**

### **IMPLEMENTING SILT SOCKS IN TILE RISERS TO REDUCE SEDIMENT AND NUTRIENT TRANSPORT**

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Given the growing environmental problems associated with eutrophication in surface waters receiving agricultural runoff, there is a need for low-cost and high impact management practice solutions. Tile risers located in closed depressions within agricultural fields act as direct pathways for sediment and nutrient transport to surface waters. This study evaluates the impact of remediation agents in silt socks to remove sediment, phosphorus, and nitrogen from surface runoff. Four series of experiments were tested: tile riser without silt sock (TWS), tile riser with silt sock only (TSO), tile riser with silt sock and charcoal (TSC), and tile riser with silt sock and steel slag (TSS). Runoff water was collected from a 9.75 m by 3.66 m laboratory soil box placed under a rainfall simulator. Treatments were exposed to 4 runoff events lasting 30 minutes each at an intensity of 50 mm h<sup>-1</sup>. Differences between treatments were conducted using Kruskal-Wallis tests. While previous findings have demonstrated silt socks to be effective at removing sediments in runoff, preliminary results suggest that flow rate is reduced by about 0.18 L/s (50%) in TSO compare to TWS, and by 0.05 L/s (13%) and 0.01 L/s (1%) in TSC and TSS. Reductions in flow rate using silt socks could serve as an initial mechanism to promote water ponding and nutrient infiltration. Remediation agents, in contrast, could serve as a second mechanism of nutrient pollution mitigation and further improve water quality. Research results will be presented and analyzed on completion of the experiment.

## **SAT-707**

### **ANALYSIS OF GRAPE CULTIVARS FOR PIERCE'S DISEASE RESISTANCE**

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Pierce's disease (PD) is a plant disease of grapevines caused by the Gram negative bacterium *Xylella fastidiosa*. This plant pathogen causes a blockage in the xylem, preventing water flow and killing the vine. This bacterium is transferred by an insect vector, and both the vector and the bacteria are found at particularly high levels along the Texas Gulf Coast, making this disease a serious constraint for the Texas wine industry. Planting PD-resistant grapevines is one strategy to deal with the deadly disease. Texas AgriLife Extension scientists through Texas A&M have planted an experimental vineyard in Industry, Texas. The vineyard includes grape varieties that may have disease resistance bred by scientists in Texas, Florida, and California. The objective of this study is to evaluate grape isolates for the levels of *X. fastidiosa* to ascertain which varieties might be the most resistant. A preliminary study during the fall and winter of 2013 demonstrated approximately half of the samples had slight positive results, indicating presence of the bacterium. Two varieties showed high levels of *X. fastidiosa* above the threshold, suggesting they would not be good choices for areas where there are susceptible vines. This was designed to confirm the preliminary results; fresher tissue will be used along

with more sensitive quantitative real time polymerase chain reaction (QRT PCR) analysis. These results will help wine growers select grape varieties that are less likely to die from PD.

#### **SAT-735**

##### **ESSENTIAL OILS OF YLANG-YLANG EXHIBITED INSECTICIDE ACTIVITY AGAINST THE COFFEE BERRY BORER *HYPOTHENEMUS HAMPEI* (CURCULIONIDAE)**

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The coffee berry borer *Hypothenemus hampei* is the main pest affecting coffee crops on a worldwide level. This beetle infects 12 commercial species belonging to the genus *Coffea*. Currently, the main insecticides used for the control of this pest are highly toxic to human health and the environment due to their slow degradation in soil. Our main objective in this project is to develop safer strategies (natural insecticides, deterrents, and attractants) to combat this pest. Previous research has indicated insecticidal activity of essential oils extracted from ylang-ylang leaves (*Cananga odorata*) against the maize weevil *Sitophilus zeamais*. Since *S. zeamais* and *H. hampei* belong to the family *Curculionidae*, we tested the potential insecticide activity of ylang-ylang components against the coffee berry borer. In order to perform this task, we obtained the essential oils from ylang-ylang flowers and leaves by hydrodistillation. To this point, the research has shown indications that the essential oil of *C. odorata* could become a prospective organic insecticide against *H. hampei*. The effect of other essential oils against the borer is currently under investigation and will be reported as well.

#### **FRI-736**

##### **EFFECT OF GYPSUM AND RESIDUE ON INFILTRATION RATE OF WATER IN TWO SOILS IN OHIO**

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Soil compaction and crusts form on the soil surface during intense rainfall events. This reduces infiltration rates of water into the soil profile and leads to increased runoff and soil erosion. In addition, water not stored in soil is unavailable for crop growth and can lead to reduced crop yields. The rate of water infiltration is influenced by several factors such as soil texture, structure, and management techniques. In Ohio, there is an abundant supply of gypsum (calcium sulfate dehydrate). Research has demonstrated that the use of gypsum as a soil amendment by farmers can improve crop yields, soil, and water quality. However, the effect of gypsum on the infiltration rate of water when applied alone or combined with plant residues is not fully understood. A greenhouse experiment was conducted to measure the infiltration rate of water from 2 contrasting soil types in Ohio, i.e., Wooster silt loam soil and Hoytville clay loam soil, treated with gypsum (cumulative of 26.9 Mg ha<sup>-1</sup> applied in 4 equal doses of 6.72 Mg ha<sup>-1</sup> each) and crop residues (13.4 Mg ha<sup>-1</sup> applied in a single dose). The effect of treatments on infiltration was measured using both the double ring infiltrometer method (Wooster soil) and the single ring infiltrometer method (Hoytville soil). Cumulative total water infiltration and the infiltration rate were calculated to determine parameters for the Philip's and Kostikov's

model. The application of gypsum and plant residues is expected to increase the water infiltration rate of both soils as compared to untreated soils.

## OTHER BIOLOGICAL SCIENCES

### SAT-336

#### TEMPORAL NICHE PARTITIONING OF FRUGIVORES AND OMNIVORES IN THE LAS CRUCES BIOLOGICAL STATION, COSTA RICA

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Competition for resources influences populations and species diversity at every trophic level within an ecosystem. With modern habitat loss and degradation, which is particularly severe in biodiverse tropical regions, understanding how different species in the same niche obtain the resources they need to survive becomes critically important if we are to prevent species loss. Many species reduce resource competition by partitioning the niche they occupy by space and/or time. Here, we observe how selected species of frugivores and omnivores partition their dietary niches in the Las Cruces Biological Station in the Coto Brus region of Costa Rica. Based on preliminary research and observations, we hypothesized that these species divide their niche by being active at different times of the day because this temporal partitioning reduces competition for food. We have placed camera traps at areas of heavy animal traffic throughout the forest and can use the timestamps on the photos to document the activity schedules of the terrestrial vertebrate species frequenting the station. We will calculate the mean time of activity for each species we record on the traps and use circular statistics to determine whether the means are significantly different. We expect to see a distinct difference in the average timing of activity of 2 common frugivorous species, the agouti (*Dasyprocta punctata*) and paca (*Agouti paca*). We also predict a less distinct but still different activity schedule for the station's omnivorous species, including the coati (*Nasua narica*), nine-banded armadillo (*Dasypus novemcinctus*), and common opossum (*Didelphis marsupialis*).

### FRI-333

#### A POINT MUTATION IN *MYH9*, THE GENE ENCODING NONMUSCLE MYOSIN II-A; HEAVY CHAIN DISRUPTS MOUSE SPERMATOGENESIS

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Nonmuscle myosin II-A (NMII-A) is a major cytoskeletal protein composed of a pair of heavy chains (230 kDa) encoded by the *MYH9* gene and 2 pairs of light chains (20 kDa and 17kDa). It is ubiquitously expressed in humans and mice and contributes to cellular processes including cell migration, cell adhesion, and cytokinesis. Humans with mutations in NMII-A have defects in blood cells, glomerulosclerosis, cataracts, and deafness. We have generated a mouse line with a

mutation frequently found in human *MYH9*: E1841K. In addition to modeling the above defects, male, but not female mice homozygous for the mutation were sterile with severe defects in sperm development. Histological analysis of mutant testis document that spermatocytes arrested at the elongated spermatid stage and degenerate spermatids sloughed off into the lumen. Additionally, some of the seminiferous tubules did not develop a lumen area or appeared degenerate with a complete absence of spermatocytes. TUNEL assays of the mutant testis showed an increase in apoptotic germ cells compared to wild-type testis. Furthermore, caudal epididymis sections showed sloughed off germ cells and a few malformed spermatozoa that were rarely motile. Heterozygous mice with similar, albeit less severe, defects were fertile. Although the expression level of NMII-A is low in mouse testis, when NMII-A is mutated at E1841K, the testis of homozygous mutant mice display an array of defects in spermatogenesis and are sterile. Collectively these observations suggest a previously unknown, critical role for NMII-A in spermatogenesis and male fertility.

#### **SAT-335**

##### **NEW ASSAY FOR ACETATE BASED ON THE OXIDATION OF AZURE DYES BY POTASSIUM BROMATE AND POTASSIUM CHLORATE**

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Azure dyes are readily used in many industries such as histology, textiles, and pharmaceuticals. Some of these dyes can irritate allergies or pollute water. Therefore, it is important to take into consideration the damage and consequences the use of these dyes can cause to the environment. Furthermore, it is important to find ways that might help degrade these dyes. In this study, the effect of acetate on the oxidation of azure A, B, and C by means of the addition of potassium bromate and potassium chlorate as oxidants in sulfuric acid media using the quenching agent sodium acetate was studied via UV-Vis spectrometry. We concluded that acetate can accelerate potassium bromate oxidation of azure A, B, and C. We also concluded there was oxidation activity seen with potassium chlorate, with a less profound acceleration. These conclusions will help us to better understand the behavior of these dyes and use the dyes more efficiently.

#### **SAT-337**

##### **THE ROLES OF LEUKOTRIENE C4 AND IL-33 IN PROMOTING LUNG INFLAMMATION AND ILC2 ACTIVATION**

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Innate type 2 lymphoid cells (ILC2) are newly discovered cells that play a vital role in helminth innate immunity and have been shown to be critical players in allergies. ILC2s produce Type 2 cytokines IL-5 and IL-13, two inflammatory interleukins present in allergic inflammation. Cysteinyl leukotriene C4 (LTC4) is a bioactive lipid and parent CysLT to LTD4 and LTE4. LTC4 is generated in allergic inflammation and its product LTD4 binds to CysLTR1 on the ILC2 surface. Interleukin 33 (IL-33) is a cytokine secreted by airway and bronchial epithelial cells that



functions as an inducer of Type 2 cytokines from ILC2s and promotes airway inflammation. Both of these molecules have been found to be independently important in hypersensitivity diseases, especially in allergic asthma. Our goal is to assess the effects of LTC4 and IL-33 on lung eosinophilia, lung ILC2 expansion, proliferation, ILC2 cytokine production, and airway cytokine levels. *In vivo* intranasal administration of LTC4, IL-33, or both will be given to mice, and bronchoalveolar lavage and lungs will be collected, processed, cultured, and analyzed for the presence of the cells and cytokines in question using flow cytometry and ELISA. We expect that mice that have been administered both LTC4 and IL-33 will have a significant increase in eosinophilia, ILC2s, and type 2 cytokines over the models that were only given LTC4 or IL-33. New findings regarding ILC2 and other innate immune cell functions and characteristics can possibly lead to the discovery of novel treatments for asthma and other forms of allergic diseases.

#### **SAT-334**

##### **THE EFFECTS OF HUMAN LEPTIN ON FOOD INTAKE IN THE AFRICAN CLAWED FROG *XENOPUS LAEVIS***

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Leptin is a polypeptide secreted by adipose and other tissues that has a dramatic inhibitory effect on appetite in mammals. Recently, the structure of non-mammalian leptin peptides has been elucidated. Despite having very little similarity based on primary amino acid sequences, vertebrate leptins are surprisingly conserved based on tertiary structure. There is some evidence to suggest that human leptin may act on leptin receptors in other vertebrate species, but the data are based on *in vitro* heterologous expression assays. In this present study, we examined the ability of human recombinant leptin (hrLeptin) to modulate food intake in a model amphibian species, the South African clawed frog *Xenopus laevis*. We hypothesized that hrLeptin will be effective in suppressing food intake in this amphibian species. In our initial experiments, juvenile frogs were injected via the dorsal lymph sac with one of 5 doses (0, 0.02, 0.2, 2, or 20 ug) of leptin, and food intake was assessed. The hrLeptin had no effect on food intake in *X. laevis* after peripheral administration in 2 independent trials. Based on qualitative reverse transcriptase PCR, we detected mRNA for the leptin receptor in the telencephalon and optic tectum of *X. laevis*. We are currently testing the effects of hrLeptin on food intake after intracerebroventricular administration in *X. laevis*.

#### **FRI-334**

##### **STUDY OF *IRGM* AS A SUSCEPTIBILITY LOCUS IN AFRICAN AMERICANS WITH CROHN'S DISEASE**

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Crohn's disease (CD) is a destructive, life-long, chronic inflammatory disorder that results in intestinal ulcers, bleeding, and weight loss and severely diminishes quality of life. Crohn's

disease affects all races and ethnicities and is thought to occur via the interaction of environmental factors with genetics in a susceptible host. Unfortunately, thus far, most of the genetic studies have been done in populations of European descent. The prevalence and disease burden of CD among the African American (AA) population is similar to that of Caucasians. Because genetic discoveries can have diagnostic, therapeutic, and prognostic value, it is important to determine if the genetic susceptibility patterns found in Caucasians are valid for the African American population. The *IRGM* gene is one of 71 or more loci that have been associated with CD susceptibility in patients of European descent. Specifically, two *IRGM* single nucleotide polymorphisms (SNPs) (rs13361189 and rs4958847) have been associated with increased CD susceptibility. The purpose of this study is to determine if these 2 SNPs have any association with CD in AA patients. DNA was extracted from the blood of 212 AA CD cases and 119 controls, then genotyped using the TaqMan method for the 2 identified SNPs. Finally we performed association analysis using PLINK to determine whether SNPs rs13361189 and rs4958847 are implicated in CD in the AA population. We found there is no association between these 2 SNPs and Crohn's disease in African Americans, which implies there are other genetic contributions increasing susceptibility in this population.

#### **FRI-229**

#### **IMPACT OF THE MAMMALIAN TARGET OF RAPAMYCIN INHIBITION BY EVEROLIMUS ON PERIPHERAL BLOOD $\alpha\beta$ -, GAMMA-, AND DELTA-T LYMPHOCYTES IN RENAL TRANSPLANT RECIPIENTS**

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The kidney is an essential organ necessary for the human body to discharge harmful toxins and is imperative for filtering blood. According to the Centers for Disease Control and Prevention, kidney disease is the eighth leading cause of death in the United States. Diabetes and hypertension, two major factors that influence kidney function, can consequently lead to end-stage renal disease. The primary method of treatment for end-stage renal disease is kidney transplantation, which requires a regimen of immunosuppressant drugs to prevent allograft rejection. Previously, our lab has shown that administration of the immunosuppressant drug sirolimus, a mammalian target of the rapamycin inhibitor also known as mTOR, impairs skin homeostasis and wound repair. In order to further understand the mechanism behind this adverse effect of mTOR suppression, we examined renal transplant recipients who were administered the sirolimus derivative everolimus. Evaluating the extent to which mTOR suppression impairs wound healing, 3 mm skin biopsies were performed and their wounds were monitored for over 7 days. The number and activation of  $\alpha\beta$  and  $\gamma\delta$  T cells in the blood of patients administered everolimus were compared to a control group of patients not administered the drug. Several T cell populations, specifically V $\gamma$ 9V $\delta$ 2 T cells, have been previously shown to home to sites of tissue damage to improve wound repair. Analysis of T-cell function was performed using ELISA and flow cytometric methods. This data explores which T lymphocyte populations require mTOR to maximize function in transplant recipients and has implications in tissue repair and graft rejection.

**SAT-333****NORTH AMERICAN PORCUPINE (*ERETHIZON DORSATUM*) HABITAT SUITABILITY AT MULTIPLE SCALES**

Tina Nguyen, Tim Bean.

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Habitat suitability models combine observations of species occurrence or abundance with maps of environmental variables to produce estimates of relative use. However, the relationship between species occurrence and its environment is known to vary at multiple scales. The North American porcupine is considered a generalist at a large spatial scale. However, at local levels the North American porcupine exhibits fine scale habitat and diet requirements. Here, we create 2 habitat suitability models comparing continental and local distribution for the North American Porcupine. At the continental level, our distribution model reveals the physiological and climatic limitations of the North American porcupine. At the local level, our model is driven by the behavior of the North American porcupine. We use “participant science” observations and museum records to construct a model of coastal California that includes Humboldt, Trinity, and Del Norte Counties. We document their presence by bait and trapping methods based on the previous 2 models. The differing scales of the models reveal additional insight about porcupine biology and habitat selection at the local level in a unique environment. This work reaffirms the importance of considering scale when mapping habitat suitability for a species of concern. Understanding habitat suitability at the local versus continental level will better help wildlife biologists manage and conserve appropriate habitats needed for the diminishing population of North American porcupines in California.

**FRI-336****NDI1 EXPRESSION IN INTESTINAL STEM CELLS EXTENDS LIFESPAN IN *DROSOPHILA MELANOGASTER***

Jacqueline Graniel, Jae Hur, David Walker.

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As organisms age, mitochondrial activity declines. Alternative internal NADH-ubiquinone oxidoreductase (*ndi1*) from yeast can increase mitochondrial activity in *Drosophila melanogaster* and extend life when expressed in neurons. The enzyme *ndi1* can substitute for all complex I functions in mammals and fruit flies except pumping out protons in the electron transport chain in metazoans. Dietary restriction (DR), reduced fertility, and beneficial bacteria have also been correlated with increased lifespan. This study focused on the influence of tissue-specific *ndi1* expression on lifespan, feeding behavior, fertility, and gut flora. We found *ndi1* flies lived longer and ate more, suggesting *ndi1*-mediated lifespan extension is not a result of DR. Furthermore, an increase in feeding frequency and an increase in sugar consumption was observed in the long-lived flies. Similarly, decreased fertility that has been previously associated with some long-lived flies was not observed in *ndi1* flies. To test if *ndi1* expression was dependent on the presence of endogenous bacteria, survivorship in media supplemented with antibiotics was conducted. The addition of antibiotics did not decrease lifespan in *ndi1* flies

back to wild-type levels, suggesting that *ndi1*-mediated lifespan extension is largely independent of gut flora. Together these results will help us better understand aging and may provide the foundation for using *ndi1* in a clinical setting to protect against age-related diseases.

#### **FRI-335**

##### **CONTRIBUTION OF CHOLINERGIC RECEPTORS TO METHYLMERCURY (MEHG)-INDUCED CYTOTOXICITY IN PC12 CELLS**

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Ca<sup>2+</sup>-mediated cell death is a common response of neurons to methylmercury (MeHg) exposure. Our previous studies have shown that cholinergic receptors (AChRs) are potential targets for MeHg-mediated Ca<sup>2+</sup> dysregulation. The extent to which these receptors respond to MeHg in the absence of ACh have not been delineated. We studied the role of AChRs in MeHg-induced cytotoxicity in rat PC12 cells. Nerve growth factor-differentiated PC12 cells were treated for 1 hr with 1, 2, or 5  $\mu$ M MeHg. Cytotoxicity was examined using the Live Dead Assay<sup>®</sup> 1 or 24 hr after MeHg treatment concluded. Mecamylamine (MEC, 5  $\mu$ M) and atropine (10  $\mu$ M), nAChR and mAChR antagonists, respectively, were used to determine the involvement of the studied receptors to MeHg-induced cell death. Viability at 1 and 24 hr after MeHg was reduced in a concentration, but not time-dependent manner. At 1 hr, MeHg-induced cytotoxicity ranged from 33% (1  $\mu$ M) to 57% (5  $\mu$ M) and at 24 hr from 35% (1  $\mu$ M) to 65% (5  $\mu$ M). Pretreatment with their respect antagonist protected PC12 cells from MeHg-induced cell death at both time points. Protection was proportional to the [MeHg], i.e., defense against low [MeHg] (1, 2  $\mu$ M) was more effective than that at 5  $\mu$ M MeHg. At 1  $\mu$ M MeHg, protection ranged from 77 to 97% (3 to 23% cytotoxicity) at both 1 and 24 hr, whereas at 5  $\mu$ M MeHg protection was only in the range of 32 to 50%. Thus, both receptors contribute to Ca<sup>2+</sup>-induced cytotoxicity by MeHg. This occurs in the absence of a cholinergic agonist, suggesting direct actions of MeHg on AChRs.

#### **FRI-337**

##### **EXPLORING GENE-ENVIRONMENT INTERACTIONS IMPLICATED IN PARKINSON'S DISEASE USING A PARQUAT AND MANEB MODEL IN *DROSOPHILA***

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Parkinson's disease (PD) is a neurodegenerative disease characterized by the loss of dopaminergic neurons and both motor and non-motor functions. Overexpression and mutations of the  $\alpha$ -synuclein (*SNCA*) gene in humans has been linked to familial forms of PD. However, the vast majority of PD cases are sporadic; thus, disease progression likely relies on an individual's genetic background and/or environmental exposures. Exposure to environmental toxins has been shown to increase the risk of developing PD in humans. In particular, prolonged exposure to the pesticides paraquat and maneb can increase the risk of

PD by 200%. Humans with variants in *SNCA* exhibited an increased risk of PD, compared to control, when they were exposed to pesticides. *Drosophila melanogaster* was utilized as a model of paraquat- and maneb-induced PD. Survival decreased by 50%, and motor ability significantly decreased when exposed to paraquat alone or when exposed to a combination of paraquat and maneb. Dopaminergic cell counts decreased only when exposed to both paraquat and maneb. This data shows that paraquat and maneb cause decreased survival and motor function, and only late in life is a loss of dopaminergic neurons observed. Additionally, paraquat and maneb are synergizing with *SNCA* to cause dopaminergic cell loss at even earlier time points than paraquat and maneb alone. Future directions include repeating the experiment using the tyrosine hydroxylase (TH) driver, which will allow for mutant *SNCA* gene expression in a manner more specifically targeted to dopaminergic neurons and observing and similarly assessing survival and DA neuron loss.

## PHARMACOLOGY

### SAT-227

#### THE USE OF FACTORIAL DESIGN TO DEVELOP A THERMO-STABLE PULMONARY BCG VACCINE

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Mycobacterium tuberculosis is responsible for 2 million global mortalities per year. The bacille Calmette-guérin (BCG) is a live bacterial vaccine and is the only approved vaccine against tuberculosis. It is administered via the intradermal route and is currently prepared by lyophilization. However, live vaccines prepared by lyophilization require constant cold chain storage at 4 °C, a problem in areas where tuberculosis is prevalent. In addition, the intradermal administration of these vaccines requires trained healthcare workers, due to the prevalence of needle stick injuries associated with this route of administration. Spray drying is another method of vaccine preparation and, although less widely used, several researchers have shown that spray dried vaccines can provide higher bacterial viability at elevated temperatures. This could potentially eliminate the need of cold chain storage in maintaining BCG efficacy. Furthermore, dry powders can be delivered via the pulmonary route, thereby decreasing training requirements for healthcare workers. In this study, we aimed to create a BCG dry powder suitable for pulmonary delivery using a factorial design to evaluate the variable parameters of excipient concentration, feed rate, and outlet temperature. The excipients L-leucine, bovine serum albumin, polyvinylpyrrolidone, mannitol, and trehalose were chosen for the experiments. Powders were characterized based on their size, yield, water retention, water uptake, and glass transition temperature (T<sub>g</sub>), and then the best performer was spray dried with BCG. We expect that dry powders formulated using factorial design will reveal ideal excipient mixtures and parameters for the formulation of a stable pulmonary BCG vaccine.

**FRI-227****CHEMICAL COMPOSITION AND ANTIMICROBIAL ACTIVITY OF WILD-HARVESTED *ACHILLEA MILLEFOLIUM* FROM THE REPUBLIC OF ARMENIA**

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For thousands of years, humans have studied plants to understand their medicinal properties. As interest in plant medicines is increasing, their components are being studied to provide evidence for their use in medicine. *Achillea millefolium*, also known as yarrow, is a plant species of the Asteraceae family that is widely spread throughout the northern hemisphere. Traditionally, *Achillea* is used as an anti-inflammatory, a hemostatic, a spasmolytic, and an anti-allergenic. Wildly growing yarrow (the entire shoot system) was hand picked in late June from the Aparan, Sevan, and Gyumri regions of Armenia. Raw materials were left to dry in a shady room at 30 °C for one week. Microscopic analysis confirmed the identity of the collected species to be *Achillea millefolium*. Its essential oil was distilled (% yield = 0.44) using the hydrodistillation method for subsequent analysis via gas chromatography-mass spectrometry (GC-MS). Following hydrodistillation, *Achillea*'s ethanol extract (% yield = 8.8) was obtained and subjected to liquid chromatography-mass spectrometry (LC-MS) to further secure its chemical composition. After GC-MS analysis, *Achillea*'s essential oil is expected to consist of mostly the sesquiterpene lactones achillin and achillicin. LC-MS analysis of its ethanol extract will likely show the presence of flavonoids such as apigenin, luteolin, and quercetin. Antimicrobial activity of *Achillea*'s essential oil and ethanol extract will be determined via disc diffusion using representative Gram-negative and Gram-positive bacteria to establish its minimum inhibitory concentration (MIC). *Achillea millefolium*'s diverse chemical composition, coupled with its antimicrobial activity, could render it useful in mainstream medicine.

**SAT-226****ANTIBIOTIC SYNERGIES WITH VANCOMYCIN IN *ESCHERICHIA COLI***

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The problem of antibiotic resistance is now a growing and urgent issue in public health. Combinatorial drug therapies provide valuable tools for treatment of multi-drug resistant pathogens. This study specifically examines drug interactions with vancomycin, a powerful drug for treatment of Gram-positive bacterial infections, which works by preventing proper peptidoglycan synthesis. However, it is not effective against Gram-negative bacteria such as *Escherichia coli* because it can't get through the outer membrane, except in extremely small amounts. We propose that a highly synergistic interaction with vancomycin has the potential to render it effective in Gram-negative bacteria. In order to study vancomycin in *E. coli*, our study exploits the deoxycytidine deaminase (DCD)-deficient and peptidyl-prolyl cis-trans isomerase (SurA)-deficient strains, which show increased sensitivity and permeability to vancomycin and other antibiotics. Using these strains as the background for our survey, we tested vancomycin

in combination with a series of antibiotics. Drug interactions were determined by measuring growth percentages of cultures in suspension using endpoint optical density analysis. In both the DCD- and SurA-deficient strains, vancomycin exhibited synergistic interactions when combined with nitrofurantoin and trimethoprim. These combinations were then examined in wild-type *E. coli* in order to determine their clinical potential, and both were found to exhibit strongly synergistic interactions in the wild-type background. These findings suggest that vancomycin could be repurposed for use in the treatment of Gram-negative bacterial infections when combined with nitrofurantoin or trimethoprim. This provides opportunities for effective treatment of multi-drug resistant Gram-negative bacterial infections using highly synergistic combinatorial drug therapies.

#### **FRI-226**

##### **DEVELOPING STRATEGIES TO REACH CHALDEAN AMERICAN WOMEN WITH HEALTH PROMOTION MESSAGES**

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Health promotion efforts are largely unknown in Iraq, so Chaldean American refugees are poorly informed about health maintenance options. Social, cultural, linguistic, and financial barriers place Chaldean Americans in further danger of missing opportunities for health promotion. This demonstration project developed and tested strategies for reaching Chaldeans with health promotion messages. The most effective strategy found for reaching Chaldean American women was through English as a second language classes (ESL). Teachers agreed to allow a female, bilingual, Chaldean cancer educator to pilot test series of ten-minute breast cancer presentations at the beginning of each class. Unobtrusive, impersonal measures facilitated the assessment of the educational strategy; e.g., if complaints were lodged, if students start coming in late, whether students asked pertinent questions, etc. Teachers of two classes agreed to test the program. This intervention succeeded in reaching Chaldean women with diverse sociodemographic characteristics. Thirty-five students were exposed to the entire series of presentations. Students gave their complete attention to the presentation; no students challenged or complained about the inclusion of the materials in class; arrival times at class continued to be on schedule; students often lingered after class to ask relevant questions; and men and women in the class seemed equally receptive to the information. Reaching this population with health promotional messages via ESL classes offers considerable promise. It warrants formal evaluation in a definitive study for diverse health issues.

#### **FRI-228**

##### **EFFECTIVE PROTEIN MODELING ALGORITHM**

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Currently, protein-rendering algorithms rely on using every single atom to create the surface of the protein. These surfaces are key to drug-macromolecule interactions, an important piece of structure-guided drug design. By using every atom, the produced surface is accurate; however,

it requires a lot of memory and time. The aim of the research is to develop an algorithm that requires less memory while striving to be as accurate as possible. To reduce the memory usage, the algorithm will focus on amino acids rather than atoms. This is done by using the C-alpha atom as the center of the amino acid and a radius determined by the distance between the C-alpha atom and the furthest atom. To determine the similarity of the two surfaces, we used the old surface's normal to compare the distance between the surfaces. We expect the algorithm to require less memory while also being similar to the original surface. By making an efficient algorithm, the ability to display large viruses such as HIV and proteins becomes easier, which can lead to significant advances in medicine and drug design.

#### **SAT-225**

##### **ANALYZING THE EFFICACY OF EPIGENETIC MODULATORS IN TRIPLE NEGATIVE BREAST CANCER**

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Triple negative (TN) breast cancer accounts for 15 to 20% of all breast cancer diagnoses, is highly aggressive, and is associated with poor prognosis. There are currently no targeted therapies available as TN breast cancer cells lack the estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2). A novel approach is the use of drugs that alter the epigenetic landscape in breast cancer cells. One such drug is entinostat, a histone deacetylase (HDAC) inhibitor of class I HDACs. The inhibition of HDACs in cancer cells results in the reactivation of tumor suppressor genes that have been silenced. It has been shown in clinical trials that entinostat alone is not an effective treatment for breast cancer. Currently, entinostat is being investigated in ER-positive breast cancer in combination with other drugs such as aromatase inhibitors. Here, we seek to determine if there is an additive or synergistic effect when entinostat is combined with JQ1, a BRD4 inhibitor that also induces epigenetic changes. We have determined the IC<sub>50</sub> of both drugs in the MDA-MB-231 cell line, which represents the claudin-low subtype of TN breast cancer. In the future, we will treat MDA-MB-231 cells with entinostat and JQ1 to determine if they exhibit a combinatorial effect. If so, this would provide foundational evidence of a potential novel dual targeted therapy that bypasses the current approach of targeting cell surface or hormone receptors.

#### **FRI-225**

##### **ROLE OF CPT1 ENZYME IN PROSTATE CANCER VIABILITY**

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As a leading cancer around the world, prostate cancer claims over 258,000 men every year. With the understanding that prostate cancer cells rely heavily on the production and availability of lipids to survive, this current study investigated the possibility of blocking different avenues in which lipids are transported to the cell in the hopes of lowering cell viability. Specifically, the project targeted the enzyme CPT1A, which resides in the outer rim of the mitochondria and is a rate limiting step to transport fatty acids into the mitochondria for oxidation. The expression of



CPT1A enzyme was knocked down in LNCAP cancer cells using lentiviral shRNA silencing technology. After selection with puromycin, we obtained mRNA expression that was decreased by 90% as well as a clear decrease in CPT1A protein expression by western blot analysis. The decreased in CPT1A expression was associated with decreased cell viability in response to the fat burning inhibitor etomoxir. These results suggest that fat oxidation in the mitochondria of prostate cancer cells is mediated by CPT1A and is important to maintain cancer cell viability.

#### **SAT-228**

##### **RESPONSES OF THE RAT BASAL GANGLIA NEUROTENSIN SYSTEMS TO LOW DOSES OF METHAMPHETAMINE**

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Administration of high doses of methamphetamine (METH), in a manner mimicking the bingeing patterns associated with abuse, reduces NT release and causes its accumulation and elevated NT levels in extrapyramidal structures by a D1 mechanism. The relevance of these findings to the therapeutic uses of METH needs to be studied. The effect of low doses of METH (comparable to that used for therapy) on basal ganglia NT systems was examined and compared to high-dose and self-administration effects previously reported. Rats were injected 4 times (at 2 h intervals) with either saline or low doses of METH (0.25, 0.50, or 1.00 mg/kg/s.c.). For the DA antagonist studies, animals were pretreated with a D1 (SCH23390) or D2 (eticlopride) antagonist 15 min prior to METH or saline treatments. Rats were sacrificed 5 to 48 h after last injection. METH at doses of 0.25 and 0.50, but not 1.00 mg/kg, rapidly and briefly decreased NTLI concentration in all basal ganglia structures studied. In the posterior dorsal striatum, the reduction in NT level after low-dose METH appeared to be caused principally by D2 stimulation, but both D2 and D1 stimulation were required for the NT responses in the other basal ganglia regions. A novel finding from the present study was that opposite to abuse-mimicking high doses of METH, the therapeutically relevant low-dose METH treatment reduced NT tissue levels, likely reflecting an increase in NT release and a short-term depletion of the levels of this neuropeptide in basal ganglia structures. The possible significance of these findings is discussed.

#### **PHYSIOLOGY/PATHOLOGY**

#### **FRI-339**

##### **FUNCTIONAL REVERSAL: SHORT-TERM AND LONG-TERM VARIATIONS IN VASCULAR ENDOTHELIUM-DERIVED REACTIVE OXYGEN SPECIES**

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Understanding the time-dependent functional reversal in reactive oxygen species (ROS) is essential in order to develop therapeutic modalities for cardiovascular disease. Previously, our laboratory found that endothelium-dependent coronary vasodilation improved in mice that

overexpressed NOX2, a component of the ROS generating NADPH oxidase complex, for a period of 4 to 12 weeks (short-term). We demonstrated that increased endogenous ROS levels aided with endothelial nitric oxide synthase (eNOS) activation and nitric oxide (NO) synthesis by activating the survival kinase AMPK. Our findings revealed that heightened levels of ROS, which are often associated with endothelial dysfunction and cardiovascular problems in advanced age, can play a protective role in endothelial homeostasis by inducing eNOS activation and NO production (a potent vasodilator). However, our research did not look at the effects that can result from exposing vascular endothelial cells to increased ROS levels for a period beyond 12 weeks (long-term). Chronic exposure of ROS on vascular endothelial cells can result in hyperfunction or dysfunction of the AMPK-eNOS pathway and lead to oxidative damage. The objective of our current project is to obtain novel insight into the mechanisms behind the temporal functional reversal of ROS in vascular endothelial cells. Future research in our laboratory will focus on measuring NO and mitochondrial ROS levels during chronic oxidative stress. We will also quantify mitochondrial ROS during short-term NOX2 overexpression and compare it with the up-regulation of superoxide dismutase (SOD2), an enzyme that catalyzes the conversion of superoxide into hydrogen peroxide.

#### **FRI-341**

##### **DEVELOPING *XENOPUS LAEVIS* AS A MODEL FOR FRAGILE X SYNDROME**

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Fragile X syndrome (FXS) is the leading known monogenic form of autism and the most common form of inherited intellectual disability. Early in development, loss of function of the *fmr1* gene in humans results in lack of fragile X mental retardation protein (FMRP), and leads to deficits including impaired sensory processing and increased susceptibility to seizure. Because FMRP is highly conserved across animals, we have sought to determine whether decreasing FMRP expression in *Xenopus laevis* embryos may help to understand consequences of loss of FMRP. We established an *in vivo* imaging assay to evaluate molecular genetic strategies to decrease FMRP expression in brain neurons of the optic tectum and investigate the effects of FMRP on the generation of neurons from radial glial progenitor cells. In general, animals treated with *fmr1a* morpholinos, which reduce expression of FMRP, showed a marked decrease in neurogenesis, whereas animals treated with control morpholinos showed an increase. To investigate whether the observed reduction in neurons following knockdown of FMRP results in phenotypic behavioral deficits characteristic of FXS, we characterized 2 visually-guided behaviors: schooling, a proxy for social behavior, and visual avoidance, an innate escape behavior mediated by circuitry in the optic tectum, as well as susceptibility to seizure, in which animals are exposed to a seizure-inducing drug. Currently, we are using these paradigms to examine whether loss of FMRP in *Xenopus laevis* embryos will impair sensory processing and increase susceptibility to seizure. These studies demonstrate promise in developing *Xenopus* as a system to study FXS.

**SAT-342****INVESTIGATING THE EFFECTS OF ACUTE OZONE EXPOSURE IN FEMALE REPRODUCTIVE FUNCTION**

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Research has shown that oxidative stress can affect the expression of hypothalamic GnRH, sex hormone levels, and fertility in rodents. In this work, we investigated the effects of ozone exposure on the female reproductive system, more specifically, on folliculogenesis and steroidogenesis leading up to ovulation. The estrous cycle of 18 mice was determined every morning. After 3 consecutive cycles, mice were exposed to ozone (2 ppm) or filter air (FA) (n = 9/group) for 3 hours on the morning of proestrous and sacrificed 4 hours post-exposure. The hypothalamus, pituitary, ovaries, and small piece of frontoparietal cortex were harvested and pulverized. RNA was extracted to determine gene expression of GnRH1 (hypothalamus), GnRH receptor (GnRH-R) (pituitary/hypothalamus), and LH receptor (LH-R) (hypothalamus/ovary). Ovarian protein expression of StAR, HSD3B1, Pro-caspase 3, and progesterone receptor were detected through western blot. Blood was collected to determine serum hormonal levels of LH, FSH, estradiol (E2), and progesterone (P4). Three FA and 2 ozone treated mice were sacrificed the morning of estrus, blood was collected, serum hormonal levels calculated and ovaries histologically analyzed to determine the number of pre-ovulatory follicles and corpora lutea. Preliminary results demonstrate that ozone exposure in the afternoon of proestrous decreased gene expression for GnRH and GnRH-receptor in the hypothalamus, potentially affecting steroidogenesis and therefore also ovarian folliculogenesis. Upon completion of the project and attaining additional information from gene expression, protein content, serum hormonal levels, and histological analysis of the mice ovaries, a more complete understanding of ozone effect on the female reproductive axis can be achieved.

**SAT-340****RENAL POTASSIUM SECRETION INCREASES DURING HEMORRHAGE IN A RAT MODEL OF HEMORRHAGIC SHOCK**

Debby Lee<sup>1</sup>, Claudia A Hernandez<sup>2</sup>, Aileen K Sato<sup>2</sup>, Lee-Ann M Murata<sup>2</sup>, Catherine F T Uyehara<sup>2</sup>.

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Trauma is the leading cause of death in young adults worldwide, and up to 50% of these deaths involve hemorrhage. Hyperkalemia has been reported to be associated with non-survival of severe hemorrhage. During shock, urine flow is dramatically decreased, and thus, in order to maintain electrolyte balance, renal handling of solute secretion must be altered. In this study, we tested the hypothesis that the kidneys respond to hemorrhage by increasing potassium (K) secretion to prevent hyperkalemia. To elucidate the acute effects of hemorrhage on renal electrolyte regulation, we compared renal handling of K and sodium (Na) in conscious, chronically-catheterized rats (n = 4) before, during, and after hemorrhage (2 ml shed blood/100 g body weight (BW)). After 1 hour of sustained hypotension, rats were resuscitated with normal saline. With shock, urine flow dramatically decreased ( $15 \pm 5$  to  $4 \pm 1$  ul/min/100g BW) between

baseline and hemorrhage periods, and Na clearance also concomitantly decreased ( $14 \pm 4$  to  $3 \pm 1$  ul/min/100g). In contrast, we discovered that K clearance was maintained and urine K levels increased ( $103 \pm 22$  to  $177 \pm 25$  mmol/L). There was an increase in the trans-tubular K gradient ( $10 \pm 0.5$  to  $14 \pm 1$ ) suggesting a relative increase in renal tubular potassium secretion. Thus, increased tubular K secretion appears to play an important role in the regulation of K homeostasis during hemorrhage. This increase in K secretion may protect against hyperkalemia in hemorrhagic shock.

#### **FRI-342**

##### **CREATING AN ONLINE ONCOLOGY TRAINING PROGRAM FOR AMERICAN SIGN LANGUAGE INTERPRETERS: WORKING ON THE LEADING EDGE OF TECHNOLOGY**

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The National Association for the Deaf (NAD), Gallaudet University, Registry of Interpreters for the Deaf (RID), and the University of California, San Diego (UCSD) Moores Cancer Center developed an online oncology program for American Sign Language (ASL) interpreters and certified Deaf interpreters. This National Cancer Institute-funded training program's goal is to help RID-certified ASL interpreters across the country be more knowledgeable about cancer and more skilled in signing cancer information. This self-paced training program would also be of considerable value to non-certified interpreters, hearing family members of Deaf persons, and members of the Deaf community across the nation. Given the wide audience intended for this program, it needed to meet the constantly changing standards of the evolving technology and platforms. Desktop computers, laptops, notebooks, tablets, and cell phones were all desired as platforms for streaming the training program. Bandwidths changed allowing more options, old software evolved, and new software was constantly being developed. Compounding these challenges was the users' diverse levels of technological skills. This presentation will discuss how the users' needs inventory was developed and addressed over the years of the program's development, as the 50-hour program was created and videotaped in ASL. The training program is available on UCSD's Deaf-friendly website that includes other ASL cancer videos and the list of essential oncology terms.

#### **FRI-340**

##### **COMPETITION AND DIFFERENTIAL BINDING OF INTRACELLULAR CARGO TO KINESIN MOTORS**

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The environment within the eukaryotic cell is a continuous, dynamic system for which survival relies heavily on vesicular transport although the cargo-motor domain largely remains a mystery. A cargo-motor receptor, the amyloid precursor protein's COOH terminus (APP-C) has been shown to mediate anterograde transport of cargo in the squid giant axon via kinesin-1(KHC). However, jun-kinase interacting protein (JIP-1) also interacts with KHC by its COOH

terminus, which mediates transport of exogenous cargo. When JIP-peptide and APP-peptide conjugated beads are co-injected into an axon, transport efficiency diminishes for each bead type, suggesting competition for motors. We hypothesize that such competition results from relative binding affinity differences between different motors and different cargo. APP and JIP peptides were covalently conjugated to carboxylated magnetic beads, washed, and incubated with homogenized lysate from frozen rat brain. Proteins bound to beads were separated; unbound proteins left in supernatant were collected by 10% trichloroacetic acid precipitation. With equal amounts of starting material, beads and supernatant were run in parallel on SDS-PAGE, transferred to nitrocellulose, and probed for KHC and kinesin-3 (Kif1A). Bands were detected by enhanced chemiluminescence. Preliminary results show that APP-C pulls down more KHC than JIP-1, and JIP-1 pulls down more Kif1A than APP-C from the same lysate. These results suggest that JIP-1 and APP-C each favor a different type of motor despite their competition. Such information furthers our understanding of vesicular transport mechanisms and has implications for neurological disorders such as Alzheimer's disease. (Supported by NS062184, NS046810, MH096093, and the Harvey family.)

### **SAT-338**

#### **REGULATION OF MITOCHONDRIAL DYNAMICS AND AUTOPHAGY BY MCL-1**

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MCL-1 is an anti-apoptotic BCL-2 family protein and essential for normal cardiac function. Recent studies from our lab have shown that cardiac specific MCL-1 ablation leads to impaired autophagy and development of heart failure. However, little is known about the molecular mechanisms by which MCL-1 regulates mitochondrial function and autophagy in the heart. Preliminary data demonstrate that MCL-1 interacts with DRP1 and Parkin, proteins responsible for mitochondrial fission and mitochondrial autophagy (mitophagy), respectively. We hypothesize that MCL-1 recruits DRP1 and Parkin to mitochondria, facilitating mitophagy under basal and stressed conditions in the myocardium. We are currently investigating whether MCL-1 interacts with DRP1 and/or Parkin directly, using co-immunoprecipitation and co-localization experiments *in vitro*. Furthermore, we are investigating whether Parkin ubiquitinates MCL-1 to facilitate MCL-1 degradation. To evaluate this mechanism, we are studying whether MCL-1 levels vary in hearts from wild-type, Parkin-knockout, and cardiac-specific Parkin-transgenic mice. These studies will elucidate the mechanism of MCL-1 mediated mitophagy in the heart, potentially providing novel therapeutic avenues for cardiac disease.

**SAT-339****SM-P80 BASED VACCINATION REDUCES EGG-INDUCED PATHOLOGY & WORM FECUNDITY IN ANIMAL MODELS**

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Schistosomiasis, a neglected tropical disease, impacts nearly a billion people, with 240 million infected and an additional 700 million at risk worldwide in tropical and sub-tropical areas of developing countries with inadequate sanitation. The chronic form of this disease causes degenerative health impacts such as stunted growth, deformities, and loss of productive life years. Although there are preventive measures, health programs, and effective chemotherapy with praziquantel to deter this disease, the disease continues to spread. Furthermore, praziquantel does not address the possibilities for re-infection and drug resistance after treatment. However, there is a potential solution using a leading schistosomiasis vaccine (Sm-p80 vaccine), which has been shown and tested for its distinct prophylactic and therapeutic efficacies in animal models of infection and disease. Sm-p80 is the large subunit of *Schistosoma mansoni* calpain, a protein that plays an important role in surface membrane renewal, a mechanism widely considered to be used for evading host immunity by the parasite. In this study, we hypothesized that Sm-p80 based vaccine will reduce egg-induced pathology and female worm fecundity of *S. mansoni*. We compared liver tissue sections from vaccinated animals to non-vaccinated animals to test our anti-pathology efficacy hypothesis. Furthermore, we exhaustively analyzed data on female worm fecundity in the baboon model, comparing vaccinated animals to non-vaccinated animals. We observed distinct reductions in tissue pathology and in egg production following Sm-p80 based vaccinations in baboons. Based on these results, Sm-p80 is a strong candidate and should be further developed for human clinical trials in vaccinations against schistosomiasis.

**SAT-341****MECHANISMS OF NA<sup>+</sup> TRANSPORT INHIBITION BY HYPERTONIC SOLUTIONS IN HUMAN BRONCHIAL EPITHELIAL CELLS FROM CYSTIC FIBROSIS DONORS**

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Hypertonic saline inhalation therapy benefits cystic fibrosis (CF) patients. Surprisingly, these benefits are long-lasting and are diminished by the epithelial Na<sup>+</sup> channel blocker amiloride. Our aim was to explain these effects. Human bronchial epithelial (HBE) cells from CF donors were grown in inserts and were used to measure amiloride-sensitive short circuit currents ( $I_{Na}$ ), and transepithelial conductance ( $G_T$ ) and capacitance ( $C_T$ ). Hyperosmotic challenge (HC) solutions were prepared by either adding additional NaCl or mannitol to the isosmotic buffer or to a buffer containing a low (6 mM) Na<sup>+</sup> concentration (6Na-HC). Exposure to apical or basolateral HC inhibited  $I_{Na}$ , and  $G_T$  and exposure to apical HC also inhibited  $C_T$ . The HC-induced inhibition of  $I_{Na}$  was protracted and required 60 minutes of re-exposure to the isosmotic solution to recover 75%. Pre-incubation with amiloride significantly accelerated the recovery of  $I_{Na}$  following exposure to HC-NaCl but not when 6Na-HC was used. Apical or basolateral

membrane permeabilization using nystatin revealed that exposure to HC inhibited the apical epithelial Na<sup>+</sup> channels (ENaC) and the basolateral Na/K ATPase. Imaging the HBE membranes using fluorescent labeling suggests that exposure to HC induces membrane endocytosis. We concluded that Exposure to HC inhibits HBE I<sub>Na</sub>, probably by inducing endocytosis of apical ENaC and basolateral Na/K ATPases and amiloride diminishes this effect.

### **FRI-733**

#### **EFFECTS OF DIABETES ON RAT TAIL TENDON FASCICLE MECHANICAL PROPERTIES**

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Collagen is a protein and major constituent in the extra-cellular matrix of connective tissue acting as a load-supporting material. Chronic diabetes causes glycation, covalent bonding of protein or lipid molecules to sugar molecules without enzymatic control, to occur as a result of hyperglycemia. These modified sugars cross-link with collagen. As a result, collagen is less soluble in diabetic tendons creating less flexible and healing-delayed tendons leaving diabetics at a higher risk of tendinopathy. To assess the effect of diabetes on the mechanical properties of rat tendons, type-1 diabetes was induced by treatment with streptozotocin as a model for human diabetes related tendinopathy. The rats were categorized into 4 groups: acute diabetes, chronic diabetes, insulin-treated diabetes, and a control. Rats were euthanized and tails were frozen. Fascicles were extracted from tails. Mechanical properties of fascicles were then tested using a Deben micro-test rig linked to a computer-controlled motor to generate mechanical stress. Diabetic tendons withstood a higher maximum load than the controls. There are no statistical differences in the data, although max force and stress both produced a p-value of 0.06, suggesting a trend in which chronic diabetes seemingly produced the highest maximum load, stress, and strain. Our findings suggest diabetic-induced tendons produced stiffer tendons, perhaps due to cross-linking of collagen. Insulin-treated and acute diabetes seemed to minimize the effects of hyperglycemic glycation.

### **FRI-338**

#### **SEX-BASED DIFFERENCES IN METABOLIC RATES AND DAILY AND SEASONAL ACTIVITY IN THE COMMON CHUCKWALLA (*SAUROMALUS ATER*)**

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Rising annual temperatures resulting from climate change are expected to cause major extinctions of lizard populations by narrowing the window of time when daily environmental temperatures are suitable for activity. Understanding how lizards use this window of time and how their physiology may adjust to rising temperatures can help make better predictions of how lizard populations might respond to climate change. Using the common chuckwalla *Sauromalus ater*, a model will be developed to predict lizard responses to climate change based on ecophysiological parameters such as metabolic rates at various body temperatures and daily and seasonal activity. Data on activity and metabolism have been collected for male chuckwallas but remains unknown for females. Copper models of the same size, shape, and reflectance as the common chuckwallas will record the lizards' available thermal environment

throughout the active season using temperature data loggers. Temperature data loggers will also be used to record body temperatures of 8 female common chuckwallas throughout the active season and then compare them to the available thermal environment to determine their thermoregulatory behavior and activity. Metabolic rates will be determined using flow-through respirometry. It is predicted that females will be less active than males on a daily and seasonal basis and that metabolic rates at different body temperatures will not significantly differ between the sexes.

## ZOOLOGY/ENTOMOLOGY

### FRI-715

#### ASSESSING MULTIPLE-PATERNITY IN THE GREEN LYNX SPIDER *PEUCETIA VIRIDANS*

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In prior studies, Ramirez et al. showed that mating copulatory plugs are not consistently produced after mating, which leads in some cases to multiple paternity in *P. viridans* broods. To better estimate the potential for multiple paternity in *P. viridans*, we are now genetically assessing whether the progeny data best fit with a single male as the father or not, based on the analysis of 18 females and their brood spiderlings and using genotypes at 2 variable allozyme loci [lactate dehydrogenase (LDH) and phosphoglucose isomerase (PGI)]. We have examined 12 broods thus far, and 3 have either shown 3 paternal alleles or a significant deviation from a Mendelian genotype ratio for either LDH and/or PGI, given the adult female involved and her presumed male partner under a hypothesis of single mating. The low frequency of multiple paternity (2 of 12 broods) reported for this species by Ramirez et al. and by our current results (3 of 12 broods) may be due to limited opportunities to encounter multiple male partners. Specifically, Arango et al. found that the female/male sex ratio shifted from 1:1.5 in April to 1:0.1 in September at a site in Mexico. Hence, females reaching adulthood later in the year may have had access to fewer males at the Mexican study site. If a similar seasonal sex ratio shift occurs in Southern California, this may be partly responsible for the low frequency of multiple mating found by Ramirez et al. and in our current study.

### FRI-705

#### RATE OF INFECTION IN VECTORS OF *TRYPANOSOMA CRUZI* IN SOUTH TEXAS

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Chagas disease, considered a neglected tropical disease, is caused by the parasite *Trypanosoma cruzi* (*T. cruzi*). Chronic infection may lead to heart tissue damage and eventually death. The disease is principally transmitted by vectors and less frequently by blood transfusions, transplants, or congenital means. Members of the insect subfamily Triatominae, commonly known as kissing bugs, are the main vectors for *T. cruzi*. Insect population control is imperative for disease prevention. Although few disease cases are reported in the United States, distribution data illustrated an expansion in the vector occurrence in South Texas, where



poverty levels are the highest in the state. This could increase the population's risk for contracting Chagas disease since the kissing bugs in this region could be infected with *T. cruzi*. This study analyzed 96 insects (94 *T. gerstaeckeri*, 1 *T. lecticulata*, and 1 *Opisthacidius* spp.) from South Texas that were opportunistically collected by residents in domestic situations and by researchers in rural environments using dry ice traps. Infection status was determined using polymerase chain reaction (PCR) tests to detect *T. cruzi* DNA in kissing bugs' intestines. Preliminary results indicated an infection rate of 54%. This high infection rate suggests that residents of South Texas are at risk for contracting Chagas disease, and human cases could be going undiagnosed. Informational talks focused on preventive measures could create knowledge about the disease among medical personnel and the local community. Ongoing research includes blood meal analysis to detect *T. cruzi* hosts, and determination of *T. cruzi* lineages.

#### **SAT-706**

#### **DENSITIES OF THE LITTLE FIRE ANT *WASMANNIA AUROPUNCTATA* IN VARIOUS HABITATS AT THE LAS CRUCES BIOLOGICAL RESEARCH STATION, COSTA RICA**

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The little fire ant *Wasmannia auropunctata* (LFA) is indigenous to Costa Rica but poses serious economic and health risks in other tropical and subtropical regions of the world. Though small in size, LFA stings may cause blindness in animals, cause irritating rashes, or cause anaphylactic shock in the case of allergic reactions. However, in its native habitat in Central America, LFA populations rarely reach the high levels commonly encountered in habitats where they are considered exotic invasive species. This study provides insight into the population behavior of LFA in undisturbed and disturbed forest and grassland areas in Costa Rica with a view to understanding the forces that regulate its population in regions where it is indigenous and the absence of which allow it to become such a devastating, invasive pest elsewhere. LFA were collected from sifted leaf litter samples extracted using Berlese funnels. These samples were collected from 5 different habitats at the Las Cruces Biological Station in southern Costa Rica. These habitats were the Wilson Botanical Garden, secondary forest recently reclaimed from grassland, selectively logged secondary forest, grassland, and undisturbed primary forest. LFA density and the densities of all other ant species collected were determined for each habitat. LFA densities were higher in the secondary forest and grassland than in the primary forest where LFA was suppressed. Similarly, the number of other ants was lower in areas infested by LFA and higher in primary forest, where LFA densities were lowest.

**FRI-706****HOW INTERACTIONS IN ITHOMIINE AGGREGATION ARE INFLUENCED BY WING PATTERN, SPECIES IDENTIFICATION, AND GENDER**

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In the Ithomiine tribe of butterflies, there are different mimetic species and color patterns such as the clear-winged and tiger-striped. Species within the Ithomiine tribe execute a rare behavior of forming aggregation sites. An aggregation site is a place where many species of butterflies come together, which can help butterflies teach predators about unpalatability, defend themselves against predators, or attract mates for reproduction. The purpose of this research is to observe interactions in Ithomiine aggregation and how frequency of interaction is influenced by color pattern, species identity, and gender. We predict Ithomiine species will interact with conspecifics in the aggregation site. We observed Ithomiine interactions within the aggregation site every day for 6 weeks during sunny weather. When observing 2 interacting Ithomiines, they were caught, identified, tagged, and then released back into the aggregation site. We found that most interactions were between members of the same species and that most interactions were between males and females. This indicates most interactions within the aggregations are males and females of the same species courting each other. Other observations of interactions between males consisted of territorial behavior and/or confusion between different species that mimic the same color and pattern of Ithomiines.

**SAT-715****THE EFFECTS OF NECTAR ROBBING ON THE REPRODUCTION OF *CUPHEA RACEMOSA***

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We studied the effects of nectar robbing on the seed production of a population of *Cuphea racemosa* (Lythracea). This herb is found in isolated patches along open areas of Las Cruces Biological Station in southern Costa Rica. We observed that *C. racemosa* was visited by 2 *Meliponinae* bee species (Hymenoptera and Apidae), one of which robbed nectar from the corolla of flowers. Two out of 6 patches studied had evidence of nectar robbing. To estimate effects of nectar robbing on seed production, seeds from 50 fruits from each of the 6 subpopulations were counted. Feeding holes caused by the bees were also quantified within each subpopulation. Receptivity of the stigmas was determined using hydrogen peroxide as an indicator. We protected 15 flowers from robbing by using a small strip of masking tape around the corolla of the flower. The effects of nectar robbing on *C. racemosa* reproduction were then estimated by means of seed production or number of pollen grains on the stigma during the receptive period. To discard self-pollination or auto fertilization as a reproductive alternative in *C. racemosa*, 60 flowers from individuals in one of the patches were isolated with fine tissue bags. A treatment was randomly designated to a group of 20 flowers. Treatments were excluding pollinators, emasculation, and hand pollination with the own plant pollen. We expect to find no significant differences between the seed production of robbed and non-robbed plants. The results will be discussed in the light of plant reproduction strategies.

**SAT-738****PLEISTOCENE ENDEMISM IN *TAMIASCIURUS***

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Pleistocene climate cycles and glaciations had profound impacts on taxon diversification in the boreal forest biome. Tree squirrels of the genus *Tamiasciurus* present a notable opportunity to examine post-glacial diversification because of their ubiquity in temperate and boreal forests of North America. In particular, we explore the role of 2 archipelagos: one oceanic in the Pacific and the other skylands of the desert Southwest. Preliminary analyses of mitochondrial cytochrome-b sequences uncovered novel genetic diversity that indicates a potentially endemic lineage located in southeast Alaska and 2 others on sky islands of the southwest U.S. (Sacramento complex and Gila/Chuska complex). We are amplifying this study with additional individuals and additional independent loci to investigate regional endemism, potential gene flow, and conservation genetics. These isolated populations are of potentially high conservation concern, and our genetic assessments will be important for future management as well as informing us of speciation processes related to refugial endemism and connectivity.

**SAT-705****IN SEARCH OF INSECT VECTORS OF ANIMAL PARASITES IN ALBUQUERQUE, NM,  
PARTICULARLY *ONCHOCERCA LUPI* (FILARIAL EYE WORM OF CANINES)**

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An emerging infectious disease caused by *Onchocerca lupi* (filarial parasitic worm) leads to blindness in dogs in arid regions of NM, including Albuquerque. Resolving the parasite life cycle will provide information on epidemiology and potentially also on control strategies for preventing infections. Considering the life cycles of related filarial parasites, we hypothesize that study of blood feeding insects can identify the specific vector host that transmits *O. lupi* infection. Canopy light and CO<sub>2</sub> traps were used for weekly overnight collection of blood feeding insects from 7 Albuquerque city parks associated with confirmed cases of *O. lupi*-infected dogs. Captured insects were identified morphologically (family level) and stored in ethanol. DNA was extracted (DNAzol) from representative insects to generate 16S PCR amplicons for phylogenetic identification. Selected insects will be dissected, and DNA from pooled samples will be tested by PCR to investigate the presence of *O. lupi*. Samples will also be tested for additional animal parasites such as dog heartworm and avian malaria for which local insect vectors remain unknown. Trapping over 2 months yielded 23 mosquitoes (Culicidae), 123 black flies (Simuliidae), and 3,764 biting midges (Ceratopogonidae), relatively drought resistant insects. Morphological and sequence data from the 2 most distant sites indicate that 2 species of black flies and at least 2 species of midges occur throughout Albuquerque. BLAST suggests these represent new species. While it is attractive to consider the abundant midges as the more likely candidate vector for *O. lupi*, this remains to be tested by our continuing investigations.

**FRI-707****EXPOSURE OF JUVENILE *DAPHNIA MENDOTAE* TO 0.3  $\mu$ M METHOPRENE FOR 14 DAYS EXHIBIT DECREASED CHANGE IN BODY LENGTH COMPARED TO UNEXPOSED CONTROLS**

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Methoprene can accumulate in lake water systems as well as in its crustaceous inhabitants. The effects of this insecticide component have never been studied in *Daphnia mendotae*.

Methoprene is a known agonist of *D. magna*'s juvenile growth hormone, methyl farnesoate (Mf), which is involved in the biochemical pathways that result in the molting process and thus growth. We assume methoprene can likewise agonize Mf in its sister subspecies *Daphnia mendotae*. We hypothesized that *Daphnia mendotae* exposed to 0.3  $\mu$ M methoprene will exhibit decreased growth rate when compared to unexposed daphnids. We obtained our daphnid samples directly from Lake Mendota using a Schindler-Patalas trap. Daphnids were placed in 1 of 3 groups: the negative control group - 30 mL of autoclaved lake water, 0.3 mL algae daily, 25 °C temperature, and a 12 hour light/12 hour dark light cycle; the positive control/TBME group - control conditions plus 0.3  $\mu$ L tertbutyl methyl ether; and the Methoprene group - control conditions plus 0.3  $\mu$ L methoprene dissolved in TBME. Daphnids exposed to methoprene had decreased body lengths as well as lower fecundity than those exposed to either control conditions. Our results imply that methoprene/USP complex binds to ecdysteroid/ECR complexes that act as transcription regulators, thus decelerating the rate of molting gene transcription, which leads to reduced molting and therefore reduced growth rate. Because daphnids grow exclusively by molting, the accumulation of methoprene in amounts as little as 0.3  $\mu$ M in lake water can prevent the maturation of a lake's entire population.

**COMPUTER/INFORMATION SCIENCES****FRI-711****THE PREDICTIVE POWER OF FUNCTION WORDS FOR ATTRIBUTING AUTHORSHIP IN BIOMEDICAL ABSTRACTS**

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Statistically based authorship attribution methods have shown their merits as alternative yet compelling means of understanding individualistic styles of writing. The present study looks at the predictive power of function words for attributing authorship of biomedical abstracts from co-authored papers. First, a word frequency analysis of all targeted abstracts in PubMed produced the list of words used to determine authorship. After creating individual authorial fingerprints made up of an author's unique usage of function words in stand-alone works, 2 author's fingerprints were compared to the frequency of function words in their co-authored paper's abstract. This stylometric model was then applied to the 332,806 co-authored papers' abstracts found on PubMed in subsequent experiments that considered differing variables such as the particular words in the initial generated list and the baseline amount of abstracts required to create representative authorial fingerprints. The current findings suggest that applying separate standards to function word analyses heavily influences the separation of writer

invariance between two authors. Furthermore, the results support the notion that certain components of co-authored papers are truly didactic enterprises.

### **FRI-730**

#### **CONSISTENCY BASED MSA WITH GENETIC ALGORITHMS AND TABU SEARCH**

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The purpose of this project is to present a set of algorithms and their efficiency for the consistency based multiple sequence alignment (MSA) problem. Two types of MSA are considered: one with sequences not related to each other (no consistency) and another one with consistency. Based on the strength and adaptability of the genetic algorithm (GA), 2 solutions are developed depending on the MSA type. The first solution, GA\_TS, involves a hybrid genetic algorithm (GA) considering also tabu search (TS). The GA\_TS is based mainly on the TS, whereas the GA method generates new members in the population. TS comes with new types of switch operations. The traveling salesman problem (TSP) is also applied determining MSA orders. The second solution deals with a hybrid GA based on the divide and conquer principle (DCGA), and it can save space. A consistent dot matrices (CDM) algorithm discovers consistency and creates MSA using dot matrices. CDM, with its internal phase, can minimize the number of pairwise comparisons in MSA, thus giving a better performance. The proposed GA (GA\_TS\_VS) also uses TS but it works with partitions (vertical sections). Our experiment shows that the GA\_TS has better running time than GA. For sequences with consistency, the GA\_TS\_VS can outperform the GA\_TS solution. In conclusion, GAs are stochastic approaches that are very beneficial for MSA. The proposed set of hybrid GAs provides better results than the simple GA. The GA effectiveness is achieved with the cooperation of TS providing a more efficient local search.

### **FRI-710**

#### **METHODOLOGIES AND ISSUES IN THE USABILITY OF ANDROID APPLICATION DEVELOPMENT**

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Usability is a quality characteristic that focuses on users' positive and negative experiences of the interface and features which are crucial to a software's success, whether on a mobile device or desktop computer. For mobile devices such as tablets and smart phones, this is especially true due to their relatively smaller display screens, scaled hardware capabilities, and virtual keyboards. Through the lens of a campus Android application, this study explores how usability can be achieved at the implementation level while also satisfying the usability expectations of the Android application users. During the beginning stages of the usability process, the proposed application underwent requirement analysis to see what features were useful to the campus's targeted audience. Following the requirement analysis, a high-fidelity paper prototype was engineered as a way to test how intuitive, easy to navigate, and aesthetically appealing the application was to participants before implementation. Participants were asked to complete a 30 to 40 minute interactive session that was followed by a questionnaire which addressed 5 quality usability attributes: learnability, memorability, efficiency, error tolerance, and satisfaction. For the implementation process, MIT's App-Inventor, a novice programming environment

(NPE) which utilizes a block and drag-and-drop interface, was used to embrace and employ usability and interactive design when coding the Android application. This research introduced new methodologies and concepts in creating applications for both novice and experienced programmers, whether it be in NPEs or other interactive coding environments, and focused on usability trends in current application development.

#### **SAT-710**

##### **EXPLORING HANDLING LARGE AMOUNTS OF RADIO SCIENCE DATA USING OODT**

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For the modern astronomy and radio-astronomy working environment, software technology has been massively implemented to the point that analog hardware is being almost completely replaced for the advantages the former offers, including lower cost and space requirements. Recent advantages in technology and computing have allowed us to record at larger ranges of radio wavelengths using arrays of smaller antennas or fully steerable dishes. With this advantage comes a problem: how to efficiently manage the data acquired from the recordings. The central focus of this investigation is to use the Python programming language with a software tool (Apache's OODT) to develop data extractors for hdf5 and configuration files. In addition to this, we developed an extractor for files containing column data and a metadata extractor that can expose distinct errors in Python codes. The extractors were successfully created using Python and were tested in the OODT framework. For all of the extractors, each obtained information about key/value pairs and general information of the file, like filename, location, etc. Also, for each individual extractor, there were exclusive extractions like parameters, section-delimited key/value pairs, and refactoring notices. Overall, the extractor codes worked very well, but there were problems due to OODT's framework.

#### **FRI-709**

##### **HEARING AIDS SPECTROSCOPY TOOLS USING AN OPEN MULTIMEDIA APPLICATION PLATFORM**

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This ongoing research deals with the problem of designing a hearing aid system using digital signal processing techniques in order to address important issues such as providing algorithmic solutions with ease of programmability and reduced computational complexity. In particular, our research participation in this area centers on the optimization of signal processing algorithms to treat acoustic signals in order to reduce unwanted noise interference, enhance spectral characteristics, and improve precision of modeled electro-acoustic parameters by simulating hearing impairment. This work presents preliminary results in the area of simulation of hearing impairment using MATLAB® and the Open Media Application Platform (OMAP) developed by Texas Instruments. For algorithm implementation, we are using the OMAP-L138 C6-Integra DSP+ARM processing unit. The types of filters being implemented are causal finite

impulse response (FIR) filters. These filters were selected due to the fact that they are always stable and can be implemented indirectly using fast Fourier transform (FFT) algorithms. Special attention is being given to the analysis, design, and implementation of FFT algorithms used in hearing aid signal filtering techniques. The language of Kronecker Signal Algebra (KSA) is being used as a mathematical language to formulate the FFT algorithms and to assist as the overall signal processing algorithm development effort.

#### **SAT-729**

##### **A CPU SIMULATOR TO TEACH BASIC COMPUTER FUNCTIONALITY: DESIGN AND PILOT EVALUATION**

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Digital technology has had a huge impact on our lives, more than any other major innovation in recent history. It has made its way into almost every part of our lives and will only continue to change and grow. In fact, 1 million more tech jobs for computer science graduates are projected to be available in the next decade, yet only 10% of K-12 schools are teaching computer science. These statistics are evidence that more computer science curriculum is needed at an earlier age to attract more students toward computer science. Given the lack of qualified teachers, especially below the high school level, and the promising effectiveness of educational games, there is a movement toward the use of educational video games as learning tools. There are already plenty of games on the market that teach children the basics of programming; after all it is the proper introduction to computer science. However, as people often erroneously think, programming is not the only component to computer science. It is known among many programmers that, when first exposed to computers, they immediately started thinking about how a computer works and how you could make programs. For that reason, we have created a tutorial that teaches students at a very basic level how a computer works, with gameplay to reinforce learning. With this learning tool, we want to see if student interest in computer science is correlated with curiosity about computer functionality and programming.

#### **FRI-712**

##### **A FIRST STEP TOWARD EVALUATING THE IMPACT OF WIDE AREA DEPLOYMENTS ON THE INTERNET**

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The Internet topology is a hierarchical system of interconnected networks. These networks are known as large, mid-size, and small Internet service providers (ISP) such as Comcast, AT&T, and RCN. This Internet topology also includes consumers as well as content providers like Google, Yahoo, Facebook, and others. Consumers as well as content providers have always accessed the Internet via smaller ISPs, but recent studies have stated that access means have been changing. Furthermore, with the emergence of applications such as Netflix, large content providers may be deploying their own wide area networks so that consumers may be able to directly have

access to their networks instead of using small ISPs. We investigated if the conclusions of previous research have proven themselves to be enduring and continuing. We are interested to see what, if any, differences emerge in our data as compared to theirs, which was collected over 4-1/2 years ago. Our method includes automating the data collection and analysis process so it can be easily replicated. Our contribution is that we will also include consumers' or students' typical top ten go-to websites as a means of validating the trend previously found. We will analyze the data collected from the traceroute paths to determine a snapshot of the Internet topology. Our preliminary results show that the previous research findings have continued to hold during the ensuing 4 years, but we have discovered that some content providers changed affiliations with delivery networks.

#### **SAT-709**

##### **EVALUATING DYNAMIC STORYTELLING IN FABLES**

Carolynn Jimenez, Stephanie Lukin, Marilyn Walker.  
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Narrative structures are a predominant form of communication across many different cultures and are an active area of research. Automated generation of storytelling has many broad impacts in question answering, summarization, dynamic retellings of stories from different perspectives, and interactive narrative. We combine technology for natural language generation with a deep story representation called the Story Intention Graph to model classic narratives such as Aesop's Fables. Our ultimate goal is to develop technology that is capable of generating different tellings of the same story and answering questions about the story. We evaluate our approach using two web-based annotation experiments. The first experiment collects human perceptions of the semantic relations between events in the stories. Participants are required to select the best discourse connective, representing a semantic relation such as cause or contrast, between clauses in twenty Aesop's Fables. We use the results to train supervised learning algorithms for predicting discourse connectives when generating story retellings. The second experiment measures focalization in automatically generated narratives. Focalization in storytelling is the act of narrowing the perspective of a narrative to one character. Dynamic retellings of stories have been demonstrated to increase reader empathy for a focalized character. We plan to evaluate focalization through reading comprehension and dialogue completion tasks aimed at measuring empathy and perception of characterization. We predict that the focalized stories will elicit empathy for the focalized characters.

#### **FRI-731**

##### **EXPLORING PATTERN RECOGNITION TECHNIQUES ON BRAINWAVE DATA FOR HANDS-FREE AND GESTURE-FREE CONTROL**

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Synchronized electrical pulses resulting from neuron communication in the brain produce brainwaves that are detectable in the human head. Categorized by electrical frequency and



found in different sections of the brain, these brainwaves (alpha, beta, delta, theta, and gamma) correspond directly with neural activity and the voltage fluctuations of neurons in the brain. This research attempts to discover how brainwave patterns correspond with thoughts and desire for action to take place so that users can interface directly with applications without the use of conventional input devices. We hypothesize that a unique pattern of brain activity occurs when a user wants a similarly unique action to take place. This project uses the ThinkGear mobile bluetooth headset to collect brainwave data and associate wave patterns with commands used to control a helicopter through IR signals. In a previous experiment, we attempted to associate patterns with commands by making our program calculate averages over time during a calibration exercise and look for those same average wave patterns during the execution phase. This technique resulted in very low accuracy. Other methods to be tested include using a hit counter and algorithms similar those seen in fighting genre video games in order to recognize a pattern. Our goal is to create a brainwave pattern recognition algorithm that will allow a user to control our helicopter (and other devices) with hands and gesture free control.

#### **SAT-711**

##### **EMOTION RECOGNITION FROM FACIAL SKIN COLOR**

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Automated emotion detection is an important problem in computer vision, with applications in human computer interaction, psychology, surveillance, and other fields. Most approaches use geometric information, such as eye gaze patterns or positions of key facial points, to determine and classify human emotion. In this study, we use facial skin color as the source of information to infer the emotional state of a human being in the valence dimension (positive or negative reaction to an event, object, or situation). Facial skin color changes are caused by fluctuations in the concentration of hemoglobin and blood oxygenation under the skin, which vary depending on the emotional and physical state of a human being. We used a dataset that contains the median skin colors of the facial regions of 48 diverse subjects compiled over time as they were shown three different videos that intended to elicit the following emotional responses: positive, negative, and neutral. We performed experiments using various machine learning algorithms, including decision trees, support vector machines, k-nearest neighbors, and locally weighted regression. Preliminary results suggest that facial skin color can be a reliable source of information for emotion recognition in the valence dimension, yielding an accuracy of 74.19%.

#### **SAT-730**

##### **USING SIMD INSTRUCTIONS TO IMPROVE BIT PARALLEL ALGORITHMS FOR FINDING LONGEST COMMON SUBSEQUENCE AND EDIT DISTANCE**

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With the development of high-throughput DNA sequencing technologies, and the enormous data sets they generate, there is a great need for programs that can quickly compute sequence

comparisons. Longest common subsequence (LCS) and edit distance (ED) are two very common types of alignment algorithms useful for DNA sequence analysis. Standard LCS and ED programs have a time complexity of  $O(m \times n)$ , i.e., proportional to the product of the sequence lengths,  $m$  and  $n$ . A newer bit-parallel (BitPal) approach has been developed that is theoretically faster by a factor of  $w$ , where  $w$  is the computer word size, currently 64 bits. We are investigating the possibility that use of special 128 bit computer registers could further increase the speed of these algorithms. We are designing and implementing modified LCS and ED BitPal algorithms in the C programming language using advanced single instruction multiple data (SIMD) instructions with 128 bit words designed for recent computer processors. We are benchmarking our algorithms with runs of 1 million alignments. Our new SIMD LCS and ED algorithms have so far achieved 25.2% and 24.6% speedups with respect to comparable non-SIMD programs. Though the speedups we have observed are good, they are not as great as expected, possibly due to extra steps needed to initialize the SIMD instructions, which we are trying to minimize. In the future, SIMD instructions could be applied to more general alignment algorithms. Additionally, recent development of 256 bit SIMD instructions could be used to further increase speed.

#### **FRI-729**

##### **MATCHING VIDEO SEGMENTS WITH RELEVANT DOCUMENTS**

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The USC Shoah Foundation has collected over 52,000 video testimonies from survivors and other witnesses of the Holocaust. The goal of this project is to improve the learning experience for the people who watch the testimonies by integrating external knowledge to the archive. For example, if a person in a testimony is talking about his experience in the Warsaw Ghetto, we would like to display more information (e.g., a Wikipedia article) related to this topic next to the video. Since the videos are indexed by keywords for each minute of video, we use these data to extend various information retrieval methods to match each segment to a Wikipedia article. These methods include the vector space model approach, latent semantic indexing (tf-idf weighing) language models and topic models. Based on the existing techniques, we will propose a new method that exploits the metadata of the document corpus to match the video segments with relevant documents. One challenge of this project is that we are searching for the most relevant documents in a specific category (in this case, the Holocaust). We predict that incorporating query-expansion procedures to our methods by using definitions for each keyword and the information provided by the corpus' metadata will improve the performance of the standard methods in all cases. We will report results from this work.

**SAT-712****DEVELOPING AND CONDUCTING USABILITY TESTS TO IMPROVE WEB CONTENT DELIVERY OF USGS COASTAL HAZARDS SCIENCE**

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The United States Geological Survey (USGS) Coastal and Marine Geology Program has compiled multiple datasets on the nature of America's coastline, containing hundreds of scientific reports representing over 15 years of research, as part of its National Assessment of Coastal Change Hazards project. This includes data on extreme storms, historical shoreline change, and coastal vulnerability to sea level rise. This information has previously been made available to the public across nearly 20 different websites. In an effort to integrate this data into a unified location and streamline public accessibility, the USGS is developing a web portal where stakeholders, such as landowners, scientists, policy makers, or students, can quickly and easily view and interact with the data within a single user-friendly web application. As part of this effort, user testing was performed to help elucidate areas where design improvements would improve the web portal to increase its effectiveness in relaying USGS science to the public. Usability testing is the testing of a product or service with potential users to identify how to best develop a product to meet its goals. Eight participants were asked to complete scenario-based tasks on the web portal using written prompts. Post-test Likert scale evaluations provided further data about portal user experience and satisfaction. The tests are evaluated against the stated goals of the web portal, which include speed in finding information, clarity of information presented, ease of access for each user group, and user satisfaction. Test results are used to inform ongoing web portal development.

**EDUCATION****EDUCATION RESEARCH/ADMIN. (EXCEPT EDUC./SCHOOL PSYCHOLOGY)****FRI-101****EXAMINE DESCRIPTIVE PATTERNS AND DIFFERENCES IN COLLEGE STUDENTS' BELIEFS ABOUT THE NATURE OF SCIENCE, UNDERSTANDING OF EVOLUTION, SCIENTIFIC REASONING ABILITY, RELIGIOSITY, AND ACCEPTANCE OF EVOLUTION**

Stephanie Gutierrez, Ann Cavallo.

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Understanding evolution provides students with an underlying framework for the discipline of biology that is essential for understanding scientific concepts. According to many researchers and educators, the public's current understanding of evolution is considered to be significantly deficient. This study aimed to increase levels of understanding college students have about evolution and investigate how these understandings, along with views about the nature of science, scientific reasoning ability, and religiosity, may impact their acceptance of evolutionary theory. The specific purposes of this study were to explore patterns and differences in students'

understanding of evolution, views about the nature of science, scientific reasoning ability, religiosity, and acceptance of evolution; to examine interrelationships among students' understanding of evolution, views about the nature of science, scientific reasoning ability, religiosity, and acceptance of evolution; and to determine the best predictive model from among students' understanding of evolution, views about the nature of science, scientific reasoning ability, and religiosity on their acceptance of evolution. This research, conducted at a large research public university in the Southwestern United States, consisted of 100 undergraduate students of diverse backgrounds enrolled in various liberal arts classes with various academic majors and undergraduate levels. Questionnaires measuring the students' understanding of evolution, views of the nature of science, religiosity, and acceptance of evolution were given to the students. The results may help educators design better instruction that could aid in students' learning process and provide understanding of how these factors may hinder or support students' acceptance of evolution.

#### **SAT-101**

#### **DEVELOPING A SURVEY INSTRUMENT TO MEASURE PROBLEM PERCEPTION, TASK INTERPRETATION, AND PLANNING STRATEGIES WITHIN SELF – REGULATED LEARNING, A WORK IN PROGRESS**

Cory Ortiz<sup>1</sup>, Bao Pham<sup>2</sup>, Oenardi Lawanto<sup>1</sup>, Andres Febrian<sup>1</sup>.

<sup>1</sup>*Utah State University, Logan, UT,* <sup>2</sup>*Louisiana State University, Baton Rouge, LA.*

Many educational researchers are interested in self-regulated learning (SRL) as a process to increase the learning capabilities of individuals. However, there are currently no methods to measure SRL competence. The purpose of this research, then, is to develop a survey instrument that will measure how well first year college students incorporate SRL in problem solving. At the time of writing, this project is in progress. This abstract will discuss what has already been accomplished in addition to next steps. This survey instrument will be developed through verbal protocol analysis. As of yet, 5 individuals with an engineering background were recorded solving ill-defined math and engineering questions while "thinking out loud." In the coming weeks, the footage will be analyzed and encoded for specific verbiage that is correlated with planning strategies, task interpretation, and problem perception. From the data, we will derive the survey instrument questions. Future work will consist of validating this instrument, followed by pilot testing. The final goal of this project is to use a completed instrument in research about using SRL in problem solving.

## OTHER EDUCATION

### FRI-103

#### **UNDERREPRESENTED SCIENCE AND MATH MAJORS' PERSPECTIVES OF EXPERIENCES SUPPORTING THEIR MATHEMATICAL SUCCESS**

Erik Muntz, Sarah Oppland-Cordell, Joseph Hibdon Jr., Katherine Bird, Ruben Echevarria, Peter Stilling, Alejandro Sanchez.

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This project uses qualitative methods to examine perceptions of experiences that supported the mathematical success of 11 underrepresented science or mathematics majors. In this study, underrepresented students refer to Latina/o students who are also low-income and/or first generation college students. Questionnaire and interview data were analyzed to explore connections among participants' perceptions of experiences that supported their mathematical success, their racial identity constructions, and experiences they managed in various sociopolitical contexts. Drawing on critical race theory, cross-case analysis indicates 3 main themes regarding experiences that supported their mathematical success: experiences involving their personal agency and resilience, experiences that strengthened aspects of their academic identities, and experiences involving various in-school and/or out-of-school influences (primarily teacher influences, family influences, and academic resources). Such experiences that supported participants' mathematical success were complexly related to their racial identity constructions, the co-construction of their racial identities with other salient identities, and experiences they negotiated in multiple sociopolitical contextual layers. Examples of emergent connections between experiences that supported their mathematical success and their racial identity constructions included: resisting racialized experiences, functioning as cultural mathematical role models, and engaging with cultural academic role models. Participants' counterstories reveal how inequities, sociohistorical forces, sociopolitical constructs, contextual influences, agency, and resilience are intimately related to their mathematical success. Authors will present a video documentary that will highlight examples of such counterstories. This study is essential to help move the mathematics education community beyond explanations that normalize underrepresented student failure to understanding how and why they succeed in mathematics.

### SAT-103

#### **SCIENCE IDENTITY DEVELOPMENT OF STUDENTS IN STEM COURSES LED BY INTERNATIONAL FACULTY**

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One out of every two students who begin college in a STEM (science, technology, engineering, and math) major will switch out before graduating according to the Business Higher Education Forum. With the shifting modern economy having so much growth in the technology job market it is imperative that, as a country, we produce more STEM qualified graduates to stay a world leader. To increase the graduation rate of students in STEM majors, research must be

done to identify and combat the problems that are keeping students from graduating in these STEM fields. Other studies have found through quantitative means that a cultural barrier exists on many campuses between students and international faculty. Over the last decade the number of international faculty working in STEM fields has grown tremendously, yet one factor that has not been looked at is how the increase in international faculty members teaching in STEM fields has impacted students' development in STEM courses. Through in-depth interviews this research will explore how international faculty members can help or hinder a student's science identity. This phenomenological qualitative study will examine how students develop in courses led by international faculty and thus succeed in STEM courses.

#### **SAT-104**

##### **INTERPRETERS' KNOWLEDGE OF CANCER: PRELIMINARY RESULTS FROM THE ONCOLOGY TRAINING PROGRAM**

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The National Association for the Deaf (NAD), Gallaudet University, Registry of Interpreters for the Deaf (RID), and University of California, San Diego (UCSD) Moores Cancer Center developed an American Sign Language (ASL) Oncology Training Program for interpreters, funded by the National Cancer Institute. The self-paced, online training program's goal is to increase ASL interpreters' knowledge and skills when signing about cancer. The program is accessible to both hearing and Deaf interpreters. The training modules, training videos, glossary of oncology terms, and questionnaires are in English and ASL. IRB-consented RID-certified interpreters across the United States (n = 493) completed baseline surveys before beginning the training program. After completion of the approximately 50-hour training program, interpreters take a post-test to determine whether the program increased their cancer-related knowledge and to request their opinions and feedback related to the program. This poster will present an overview of the IRB-consented RID-certified participants' sociodemographic characteristics and baseline knowledge generated from the 85 true/false questions. The presenter will show several English items from the survey and their ASL translation and explain how that data will be used to evaluate the training program.

#### **SAT-102**

##### **A FEMINIST OF COLOR APPROACH TO DEFINING SUCCESS IN MATHEMATICS EDUCATION**

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With a very low representation of students from marginalized communities in higher level mathematics courses and mathematics-related careers, we consider how mainstream definitions of student success (based on grades, test scores, course-taking patterns, etc.) in mathematics affects how students perceive themselves in relation to mathematics and, in turn, how mainstream definitions deem this population "unsuccessful." The methodology for this

project was to explore explicit and implicit definitions of success based on what researchers wanted students to get out of their mathematics courses. We reviewed mainstream/dominant mathematics education articles and articles/chapters written by faculty who had long histories of studying marginalized students. Then we used theories from feminists of color to give new interpretations of how students and researchers negotiate and resist dominant discourses to provide alternative ways to define success for students of marginalized communities. The following questions were investigated: How are mathematics researchers defining identity and success? In what way(s), if any, are their definitions of success related to theories put forth by feminists of color who have focused more exclusively on issues of identity and liberation? What implications, if any, does focusing on identity and liberation have for improving teaching and learning for students of marginalized communities? We find that it is through social agency and the ability to negotiate different contexts that students, teachers, and researchers are able to define mathematical success beyond standard definitions. These findings and future work can help the latter groups assist students in having a more positive image of themselves in relation to mathematics.

## **FRI-102**

### **ASSESSING THE IMPACT OF A MULTICULTURAL ONLINE STEM COURSE ON STUDENTS' SCIENCE IDENTITY**

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The STEM (science, technology, engineering, and math) workforce in the United States has few individuals in underrepresented minorities (URMs; e.g., African, Latin, and Native Americans). This may be due to a lack of cultural support during students' education, which makes it difficult to self-identify as scientists. When cultural support is provided in a STEM course, there may be a greater commitment to a science career. This study will assess the impact of a multicultural online STEM course on students' science identity. We hypothesize that ultimately, non-White students will improve their self-identification as scientists. We conducted a pilot study of students ( $n = 11$ ) in a multi-institutional, online STEM course. A spring, 2014 quasi-experiment will be conducted on a larger number of students. The culturally sensitive course is offered at two mainstream and two Tribal universities. Pre- and post - course surveys are administered to participants. Student science identity will be assessed and analyzed by ANOVA. Due to the low number of pilot participants, statistical power was low. However, our preliminary data demonstrates trends. The post-course survey data show a weak trend that White students are more interested in STEM than non-White students ( $p = .80$ ). Furthermore, non-White students show a trend to self-identify as a scientist more so than White students ( $p = .31$ ). The preliminary trends suggest that a multicultural STEM course may play a role in students' science identity. URMs demonstrated a possible relation between their ethnic and science identities. The findings suggest that a culturally sensitive STEM course may positively affect students' scientific self-identity. The upcoming spring, 2014 intervention study will test this hypothesis.

## **FRI-104**

### **DEVELOPMENT OF A COLLABORATIVE LEARNING CLASSROOM**

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Collaborative learning, argumentation, and development of critical thinking are skills students need to succeed in the STEM (science, technology, engineering, and math) fields. These skills are necessary for enhancing academic performance and developing life-long learning skills. Collaborative learning is built on the ideas of inquiry, communication, and application. We converted a traditional lecture to a flipped classroom, taught as a collaborative learning course in an active learning with technology (ALT) classroom. The approach included online tutorial-based homework, in-class problem sets, and a combination of individual and collaborative assignments and assessments. Information about student motivation, study techniques, and exam scores were collected and analyzed based on the ALT classroom experience. Results from fall 2013 semester indicate active and reflective students have the potential to succeed in an ALT classroom. Students who objected to the collaborative approach and refused to participate performed poorly. Daily quizzes indicated students' attendance and engagement, which is reflected by Exam III scores. Fall 2013 semester course scores conclude that both active and reflective students can succeed in a collaborative learning environment. Further analysis is needed to establish efficient ways to motivate students, effective ways to connect with students, and solid structure so that all students feel they can succeed through collaborative learning. The American Chemical Society (ACS) analytical exam (standardized exam) has been administered as the final exam for this course over the transition from a tradition lecture to a collaborative learning environment. This exam tracks the effectiveness of the modifications to learning styles employed and compares to student performance nationally.

## **ENGINEERING**

### **AEROSPACE/AERONAUTICAL/ASTRONAUTICAL ENGINEERING**

## **SAT-906**

### **CLOSED-LOOP FEEDBACK TEMPERATURE CONTROLLED ENCASEMENT TO TEST OPTIMAL TEMPERATURE FOR POLY LACTIC ACID AND ACRYLONITRILE BUTADIENE STYRENE POLYMERS FOR THE PUNCHTEC CONNECT XL 3D PRINTER**

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There are a wide variety of 3D printers, most of which utilize acrylonitrile butadiene styrene (ABS) or poly lactic acid (PLA) as print materials. These polymer-based thermoplastics behave similarly yet adhere best in material-specific environmental temperatures. The objects produced the strongest prints when the environment was between 40 to 50 °C (104 to 122 °F). For this project, we analyzed and optimized the quality of the printed objects by creating an enclosed environment for a Punchtec Connect XL 3D printer. By utilizing an Arduino



microcontroller, CPU fan, thermocouple, LCD digital display, and heating elements, the temperature of the enclosure was controlled using a closed-loop feedback control algorithm. The CPU fan in combination with the heating elements caused heated air to flow into the enclosure, while the thermocouple measures the temperature near the part. Using the Arduino to interpret commands from the user interface, multiple temperature profiles can be set. The enclosure was constructed from acrylic and has a volume of 13,824 in<sup>3</sup>. Various quantitative tests were performed to compare an enclosed versus a non-enclosed system, which included resistance to delamination, surface roughness, linear resolution, and temperature precision to determine the quality of prints and the effectiveness of the enclosure.

## BIOENGINEERING/BIOMEDICAL ENGINEERING

### SAT-908

#### PERIODONTAL LIGAMENT CELLS IN TREATING DIABETIC PERIPHERAL NEUROPATHY

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Diabetic peripheral neuropathy (DPN) is a painful and slow-developing affliction caused by diabetes mellitus, often manifesting as hyperalgesia. In rats, damage to the peripheral nerves in the form of diabetic injury induced by streptozotocin (STZ) has been used as a reliable model for DPN. We wish to determine if injecting periodontal ligament stem cells (PDLSCs) near the sciatic nerves of rats will be effective in treating/alleviating DPN. To this end, our lab has induced 5 male Sprague-Dawley rats with diabetes, leaving 5 animals as controls, using a 50mg/kg dose of STZ injected intraperitoneally. Diabetes was considered induced if the rats had a blood glucose level above 250mg/dL. Pain-evoking behavioral tests were used to assess the development of hyperalgesia, began the fourth week after induction, performed on a weekly basis, and include the von Frey test, the Hargreaves test, and the acetone test. In the eighth week, saline was injected in the thigh muscles of the rats; PDLSCs will be injected in later groups. Testing then continued for 4 more weeks, after which the animals were euthanized. Our results suggest that the rats have been induced into a diabetic state as they experienced weight loss, hyperglycemia, and frequent urination. Although, a statistically significant change in behavior corresponding to DPN was not observed, increasing the sample size and STZ concentration will most likely remedy the problem. In conclusion, this project has allowed our group to produce a diabetic state and begin optimization of DPN conditions in rats.

### SAT-926

#### POLY(LACTIC-CO-GLYCOLIC ACID) MICROPARTICLE DELIVERY SYSTEM FOR THE DEVELOPMENT OF A PROTEIN-BASED CHAGAS VACCINE

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Chagas disease, a neglected tropical disease (NTD) caused by the parasite *Trypanosoma cruzi*, affects approximately 10 million people from which 20 to 40% present cardiac alterations that

can lead to heart failure and death. A promising approach against NTDs is the development of recombinant protein vaccines. Since the protein alone is poorly immunogenic, these vaccines require the use of adjuvants to enhance the immune response. Biodegradable polymeric microparticles (MPs) are used as a delivery system to potentiate the immune response by facilitating the access of antigen-to-antigen presenting cells (APCs). We studied the antigen depot effect of 50:50 poly(lactic-co-glycolic acid) (PLGA) MPs *in vivo*. Tc24, a *T. cruzi*'s 24k Da excretory-secretory protein, was labeled with Alexa fluoro 660 (AF660) fluorescent dye and encapsulated in PLGA MPs using a double-emulsion, solvent-evaporation method. To study the effect of MP properties, we formulated MPs with cationic surface charge using DEAE-dextran and slow degrading MPs using 85:15 PLGA. BALB/c mice were subcutaneously vaccinated with equivalent doses of AF660-Tc24. Our control groups included AF660-Tc24 formulated with Alhydrogel® (Alum) and AF660-Tc24 dissolved in PBS. Injection sites were imaged using a Lumina II *in-vivo* imaging system. The antigen concentration was measured over a month-long time course. Radiant efficiency counts indicate that AF660-Tc24 MPs resulted in a greater retention of antigen than PBS-AF660-Tc24 but lower than Alum-AF660-Tc24. Antigen concentration of PLGA50:50 MPs and cationic MP groups decreased in parallel. This study provides a better understanding of the properties of MPs and their effect on antigen retention.

#### **SAT-907**

##### **INTRODUCTION OF CANCER MUTATIONS INTO HUMAN CELLS**

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Gliomas are the most common malignant primary brain tumors diagnosed in the United States. They arise from 3 types of glia cells of the brain known as astrocytes, oligodendrocytes, and ependymal cells. Gliomas are classified according to their grade level. Grade 2 gliomas are known to be less cancerous and slower growing. On the contrary, Grade 3 gliomas are very cancerous and exhibit a malignant tendency. While grade 2 and grade 3 gliomas are known to be associated with mutations in genes *IDH1* and *ATRX*, the exact tumorigenic mechanisms of these mutations remain unknown. Using the CRISPR-Cas9 system, *IDH1* and *ATRX* mutations will be introduced into human embryonic stem cells. The construction and testing of special guide RNAs will be utilized to verify the introduction of the mutations at the sites of interest. Successful generation of embryonic stem cell lines carrying glioma mutations would provide an invaluable model system to study glioma development in the laboratory and develop new therapies for the disease.

**SAT-922****SYNTHETIC POLY(ETHYLENE GLYCOL)-OXIME HYDROGEL DOES NOT EXHIBIT CYTOTOXICITY OR CELLULAR INTERACTION**

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Hydrogels derived from natural or synthetic polymers have been utilized in many tissue-engineering applications including cell encapsulation, drug delivery vehicles, and space filling agents. Naturally-derived hydrogels have been used frequently due to their similarities in chemical structure to natural extracellular matrix. However, naturally derived materials exhibit predefined structure, limited physical properties, and, due to required synthesis from natural sources, batch-to-batch variability. A solution to these limitations is synthetically derived hydrogels where physical properties including degradation rate, stiffness, porosity, and gelation time can be controlled precisely. Previous studies have demonstrated the ability to synthesize oxime crosslinked hydrogels for cell encapsulation and injection through a catheter. Biocompatibility, specifically cellular interaction and cytotoxicity, of the synthetic poly(ethylene glycol)-oxime hydrogel will be tested at different functional group ratios. An agar diffusion test with L929 mouse fibroblasts will be utilized to test cytotoxicity, and a phalloidin stain will be used with 3T3 mouse fibroblasts and RAW macrophages to investigate if cells react with the hydrogel functional groups. The expected observation is that the synthetic poly(ethylene glycol)-oxime hydrogel does not exhibit cytotoxicity. Biocompatibility of the synthetic poly(ethylene glycol)-oxime hydrogel is crucial to assessing its potential for *in vivo* and *in vitro* use.

**FRI-915****QUANTIFYING DEPTH OF INJURY FROM NPE6-MEDIATED PHOTODYNAMIC THERAPY**

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The focus of this project is to try to quantify the depth of injury that comes from photodynamic therapy (PDT) when using the photosensitizer Npe6 from PDT histology slides. Photodynamic therapy is a treatment requiring 3 components: a photosensitizer, the presence of oxygen, and a continuous light source that can activate the specific photosensitizer. After the photosensitizer is administered, the light source is aimed at the vessels of interest which have absorbed the photosensitizer and allowed the photosensitizer to react in the blood. This causes oxygen to go from triplet state to singlet state, making it highly cytotoxic, killing the cells and blood vessels. The histology slides have been gathered from PDT experiments on rodents at different radiant exposures. A Point Grey FireWire Grasshopper camera, Photoshop, and Flycap software were used to translate the histology slides into digital images that will then be analyzed in hopes of quantifying damage to tissue in relation to the radiant exposures used to cause the injury. Specifically, the focus will be on observing changes between the different layers of skin, changes between normal and damaged tissue, and observing how the amount of

light that cause the injuries affects the depth of injuries since previous studies have shown that high radiant exposures can cause greater tissue damage.

#### **FRI-923**

##### **BIO-BASED NEW MATERIALS DERIVED FROM BA-, CA-, MG-TARTRATE/PHOSPHATE INTERACTIONS: NEW INSIGHTS IN SOL-GEL MATRIX DIFFUSION AND PHYSICAL DETERMINATIONS**

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Crystal growth methodology for metallic biomaterials has been extensively studied in our group over the past several years. Our current efforts involve Mg-, Ca-, and Ba-. The importance of these soft metals in the body stems from the fact they are bivalent ions that are used to form biomaterials such as hydroxyapatite  $[\text{Ca}_{10}(\text{OH})_2(\text{PO}_4)_6]$  within the bone matrix. They are also responsible for several metabolic processes within the soft and hard tissues. Today, different techniques have been used to prepare uniform particles. We found the sol-gel method advantageous for use in homogeneous solutions because of its experimental simplicity and its broad applications. This simple procedure allows critical honing of the synthesis route, and no special conditions are needed to do so. The aim of the present study is to grow magnesium-tartrate and phosphate biomaterial crystals by the single diffusion gel-growth technique and characterize them by several physical methods. Elemental analysis as well as FTIR, UV-VIS, TGA, and X-ray measurements show that the magnesium compound supports the proposed composition  $[\text{Mg}(\text{L-tart})_2 \cdot 4\text{H}_2\text{O}]$ . The as-synthesized micro spheres crystallize as a 2-dimensional, 6-sheet polymer, as determined by preliminary powder X-ray diffraction (PXRD) experiments that verify the crystallinity of the as-synthesized spherical materials. The experiments were conducted from  $2\theta = 10$  to  $70^\circ$  at  $0.040^\circ$  step size increments and a step time of 2 sec/step at room temperature (298.15 to 303.15 K).

#### **FRI-922**

##### **THE EFFECT OF NON-SYNONYMOUS MRP4 VARIANTS ON EXPRESSION**

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Multidrug resistance protein 4 (MRP4) is a transmembrane protein responsible for the efflux of a broad range of endogenous and xenobiotic compounds and has been found to play a role in cellular signaling, cellular toxicity, drug elimination, and antiviral resistance. The *MRP4* gene is highly polymorphic, and many nonsynonymous variants have been identified. Previous studies demonstrated that MRP4 variants differ in their ability to efflux antiretrovirals and marker substrates from the cell. One possibility is that these proteins may have altered overall expression or differences in trafficking to the cell surface. The E757K variant of MRP4 has previously been shown to have reduced membrane localization but no change in overall expression. However, this has not been tested for any other MRP4 variants. We hypothesize that some MRP4 variants will have altered expression relative to the reference sequence. To

test this, variants were generated via site-directed mutagenesis and transfected into HEK293 cells. Cell surface biotinylation will be used to pull down surface proteins, and western blot will be performed on both biotinylated proteins as well as whole cell lysates. Overall expression will be compared between variants, and the ratio between surface expressed MRP4 and total MRP4 will be evaluated. Understanding membrane expression of different MRP4 variants will help predict which variants are likely to cause reduced function. Reduced functional variants of MRP4 may contribute to interindividual differences in drug response and toxicity.

#### **FRI-921**

##### **ENGINEERING MEMBRANE TRANSPORTERS TO INCREASE THE AVAILABLE CYTOSOLIC ACETYL-COA IN *S. CEREVISIAE***

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The acetyl coenzyme A (AcCoA) molecule plays a key role in cellular metabolism in numerous pathways. As a link between catabolic and anabolic processes, AcCoA is an important starting point in the biosynthesis of many biotechnologically relevant metabolites, such as isoprenoids used as flavors and fragrances, biodiesels, and anticancer drugs. In the yeast *Saccharomyces cerevisiae*, AcCoA metabolism occurs in at least 4 subcellular compartments. Because the intracellular membranes are impermeable to AcCoA, no innate pathway exists for direct transport between compartments, limiting the biosynthesis of such compounds to the available cytosolic concentration of AcCoA where the pathway for their synthesis exists. Here, we aim to increase cytosolic AcCoA levels by using transporters to move the molecules from the mitochondrial compartment into the cytosol. The human AcCoA transporter AT-1, which moves AcCoA from the cytosol to the ER lumen, and a homolog (YBBR220C) in *S. cerevisiae* have the potential to fulfill this role. We investigate the insertion of targeting sequences for the mitochondrial inner membrane into AT-1 and YBBR220C under constitutive promoters of varying strength to properly localize these proteins. Thus far, fluorescence microscopy imaging confirms the correct localization of green fluorescent protein (GFP) to the mitochondria using the Oxa1p-targeting sequence. Restriction enzyme digest followed by agarose gel electrophoresis and DNA sequencing were used to determine successful plasmid recombination. Future work is aimed at correct localization of the transporters and will be important in assessing their ability to transport AcCoA into the cytosol to increase yeast metabolic production.

#### **FRI-919**

##### **INVESTIGATION OF THE CYTOTOXICITY OF COMMERCIALY AVAILABLE POLY(N-ISOPROPYLACRYLAMIDE)-COATED SURFACES**

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Poly(N-isopropylacrylamide) (pNIPAM) is a thermoresponsive polymer that undergoes a phase change at a physiologically relevant temperature range, which leads to cell release. Below its

lower critical solution temperature (LCST approximately 32 °C), pNIPAM becomes hydrated and is hydrophilic. In this state, its chains become more extended, and cells detach as intact cell sheets. Before the detached cell sheets can be used on humans, the cytotoxicity of the surfaces must be assessed. In previous studies, we found that although most techniques for polymerizing NIPAM, for example, plasma polymerization, ppNIPAM, and sol-gel preparations of NIPAM (spNIPAM), yielded biocompatible films, those from commercially available NIPAM (cpNIPAM) were relatively cytotoxic. In this work, we investigate the reasons behind this anomaly. The cpNIPAM-coated surfaces were evaluated for their thermoresponse and surface chemistry using standard surface science techniques (e.g., goniometry, X-ray photoelectron spectroscopy). The relative biocompatibility of the substrates with cultured bovine aortic endothelial cells (BAEC) and monkey kidney epithelial cells exposed to extracts from the cpNIPAM, spNIPAM, and ppNIPAM films was assessed using live/dead assays. In addition, the extract solutions themselves were analyzed by NMR and mass spectroscopy. We find that the diminished cell viability of BAECs exposed to cpNIPAM substrates is most likely due to a combination of factors, including the inclusion of short chain length polymers, the presence of unreacted catalyst, and other factors. This work will have valuable insights into the cytotoxicity of cpNIPAM-coated surfaces, and therefore, into the applicability of cells grown on this surface for human subjects.

#### **SAT-920**

#### **JET-PROPELLED SWIMMING BY SIPHONOPHORES, A COLONIAL GELATINOUS ZOOPLANKTON** **MC Hannon<sup>1</sup>, Kakani Katija<sup>2</sup>.**

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Siphonophores (Cnidaria: Hydrozoa) inhabit pelagic waters where representative species occupy depths ranging from the surface to the benthos. Three suborders of the siphonophoran clades exist: cystonects are surface dwellers and lack nectophores (swimming zooids); physonects bear many nectophores in their nectosome; and calycophorans, whose nectosome is comprised of up to 2 nectophores. The swimming mechanisms utilized by siphonophore nectophores to traverse depths in the ocean have been shown to influence their ecology and predation impact. Previous work has revealed a size threshold in hydrozoan swimmers (velar diameter > 5 mm) that causes a significant decrease in proficiency and decline of efficiency of jet propulsion. Siphonophore nectophores have relatively small exit diameters, and it is unclear as to where these organisms fall on the spectrum of jet-propelled swimming efficiencies and if there is a size-specific trend. Here we analyze the wake structures created by organisms in the two sub-orders, physonects and calycophorans, where the nectophore size represents different size classes (i.e., velar diameter < 5 mm and velar diameter > 5 mm). Using high-speed video analysis of nectophore contraction, the resultant fluid dynamic wake structure can be determined to inform the energetic cost and ecology of swimming siphonophores.

**SAT-913****PHARMACOLOGICAL INHIBITION OF 11 $\beta$  HYDROXYSTEROID DEHYDROGENASE TYPE 1 (11HSD1) AND THE BIOMECHANICAL TISSUE PROPERTIES OF SCARRED MYOCARDIUM**

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The inhibition of the 11HSD1 enzyme has been recognized as a potential novel therapeutic target for the treatment of myocardial infarction (MI). This study investigates the hypothesis that the pharmacological inhibition of the 11HSD1 enzyme will improve the local biomechanical tissue properties of infarcted (i.e., scarred) myocardium. We used normal and infarcted hearts from mice that were either untreated or treated with an 11HSD1 inhibitor compound at 2 doses. To evaluate the biomechanical tissue properties of mouse hearts, we excised them after a diastolic arrest and placed them onto an infusion system attached at the level of the mitral valve. Using a small cannula and a balloon, we inflated and deflated the left ventricle. We painted three dots onto the infarcted myocardial region of interest (scar), and we recorded the displacement of the dots during the inflation/deflation process in order to later transform their movement into 2 dimensional epicardial strains. Our results indicate that the stiffness of scar myocardial tissue from animals subjected to a pharmacological inhibition of 11HSD1 increases in a dose dependent manner as compared to the elasticity of untreated animals. These results suggest that the inhibition of 11HSD1 increases scar stiffness likely by enhancing the function of the cells that produce fibrous tissue. These actions may result in improved *in vivo* structure/function of infarcted hearts.

**FRI-909****DESIGNING MUTANT CATHEPSINS TO PROTECT AGAINST CATHEPSIN CANNIBALISM**

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Human cysteine cathepsins are proteases that are involved in the degradation of various proteins. The diversity of cathepsins is remarkable, particularly for their upregulation in tissue remodeling diseases such as cancer, atherosclerosis, and osteoporosis. Cathepsins also play a vital role in extracellular matrix degradation. Recently, a new phenomenon called cathepsin cannibalism has been discovered by this lab. Cathepsin cannibalism is the idea that one cathepsin species will preferentially degrade another species over the substrate protein. There are 11 different types of human cathepsins, but we focus on cathepsins K, S, L, and V because they are the body's most powerful collagenases and elastases. The objective of this project is to make mutant cathepsin K, L, S, and V that are resistant to cannibalism by other cathepsins previously studied in the lab. We are trying to create cathepsin K mutants that are resistant to cannibalism by cathepsin L, i.e., cathepsin L cannot degrade the mutant cathepsin K. We aim to create mutant cathepsin K proteins that are still catalytically active toward collagen and elastin substrates, but cannot be cleaved by other cathepsins. In order to create the mutant proteins, we performed site-directed mutagenesis using overlap extension polymerase chain reaction

(PCR). We designed mutagenic primers and, with multiple rounds of PCR, we were able to make mutant cathepsins. At the conclusion of the project, we will assay the cathepsins' activity using multiplex cathepsin zymography. Our findings will help to enrich the knowledge of proteolytic processes and the implications of the cannibalism in tissue remodeling and destructive diseases.

#### **FRI-906**

##### **REAL-TIME ANALYSIS OF PROTEASE SUBSTRATES USING FLUORESCENT PROTEIN PAIRS EXHIBITING FRET**

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Proteases are a diverse class of enzymes involved in several physiological interactions ranging from blood coagulation to apoptosis. Abnormal proteolytic activity has been shown to lead to diseases such as Alzheimer's and cancer. Because of this, studying the relation between proteases and their substrates allows for a better understanding of the development and treatment of diseases caused by aberrant protease interactions. Identification of protease substrates, however, remains one of the most daunting obstacles to understanding these interactions. Previous studies have used cellular libraries of protease substrates (CLiPS) to develop potential protease substrate motifs. However, this method is limited to *in vitro* analysis and does not offer information about a protease's catalytic activity with its substrates exclusively. To address this issue, we engineered protease substrates, FRET X<sub>1</sub>-X<sub>6</sub>, between the FRET protein pairs Cy-PET and Y-PET in order to measure the activity of a specific protease in tissue lysates. Fluorescent proteins that exhibit FRET are unique as they enable measurement of molecular-scale distances through changes in fluorescence. FRET-based approaches mitigate the difficulty of quantifying molecular concentrations, binding interactions, and catalytic activities of proteases. Here we demonstrate that this method allows for *ex vivo* measurement of protease activity from tissue lysates on a specific substrate sequence by assessing changes in fluorescence.

#### **FRI-911**

##### **EFFECTS OF OVER EXPRESSION OF ETS TRANSCRIPTION FACTORS ON EMBRYONIC STEM CELLS**

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The prevalence of vascular diseases and tissue ischemia in pathological circumstances raises a great need for a therapeutic population of endothelial cells (ECs) that form the internal layer of blood vessels. Embryonic stem cells (ESCs) are an attractive source for ECs because they are pluripotent and can be differentiated into ECs. However, current methods have a low yield and poorly maintain their identity. We hypothesized that overexpression of members of the E-26 (ETS) family, which have been shown to regulate vascular development and angiogenesis, may increase EC generation from ESCs and stabilize EC identity. ESCs were infected with lentiviral vectors encoding the ETS family members *Etv2*, *Erg*, and *Flt1* (EEF). At day 7, transcripts of EC



markers, *Vecad*, *CD31*, *Flk1*, *CD62e*, and *Tie2* were evaluated by QPCR. Surface protein expression of *Vecad*, *CD31*, and *Flk1* was also tested by flow cytometry. We observed an increase in all EC markers *Etv2*, *ERG*, *Fli1*, *Vecad*, *CD31*, and *Flk1* in the EEF-infected cells compared to controls. We isolated the *CD31*<sup>+</sup> fraction by FACS and, after differentiation, found that most EC transcripts were higher than in the *CD31*<sup>+</sup> population, except for *Etv2* levels, which were lower compared to the *CD31*<sup>-</sup> cells. However, *Etv2* levels were higher in the *CD31*<sup>-</sup> cells, suggesting that *Etv2* may block *CD31* gene activation. Future studies will explore the role that *Etv2* is playing in ESC differentiation. (Partially funded by GM007717.)

#### **SAT-919**

##### **CONTINUOUS FLOW CTC CELL LABELLING USING MICROFLUIDIC FLOW FOLDING TECHNIQUES**

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The study of circulating tumor cells (CTCs) from low volumes of patient blood can provide information on primary tumor characteristics, response to certain treatments, and mean survival time. This diagnostic tool requires separation of CTCs from other blood components and is based on manipulating the unique characteristics of CTCs (size, surface protein expression etc.). Cellsearch, the only FDA-approved CTC isolation device, is limited in that its function is only semi-automated, and the isolated CTCs are not viable after processing, making secondary analysis difficult. Microfluidic devices with functional requirements of high isolation purity, high separation efficiency, and high throughput processing are currently being developed to effectively isolate CTCs from blood. Microfluidic designs can either operate under passive and/or active mixing principles. Active mixers use external energy (i.e., electrical) to mix fluid flows, while passive mixers require no energy input and rely on channel geometry. Our passive mixing device is made using soft lithographic techniques and offers continuous on-chip labelling of CTCs with antibody-functionalized beads using various embedded groove flow-folding designs. This study characterizes the labeling efficiency of these grooved microchannels by combining separate streams of calcein-stained MCF7 cells and anti-EpCAM coated fluorescent microbeads in the flow. Video analysis using fluorescence microscopy allows for optimizing the groove pattern, height, and location within the microchannel in addition to flow rates. Future work entails using these optimized devices to label the CTCs with magnetic beads and manipulate the labeled cells using a magnetic tweezer/permalloy disk array to make downstream analysis possible.

#### **FRI-912**

##### **DEVELOPMENT OF CELL SHEETS FROM MAMMALIAN CELLS CULTURED USING VAPOR-PHASE DEPOSITION OF A "SMART" POLYMER**

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Poly(N-isopropylacrylamide) (pNIPAM) is a thermoresponsive polymer that is widely used in bioengineering applications. Although it is not the only polymer that responds to a stimulus

such as temperature, pH, light, or magnetic field, pNIPAM is of special interest due to the phase change that it undergoes in a physiologically relevant temperature range. The significance of this property is apparent in cell sheet engineering, where the thermoresponsive polymer allows cell sheets to detach from the surface while retaining most of their extracellular matrix proteins. We investigated this method of cell detachment by coating silicon and glass chips with pNIPAM using a plasma polymerization reactor. We then tested the thermoresponsiveness of the coated surface by taking contact angle measurements of the silicon chips at different temperatures using a goniometer. We then seeded bovine aortic endothelial cells (BAECs) on both the pNIPAM coated and uncoated control glass surfaces. After reaching confluence, we investigated the cell detachment from the pNIPAM coated surfaces against that of the control group by introducing cold serum-free media to well plates containing the cell cultures. By further analyzing the images using phase-contrast microscopy in half-hour intervals for 2 hours, we found that cells achieved successful detachment (71% detached) from the pNIPAM coated surface, most of which occurred during the first hour. The relevance of these results is manifest in one method of engineering tissues, which requires the layering and assembly of intact cell sheets.

#### **FRI-908**

#### **EXAMINATION OF DIVERSE 3-D MICROENVIRONMENTS USING ATOMIC FORCE MICROSCOPY**

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The physical parameters of the microenvironment, such as extracellular matrix (ECM) rigidity and ligand density, can govern cell migratory responses on simple 2-dimensional (2D) substrates. However, little is known about how a complex 3-dimensional (3D) ECM can impact cell migration. Atomic force microscopy (AFM) can image, with nanoscale resolution, both the topological and mechanical properties of biological samples in a fluid environment. Here, we measure the local physical attributes of 3D collagen gels to further our understanding of how the ECM can alter the mechanisms of cell migration. Through AFM, we explore the topological and mechanical properties of collagen with different architectures. Various gels were created by polymerizing collagen solutions (3 mg/mL) at different temperatures (37 °C, 21 °C, 16 °C, and 4 °C). This generated ECMs with different architectures. We used the AFM force-volume feature to capture force-displacement curves in 32  $\mu\text{m}^2$  areas for each gel. We obtained height maps showing local topographical features of the different ECM architectures together with mechanical properties derived from the full force-displacement curves. Analysis of the measurements showed an overall similar average elasticity for all the collagen gels at the macro/cellular scale. However, at the micron/cell protrusion level, while gels with homogeneous architectures (37 °C) showed relatively small changes in local stiffness or topography, heterogeneous gels (16 °C and 4 °C) demonstrated more than 10-fold local variability. These results show that the presence of stiff, parallel-bundled fibers can impact the properties of a 3D ECM. These differences within a 3D microenvironment have direct effects on cell adhesion and migration.

**SAT-912****NANODRUG COMBINED WITH ENERGY-BASED THERAPY OF CANCER STEM-LIKE CELLS**

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Cancer stem-like cells (CSCs) are rare subpopulations of cancer cells that are capable of self-renewal and differentiation into multiple types of resident cells in tumors. Mounting evidence shows that CSCs are responsible for cancer resistance, recurrence, and metastasis. These highly tumorigenic cells have been shown to be resistant to chemo and radiotherapies, making them difficult to treat using conventional approaches. Our preliminary data showed the effectiveness of several nanodrugs combined with thermotherapy on non-stem cancer cells, but the same therapeutics appear to be less effective in destroying spheroids enriched with CSCs, suggesting the resistance of this particular subpopulation of cancer cells. To resolve this challenge, we have developed a new multifunctional nanoscale therapeutic system using the anticancer drug doxorubicin for chemotherapy and photosensitizer indocyanine green (ICG) to achieve photothermal therapy. In addition, fullerene is also encapsulated to achieve photodynamic therapy with the generation of reactive oxygen species (ROSs) under near infrared laser irradiation. Results from cell viability assays indicate the destructive capabilities of this multifunctional nanodrug on CSCs. Further work is necessary to confirm our findings and to clarify the biological mechanisms of the synergistic effect of photothermal/photodynamic therapy in combination with chemotherapy. Overall, this novel therapy could contribute to the development of a combined cancer treatment modality for enhanced destruction of CSCs to overcome cancer resistance, recurrence, and metastasis.

**SAT-923****SYNTHESIS OF HEXA-PEPTIDE ANALOGUES TO OPTIMIZE CELL DISRUPTION**

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Cyclic peptides naturally occur in plants, fungi, and animals and have the potential to treat diseases. The purpose of this project is to optimize the bioactivity of a cyclic hexa-peptide that is known to disrupt cell division in certain cells. A set of side chain analogues will be synthesized using solid-phase peptide synthesis. The synthetic products will be analyzed by mass spectrometry, and their biological activity will be assessed in HeLa cells. Based on these results, a strategy will be developed to improve cyclic peptides as drug candidates by changing non-essential side chain amino acids and observing the effects on the disruption of the cell cycle. The outcomes will help future efforts toward improving this drug scaffold.

**FRI-913****GENETIC ENGINEERING OF ARCHAEAL FATTY ACID METABOLISM IN *HALOFERAX VOLCANII* FOR THE PRODUCTION OF BIOBUTANOL FROM CELLULOSE**

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In recent years, petroleum-based fuels have become increasingly difficult to obtain. They have also resulted in increased pollution due to their long carbon cycles as well as the increasing rate at which they are being burned. As a result the development of energy dense, shorter carbon cycled biofuels has become an increasing area of research. One such prominent biofuel is butanol, a 4-carbon alcohol that can be metabolized naturally from glucose in many microorganisms as well as from cellulose, a plant-based polymer consisting of  $\beta$ -glucose subunits. Industrial conditions required to produce butanol from cellulose at a scale equal to petroleum-based fuels require exposure to ionic liquids, a class of highly saline organic solvents that can be used to extract cellulose from plant materials, to which many of the mesophilic bacterial enzymes and hosts are not accustomed. Many archaeal organisms thrive naturally under these conditions and thus provide a distinct advantage, notably, the halophile *Haloferax volcanii*. Using *Haloferax volcanii* as a host, we intend to produce butanol from cellulose through the use of these ionic solutions in conjunction with modification of the pathway responsible for fatty acid synthesis. Within this pathway we have identified seven possible paralogous Acyl-CoA dehydrogenase genes (*acd1-acd7*), each thought to favor activity on certain fatty acid carbon chain lengths. By interrupting the *acd* responsible for the 4C (carbon) to 6C product, we can accumulate butyryl-CoA, a product which may later be converted to butanol through the overexpression of certain aldehyde dehydrogenases.

**SAT-909****LOW-COST, BIOCOMPATIBLE PACKAGING TECHNIQUE FOR IMPLANTABLE BIOMEDICAL DEVICES**

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Traditional commercial packaging for biomedical devices makes use of titanium as a biocompatible material, but this has expensive manufacturing costs and absorbs radio frequency (RF)-signal communication. Polymer-based packaging for medical devices *in vitro* has shown biocompatibility and wireless communication compatibility with low-cost manufacturing. Our studies present a packaging technique for micro devices that makes use of polymer-based packaging that offers longevity. This technique uses 5 layers consisting of polydimethylsiloxane (PDMS), Parylene C, and rigid acrylic. The fabrication begins with laser machining of the rigid acrylic case and Parylene C coating of the device. The casing is an assembly of three acrylic pieces: a 5mm spacer and two 2mm pieces for the top and base. The base is bonded to the spacer with acrylic adhesive and the Parylene C-coated device placed inside the casing. The casing is filled with PDMS that cures before the top acrylic piece is adhered. The casing is coated with a 32  $\mu$ m thick layer of Parylene C and placed in a mold to be

engulfed within PDMS, completing the manufacturing process. These packages were tested *in vitro* in a phosphate buffered saline solution at 40 °C and 80 °C representing body temperature and acceleration temperature, respectively. The phosphate buffered saline was dyed to expose leaking. Ten packages were placed in 80 °C and 9 in 40 °C. After 1 month at 80 °C, there were 2 failures due to leaking and 1 due to mishandling. There were no failed packages in 40 °C. Our studies show the development of a novel polymer-based packing technique useful at human-body temperatures.

#### **FRI-926**

##### **THE USE OF A SENSITIVE MICROSCOPIC PRESSURE SENSOR TO DETERMINE THE PRESSURE CHANGE FROM INTRANEURAL EDEMA RESULTING FROM AN INJURY TO A NERVE**

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Nerve injuries such as tensions or compression events can lead to intraneural edema and subsequent functional limitations. Intraneural edema is a watery fluid that builds up in the epineurium of the nerve after a nerve injury. Edema causes the nerve to render an abnormal amount of pressure which may prevent proper flow of blood and other viable nutrients that are pertinent to maintain a healthy nerve function. Human nerves can be extremely small, about the diameter of a pencil. The use of a sensor to determine the differential amount of pressure change that occurs when the nerve swells will help researchers understand nerve injuries more completely. Southern Methodist University developed such technology using the principle of whispering gallery modes (WGMs). The sensor is made of polydimethylsiloxane (PDMS) and can range from 50 microns to 1,000 microns in size. Pressure changes within a nerve are calculated by evaluating a change in radius of the sensor as small as 0.02%, which represents about 0.15 mmHg in pressure change. The technology behind the sensor is based on the amount of light captured in a translucent substance. The morphology of the transparent substance is based on the amount of pressure being subdued on the sensor. The sensor can measure the pressure by the refraction of light due to the morphology of the probe. Evidence has shown that the microscopic sensor is extremely accurate, and the use of this technology may help to obtain information regarding the pressure change resulting from the intraneural edema.

#### **FRI-925**

##### **DETERMINING THE EFFECTS OF SLIDING, LOADING, AND LUBRICANT OF CARTILAGE WEAR OF THE RABBIT HEMI-CONDYLE**

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Osteoarthritis (OA), or wear-and-tear arthritis, is the most common form of arthritis, known for its gradual fibrillation and loss of articular cartilage. The rabbit model for anterior cartilage ligament transection (ACLT) simulates many of the changes which occur in cartilage following an injury and in the development of OA. A quantitative imaging study using India ink-stained articular surfaces in the rabbit ACLT knee has revealed common regions of degeneration post-

surgery. Abnormal loading/sliding and joint lubrication may be the root of cartilage deterioration through direct mechanical wear or mechanobiological regulation. However, it is unclear what the systematic, structural, biochemical, or biomechanical causes are for the development of OA. The objective of this study is to complete a range-finding pilot study and establish parameters to generate time-dependent cartilage wear in a physiologically-motivated, *in vitro* wear test using the rabbit hemi-condyle. A pin-on-disc wear test system will be utilized to determine the effect of load with superimposed sliding and lubricant on the cartilage wear rate of a rabbit hemi-condyle. The pattern and extent of wear will be evaluated by imaging and biochemical methods. Fluorescence microscopy will be used to visualize cell organization and density. The amount of tissue released into the lubricant solution will be determined by glycosaminoglycan and collagen loss. Understanding the biomechanical and biochemical basis of cartilage wear may help us find better therapeutic methods to treat OA and other debilitating joint problems.

#### **SAT-915**

##### **REMOVAL OF ENDOGENOUS ESTERASE ACTIVITY IN *S.CEREVISIAE***

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The peroxisome is an organelle in the yeast *Saccharomyces cerevisiae* which can potentially be engineered to serve as an efficient, isolated reactor for proteins and chemicals. In order to use the peroxisome, we must learn about its membrane including the possible existence a pore of undefined shape and size. Esterases are useful for *in vivo* cell labeling and could be used to assay the permeability of the peroxisome membrane, but first we must identify the level of endogenous background activity. In *S. cerevisiae*, there are 6 endogenous genes which produce the background esterase activity. We aim to produce a yeast strain with no esterase background activity. We will remove the esterase genes and leave a barcode to identify the removed gene. This editing will be done using the new genetic engineering technology CRISPR/CAS9 (Jinek). Furthermore, we will use fluorescein diacetate (FDA) as a chemical marker to assess the permeability of the peroxisome membrane. FDA glows and changes from nonpolar to polar when reacted on by an esterase and is of a known size and shape. With these properties, it should be able to enter the peroxisome and, once reacted, fluoresce and not leave unless it is smaller than the pore.

#### **SAT-924**

##### **CELL SURFACE MECHANOSENSING**

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Cellular response depends on its environment. Mechanical properties of the environment have been of specific interest, stiffness being the most frequently cited of these. Cells are able to attach and live on hydrogels, the most frequently used being polyacrylamide. On polyacrylamide gels, changing substrate stiffness changes cell response; for example, spread area increases as stiffness increases. On polydimethylsiloxane (PDMS) substrates, however, cell

spread area is insensitive to substrate stiffness. We hypothesize that this difference is explained by the change in porosity between polyacrylamide and PDMS. To test this, we fabricated mixed media gels with a layer of polyacrylamide on top of PDMS. To change the degree of stiffness of the substrate, we varied the thickness of the polyacrylamide gel. For thin layers of polyacrylamide, cells sense the mechanics of the underlying PDMS. By changing the stiffness of the PDMS, we can independently change the effective substrate stiffness while maintaining constant porosity set by the polyacrylamide. Preliminary results have confirmed spread area behavior on pure polyacrylamide and PDMS with remaining experiments ongoing. When complete, our measurements will clarify the role of porosity in cell sensing of its local mechanical environment.

#### **FRI-910**

##### **HIGH-THROUGHPUT DRUG SCREENING *IN-VIVO* USING DROPLET MICROFLUIDICS**

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High-throughput biological assays, like cell-based drug screenings, conducted through various cutting-edge technologies have significantly advanced different areas of bio-medical research. Even though these technologies have become essential to the progress of scientific research, the costs associated are exorbitant. The effect of such costs limits scientific progress. Polydimethylsiloxane (PDMS)-based microfluidic devices provide a well-known lab on a chip technique where reagents may be combined in sub-nanoliter volumes in a fast and controlled manner. PDMS is a cheap, transparent, bio-compatible substrate that affords rapid prototyping and an efficient platform for drug screening. We use such devices to generate water-in-oil emulsion droplets at high throughput (approximately 5,000 drops per second) that efficiently encapsulate cells in the presence of drugs. The emulsion provides millions of individual reaction compartments for *in-vivo* drug screening assays at different physiologically relevant concentrations. Reducing the size of the reaction compartments to sub-nanoliter volumes allows us to be parsimonious with reagents, while the large number of droplets provide superior statistical resolution. In this project, we design, fabricate and use microfluidic devices to observe the efficacy of anti-cancer drugs in comparison to a commonly used chemotherapy drug, 5-fluorouracil (5FU), using a human cancer cell line (human lymphoblast) where the drug concentration is systematically varied. The effectiveness of the test drugs are estimated from the cell fates of the lymphoblast cells in each drop in their presence, using commercially available fluorescent reporter kits.

#### **FRI-924**

##### **DEVELOPMENT OF TARGETED MESOPOROUS SILICA-SUPPORTED LIPID BILAYER NANOPARTICLES FOR DELIVERY OF NUCLEIC ACID CARGO**

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Gene therapy remains a promising approach for treatment of a diverse range of diseases. However, providing reliable, cell specific delivery of nucleic acids to cells *in vivo* remains a

significant challenge. Improvement of gene delivery efficacy likely requires a greater level of control over cargo stability, cellular specificity, and gene integration and expression. Current non-viral methods of *in vivo* gene delivery in mice such as cationic liposomes, polymers, peptides, or other nanoparticle-based complexes, have emerged as safer and cheaper alternatives to their viral counterparts. However, maximizing efficiency and specificity while minimizing toxicity using these methods is currently limited. Mesoporous silica nanoparticles (MSNPs) serve as an attractive option for targeted interaction with cells due to their ability to undergo surface modification while maintaining stability. Having recently developed MSNPs with larger pore sizes, we have attempted to modify these particles to deliver nucleic acid cargos. We used cationically modified, torus-shaped MSNPs to deliver plasmid DNA to HeLa cells *in vitro* and highly vascularized chicken embryo tissue *in vivo*. Variables such as nanoparticle charge and size, DNA concentrations, lipid mixtures, and incubation times were explored to understand their effects on nucleic acid delivery. Currently, efficiencies greater than 50% have been achieved *in vitro* 24 hours after plasmid delivery. It remains the goal of this research to modify MSNPs to deliver genes to targeted cells with high efficiency *in vivo*. By developing a generic nucleic acid carrier, current gene delivery methods could be dramatically improved to achieve higher specificity and lower toxicity.

#### **SAT-925**

##### **DIGESTION OF POLLEN GRAINS IN PLASMA**

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Oral vaccine delivery has been a longstanding goal in the field of vaccination. Pollen grains (PGs) can be used as a novel material for oral vaccine delivery. In order to be used for vaccinations, it is imperative to determine what happens to the PGs once they enter the bloodstream. We expect the PGs that enter the bloodstream to get digested by the enzymes present in the plasma, thus enabling the release of their contents and facilitating their removal from the body. Our purpose was to determine the time needed to digest the PGs in plasma. For our experiment, we used mouse plasma and processed *Lycopodium clavatum* spores (LSs). The LSs and plasma were mixed and incubated in a 37 °C incubator for 24 hours. Then we removed the plasma from the LSs using water, ethanol, and acetone. We gathered SEM images of the pollens after they had dried. The images showed the pollens were not digested, but did look slightly worn. After observing the pollens that had been put in plasma and washed, we think the pollens could be digested if they were incubated for a longer period of time. Based on our results, we can say that PGs may get digested in plasma if incubated for longer periods of time.



**SAT-911****EVALUATING THE PRECISION OF T2\* MAPPING METHODS FOR MRI TISSUE CHARACTERIZATION**

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T2\* mapping is a widely used magnetic resonance imaging (MRI) technique for detecting iron overload in tissue. T2\* is the apparent exponential time constant of transverse relaxation estimated from measurement of MRI signal intensity. A non-linear regression is performed to estimate the time constant on a pixel-wise basis creating a T2\* map. The map is analyzed to find abnormally high iron concentrations that result from diseases such as hemochromatosis or thalassemia, which cause reduction in T2\*. Reliable identification of T2\* abnormalities is limited by measurement noise which reduces the precision of the T2\* estimate. Measurement precision depends on many variables including signal-to-noise ratio (SNR), T2\* length, echo times used in the measurement, and the specific regression method. T2\* measurement errors may affect the diagnosis between healthy and diseased individuals as well as the ability to track the efficacy of treatment for iron overload. We propose a method for evaluating the precision of T2\* mapping techniques by estimating the standard deviation (SD) of the T2\* based on the fit residuals which were transformed analytically to compute the parametric error. This method was validated by Monte Carlo analysis in which we measured the T2\* repeatedly ( $n = 64$ ) for a set of phantoms with varying iron concentrations. We compared the estimated and measured SDs and found them to be in excellent agreement with > 99% correlation. The pixel-wise SD map has the potential to improve confidence in the diagnostic assessment and is useful in comparing and optimizing imaging protocols for T2\* mapping.

**SAT-927****THE INFLUENCE OF HUMAN ACTIVITIES ON CORAL COMPETITION AND SURVIVABILITY**

Zengxing Pang, Christy Nguyen, Brittney Cox, Hristo Kojouharov.

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Coral reefs play a vital role in maintaining the balance of the ocean's ecosystems. In the past few decades, these underwater structures in the Caribbean have sustained substantial damages from human practices such as overfishing and agriculture runoff, which consequently disrupts the previously balanced interactions between corals and their competing species. As a result, coral coverage is experiencing rapid declines, allowing competitors to become more dominant in the region. To contribute to solving this ongoing issue, we are modeling changes in the populations of corals and 3 of their major competitors near Jamaica: macroalgae, turf algae, and sponges. Adding parameters to represent the effects of human activities on these species, we can run simulations to estimate how the corals will continue to survive under the influence of current practices. Further, to gain a better understanding of the competition dynamics, we are conducting analysis on our model of 4 ordinary differential equations by solving for equilibria values and determining their stabilities. In addition, by finding sets of parameter values that optimize coral resilience, we can propose methods to restore coral reefs through altering human conduct in the Caribbean.

**SAT-910****MODIFICATION OF HEMATOPOIETIC STEM CELL DIFFERENTIATION USING INHIBITORS OF HISTONE MODIFYING ENZYMES**

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Hematopoietic stem cells (HSCs) uniquely possess the ability to self-renew and produce all blood lineages. During differentiation, key changes in chromatin occur as HSCs differentiate toward final mature lineages; their relatively open chromatin converts to increasingly more closed heterochromatin. To identify the role of specific chromatin modifiers during HSC differentiation, inhibitors were used to target histone and DNA methylation. We focused on 4 chromatin-modifying inhibitors: SGI-1027, EPZ-5676, Decitabine, and DZNEP. In addition, we used inhibitor UNC0638 as a comparison for the other inhibitors. *In vitro* treatment of HSCs with UNC0638 shows an increase in stem/progenitor cells, defined as ckit+lin-Sca1+ (KLS) cells. UNC0638 targets the G9a histone methyl transferase, G9a-mediated methylation of histone H3 promoting heterochromatin formation. Each inhibitor was combined with UNC0638 to investigate whether our observed accumulation of KLS is specific to G9a inhibition. To test whether the accumulated KLS cells were functional hematopoietic stem and progenitor cells, we transplanted these populations into irradiated mice and analyzed their ability to reconstitute mature blood lineages. Cell sample data for the mice with just the UNC0638 drug confirmed that the cells are, in fact, KLS cells. Each of the other 4 inhibitors show similar results but at a much lower KLS percentage and, when treated in sync with UNC0638, the KLS fraction represented the same results as those of the UNC0638 only. These results highlight the importance of G9a in the transition from HSCs to more mature lineages and emphasize the role of chromatin condensation during stem cell differentiation.

**FRI-907****REPROGRAMMING OF ORANGUTAN FIBROBLASTS FOR INTEGRATION-FREE INDUCED PLURIPOTENT STEM CELL LINES**

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Understanding neural development has been a key to solving the mystery of what makes humans so different from other primates. Our lab has developed a pluripotent stem cell cortical neuron differentiation protocol that recapitulates many of the earliest events of cortical brain development in a cell culture dish using both human and rhesus macaque cells. We wanted to add pluripotent stem cell lines from great apes, since they are more genetically similar to humans than rhesus macaque and could point to more recently evolved features in human brain development. As embryonic stem cell lines are not available for great ape species, we have turned to engineering induced pluripotent stem cells (iPSCs) from orangutan fibroblasts. Using the same transcription factors Takahashi et al. used in 2007 to reprogram human fibroblasts into an embryonic-stem-cell (ES) like state, our aim is to create a comparative model for development between multiple primate species. In the process, reprogramming protocols

were applied to primary fibroblast cultures from Sumatran and Bornean orangutans provided by the San Diego Frozen Zoo collection. Although episomal transfection and Sendai virus transduction methods were tested, only the Sendai virus transduction was successfully used to generate integration-free iPSC cell lines. Our characterization of these orangutan iPSC cultures demonstrates their utility as a source of pluripotent stem cells for comparative analysis of neural differentiation with a variety of primates. This project represents the first step toward comparative studies using *in vitro* models of development within the great ape lineage.

#### **FRI-914**

##### **USING WEIGHTED GENE-CORRELATION NETWORK ANALYSIS TO IDENTIFY GENE CLUSTERS OF SIGNIFICANCE FOR HEAT, SALT, AND DROUGHT RESISTANCE IN *P. TRICHOCARPA***

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Hybrid poplar trees are one of the fastest growing biomasses used for biofuel production. The large land and water demand by poplar trees however has pushed interest in growing biomass crops in more marginal land that is drier, warmer, and could have more saline soils. In order to better understand the mechanisms of abiotic stress response in poplar, we investigated gene expression pattern changes in poplar tissue types in response to these stresses. Gene coexpression associated with drought, saline, and heat resistance in *P. trichocarpa* was investigated using Weighted Gene Co-Expression Network Analysis package run in R. Triplicate gene expression values for over 10,000 genes were found using RNA-seq from root tissue under drought, salt, and heat stress. We used 2,300 of these genes with statistically significant differential expression to examine the utility of WGCNA to identify clusters of genes that are significantly correlated in expression when responding to heat, salt, and drought stresses. Preliminary results examining root samples of *P. trichocarpa* under these stress conditions identified 8 distinct clusters of genes, 5 of which were specifically correlated to drought, saline, or heat stress conditions. Many genes in these condition-specific clusters were significantly upregulated. In the future, data from root, xylem, and leaf tissues will be analyzed for gene coexpression at different times to analyze the difference in stress responses in different tissues. These gene clusters will then be examined for their biological importance as well as their response similarities and uniqueness with respect to different stress conditions.

#### **SAT-921**

##### **ULTRASOUND-MEDIATED TRANSFORMATION OF *CHLAMYDOMONAS SP***

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Biotechnology can be used to manipulate microalgae to produce desirable recombinant proteins such as insulin. Efficient and stable transformation is therefore essential for the successful generation of transgenic microalgae and remains an area of intense research. This study introduces ultrasound-targeted microbubble destruction (UTMD) as a technique for transferring DNA into eukaryotic microalgae cells. To validate and optimize this novel method

of transformation, our study used green fluorescent protein (GFP) and focused on 3 key transformation parameters: voltage input, algae density, and microbubble input. Fluorescent microscopy, qPCR, and western blotting were used to optimize the UTMD technique. Lower voltage input, lower algae density, and higher bubble input have been shown to be the most optimal parameters through correlational analyses. Our data demonstrated 85 times higher than typical rate of transformation of *Chlamydomonas* sp. with the GFP reporter. With this novel and optimized method of transformation, we hope to advance the power of biotechnology and microalgae to enhance the manufacturing practices of industrial, nutritional, and biopharmaceutical products.

#### **FRI-920**

##### **ACELLULARIZED HEART TISSUE FOR DELIVERY OF FUNCTIONAL CARDIOMYOCYTES**

Alejandra Preciado, Kara McCloskey.

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Cardiovascular disease is the leading cause of death in the United States, often due to myocardial infarctions. During myocardial infarction, cardiac cells are deprived of oxygen and die. This ischemic tissue becomes a scar in the heart and can no longer contract with the rest of the heart, weakening the heart's ability to pump blood. Tissue engineering approaches are currently being investigated as reparative/replacement therapies for the broken heart. Various biomaterials for cell delivery have been explored; however, most of these methodologies use either single cell populations and/or single biomaterial systems. A highly functional cardiac tissue patch requires combinations of factors, including biomaterial architecture, material strength, compliance, cell patterning, and incorporation of multiple cell types. In order to address this chasm, our group has developed a tissue delivery system that incorporates combinatorial synthesis of acellularized tissues, moldable hydrogels, cell patterning, and cell-sheet engineering to develop an organized patch for treating myocardial infarctions based on the hypothesis that alignment of cardiomyocytes will increase patch integration, cellular retention, and cardiac function. The acellularized porcine heart tissue addresses many of these design concerns, providing increased compliance, material strength, and architecture for cell patterning. This project will slice porcine heart tissue, acellularize the tissue, examine the biomaterial for removal of all porcine cell products, and seed and attach human cardiac cells. This material will then provide a base for the cardiac tissue graft being developed in the laboratory.

#### **CHEMICAL ENGINEERING**

##### **SAT-928**

##### **MINIATURIZED ANTIMICROBIAL SUSCEPTIBILITY TEST**

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Effective treatment of bacterial infections relies on timely diagnosis and proper prescription of antibiotic drugs. We propose a simple microfluidic device to perform on-chip antimicrobial susceptibility testing (AST). A microfluidic device (20 x 20 mm) is constructed for determining

the concentration level of antibiotic that inhibits bacterial growth. We miniaturized AST by combining a concentration gradient generator with cell-culture chambers. A gradient delivery system supplies 7 reservoirs (30 nL) each of whose concentrations vary by a factor of 2. An eighth reservoir is used as a control. The material of the device, namely polydimethylsiloxane, allows for oxygen diffusion which promotes rapid bacterial growth inside the device. Tests were performed on a 20  $\mu$ L sample of *E. coli* ATCC 25922 using ampicillin and streptomycin. The minimal inhibitory concentration could be determined in 3 hours, which is almost a factor of 10 more rapid than standard broth microdilution antimicrobial susceptibility tests. This microfluidic device has the capacity to prevent the intake of ineffective antibiotics by providing quick and inexpensive measurement of the concentration of an antibiotic drug that will suppress bacterial growth. This could help prevent the spread of bacterial resistance or further exacerbating the infection.

### **FRI-931**

#### **DELIVERY OF OVALBUMIN THROUGH MICRONEEDLES TO PREVENT OVA ALLERGY IN MICE**

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*Texas Tech University, Lubbock, TX.*

Worldwide, approximately 30% of the population is affected by IgE mediated allergies. Disease modifying treatments, such as specific immunotherapies, are a common way to treat them. Specific immunotherapies typically involve repeated subcutaneous administration of allergens with gradually increasing dosages. Once a dosage reaches its optimum level, it is then given repeatedly, every month, for 3 to 5 years. Repeated allergen injections may cause inflammation, irritation, and sometimes anaphylaxis in severe conditions. Moreover, a low number of patients prefer immunotherapy with antihistamines and other steroids. The cellular mechanism of specific immunotherapy is also still unclear. Therefore, specific immunotherapy use requires good expertise and consultation. In the last few years, non-invasive and painless immunotherapies have been introduced in order to treat allergies effectively while simultaneously reducing patient discomfort. Generally, they include oral, sublingual, and epicutaneous ways of allergen administration to the body. In this perspective, we are proposing painless, epicutaneous delivery of ovalbumin allergen through microneedles to prevent OVA allergy. The epidermis is a rich source of dendritic cells, which are professional antigen-presenting cells that induce immune response against the allergen. Microneedles have been designed to address need and supersede the hypodermic needles. These are micron-scale needles measuring only 50 microns thick. They are minimally invasive and only penetrate the stratum corneum. In our initial experiments, microneedle arrays were coated with ovalbumin antigen on microneedles and delivered in mouse skin repeatedly at different times. Immune responses in serum will then be evaluated through enzyme linked immunosorbent assay.

**FRI-930****INCREASING PRODUCTIVITY OF ALGAL BIO-MASS CULTURE FOR BIO-CRUDE OIL PRODUCTION**

Tim Torres II, Peter Lammers, Nicholas Csaken.

*New Mexico State University, Las Cruces, NM.*

An alternative to fossil fuel oil is to generate crude oil from plant material such as algae. Algae also convert carbon dioxide (CO<sub>2</sub>) into oxygen via photosynthesis, increasing its utility as a green-energy source. Scaling cultivation is difficult due to water and sunlight exposure requirements. We estimate approximately 30,000 acres of land is needed to grow enough algal biomass to supply the closest small oil refinery in California. The growth footprint could be reduced if we grew algae at greater water/media depths (increasing the volume) and if evaporation was reduced by enclosing the culture in bags. We chose a known robust strain of algae that originates in hot springs. Our setup includes 2 separate 10 feet x 5 feet bioreactor bags with a paddle wheel and moat system to mix growth media and algae. The bags are fed 2 L/min of CO<sub>2</sub> and air mixture in the same light and temperature environments. We are looking at growth rates of algae at 10 cm and 20 cm depths, holding other variables constant. We observed self shading and decreased temperatures in the 20 cm bag, reducing growth rates by 36%. By doubling the volume, the rate decrease still produced 2 g/m<sup>2</sup>/day more biomass. We know that biomass can be grown at higher aerial productivity by increasing the depth of bioreactors. However, the point of diminishing returns has yet to be reached. We hope to experiment with increased depths and other sunlight exposure techniques reducing the footprint even more, making algal biomass a viable feedstock for the production of bio-crude oil.

**FRI-929****ENGINEERING NANOPARTICLE SHAPE FOR INCREASED ADHESION ACROSS THE INTESTINE THROUGH DRUG DELIVERY AND TRANSPORT**

Jessica Wong, Amrita Banerjee.

*University of California, Santa Barbara, Santa Barbara, CA.*

Oral delivery of drugs to the small intestine is an important topic in the research and development of more effective oral dose forms. Pills offer a non-invasive and patient-compliant way of delivering drugs. However, the disadvantage of oral drug delivery reflects the fact that achieving the desired biodistribution of drugs in the body is limited by the body's natural metabolic processes and transport barriers. Uptake of macromolecular drugs across the intestine is very low due to low permeability of the mucosal membrane and susceptibility of drugs to enzymatic degradation. Our lab has developed small organic polymers as well as novel polymer devices to protect the drug in the stomach and promote their adhesion on the intestine, which enhances oral bioavailability. Our research aims at developing a fundamental understanding of these transport barriers using *in vitro* models. In particular, we study, using experimental and theoretical tools and methods, the effect of chemical penetration enhancers on drug transport across the intestine, exploring the effect of various particle shapes and distinct characteristics on the performance of nanoparticles. Our lab hopes to show the

influence of shape in polymeric nanoparticles on the various processes of adhesion and targeting which are exploited for enhanced targeting.

#### **SAT-931**

##### **STUDYING INTERMEDIATES OF OLEFIN METATHESIS USING PARAHYDROGENS TO INDUCE HYPERPOLARIZATION**

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*University of California, Los Angeles, Los Angeles, CA.*

Olefin metathesis is an important reaction in the petrochemical industry, which provides high energy hydrocarbons that are used in everyday life. The reaction takes two smaller carbon chains and connects them through their double bond creating a longer hydrocarbon chain with high energy. In order to develop an efficient, synthetic alternative to our diminishing natural supply, understanding the mechanism and the intermediate molecules of the olefin metathesis reaction are needed. This knowledge will allow us to prepare a continuous-flow alkane metathesis reaction that would be beneficial to the industry. Dimethyl acetylenedicarboxylate was hydrogenated with parahydrogens and then pushed in the reactor in an NMR magnet. Inside the reactor, the dimethyl maleate (after hydrogenation) will undergo olefin metathesis catalyzed by Grubb's catalyst. Using NMR spectroscopy and gas chromatography mass spectrometry, we will determine the optimal conditions and mechanism of the metathesis reaction. By using parahydrogens during the metathesis reaction, we observed a heightened signal approximately  $10^2$  -  $10^4$  times stronger and sharper in contrast to orthohydrogens. The double bond in the catalyst attached to our reactant creates a unique, intermediate molecule that is visible in the NMR machine with a hyperpolarized signal. The experiments gave us a good understanding of the mechanism and conditions under which the metathesis is more efficient. These results can help in developing these longer hydrocarbon chains and biofuels through alkane metathesis and other catalyzed reactions that produce efficient, clean energy.

#### **FRI-927**

##### **STUDIES OF STERIC AND ELECTRONIC BEHAVIORS OF PALLADIUM COMPOUNDS BONDED TO DIPHOSPHORUS**

Stephanie Pacheco, Quinetta Shelby.  
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The overall goal of our research is to produce a palladium catalyst that has been proven to effectively control the stereochemistry of its product. Its effectiveness will be expressed through the reaction of allylsilanes and aldehydes. This reaction will show the efficiency of the catalyst by producing its product with a desired, specific stereocenter. This catalyst would be able to affect the reaction greatly and still be regenerated since it is not directly influencing the reaction it aids. Having a diphosphorus compound that is negatively charged has been proven to be a better method to synthesize the desired palladium diphosphine dimer. This dimer compound is the only one known in which the ligands are unsymmetrical and not neutral. This gives the desired negative charge needed since it is known to be the better method of synthesis. Therefore, the focus is on unsymmetrical diphosphine ligands that contain only

aromatic substituents with different electronic and/or spatial character to further examine conditions that favor the diphosphine becoming negatively charged. Having completed 3 reactions out of the 5 necessary, we have produced a relatively pure product with a 26.5% yield. The next step of this reaction sequence is to increase the purity of the third reaction product as well as the percent yield.

#### **SAT-932**

##### **ENGINEERING OF TRANSGENIC OUTPUTS FROM THE INTERLEUKIN-6 RECEPTOR**

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Cytokine release syndrome (CRS) is a potentially fatal toxicity that can be triggered by bacterial and viral infections, the administration of immunotherapeutics such as antibodies, and adoptive T-cell therapy. A key component in both the onset and the intensity of CRS is increased serum levels of the immunoregulatory cytokine interleukin-6 (IL-6). When IL-6 binds to the IL-6 receptor (IL-6R), gene-expression of acute phase proteins (APPs) is upregulated by the transcription factor STAT3, causing inflammation. Previous studies show the antibody tocilizumab blocks IL-6 signaling by binding competitively to IL-6R. The aim of this study is to change the genetic output of IL-6 signaling to the production and secretion of a tocilizumab single-chain variable fragment (scFv) that can block IL-6 signaling and ameliorate CRS. Specifically, a DNA plasmid encoding a secretable form of tocilizumab scFv behind a synthetic, STAT3-inducible promoter is being constructed. The presence of IL-6 is expected to trigger IL-6 signaling, resulting in STAT3 activation and induction of the STAT3-responsive promoter, ultimately leading to scFv production and secretion. The scFv blocks further IL-6 signaling, thereby downregulating APP production and alleviating inflammatory damages associated with CRS. The efficacy of this system will be evaluated using HepG2 human hepatoma cells, which produce the acute-phase protein  $\alpha$ 1-antichymotrypsin. This research aims to develop an approach to alleviate CRS and enable more cancer treatment options such as adoptive T cell therapy for patients who currently cannot withstand CRS.

#### **SAT-929**

##### **ENGINEERING OF RECOMBINANT CELLULOLYTIC COMPLEXES FOR BIOETHANOL PRODUCTION**

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<sup>1</sup>*University of Miami, Coral Gables, FL,* <sup>2</sup>*University of Michigan, Ann Arbor, MI.*

The finite nature of fossil fuels is an urgent problem due to their central role in modern life. A promising alternative is the use of genetically modified organisms (GMOs) that break down cellulosic biomass, the most abundant form of sugar on earth, and convert it to biofuels. We are working on constructing a recombinant protein complex for this purpose. The complex consists of several different enzymes that are attached to a protein scaffold through highly specific protein-protein interactions. The enzymes are expressed in *Escherichia coli* while the scaffold, which has already been constructed, is expressed on the surface of *Saccharomyces cerevisiae*. The protein complex attaches to cellulose, and the enzymes break cellulose down to simple sugars, which are converted to ethanol by *S. cerevisiae*. The protein scaffold places the



enzymes in close proximity to each other, causing them to work in synergy. We engineered several different cellulases appended with domains that bind specifically to the protein scaffold, expressed them in *E. coli*, purified the enzymes, and examined their functions through activity assays. The work to construct the full protein complexes is in progress.

#### **SAT-930**

##### **MAKING DROPS MOVE FASTER, THE ROLE OF TOPOLOGY ON PEM FUEL CELLS**

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<sup>1</sup>*California State University Los Angeles, Los Angeles, CA*, <sup>2</sup>*Princeton University, Princeton, NJ*.

Polymer electrolyte membrane (PEM) fuel cells can contribute to the production of clean energy for power and automotive applications. PEM fuel cells separately react hydrogen and oxygen on either side of the PEM. Hydrogen is oxidized to protons at the anode. Protons are conducted through the PEM to the cathode where they react with oxygen to form water. Water must be removed to avoid blocking the flow of oxygen to the cathode. The removal of liquid water from the gas flow channel is a major challenge for fuel-cell engineers. We have observed how the topology of the surfaces in the flow channel affects water drop detachment and motion by examining water drop growth and movement over corrugated surfaces. Water flows from a 1/64-inch hole and forms a drop on the plate with a patterned surface. The pressures for drop detachment and drop sizes have been monitored with pressure transducers and photography as a function of the tilt angle for the plate. Elucidating the physics of drop detachment and motion will allow for a more efficient engineered PEM fuel cell.

#### **CIVIL ENGINEERING**

#### **SAT-934**

##### **COLUMN-BEAM CONNECTION TESTING FOR A NONLINEAR MOMENT-RESISTING STRUCTURE**

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Earthquake-induced soil liquefaction is the process in which the relative strength and stiffness of soil decreases due to large cyclic earthquake motions. When this happens, the ability of the soil to support the foundations of structures decreases, leading to detrimental damages on surrounding infrastructure such as foundation settlement, tilting, and damaging of underground facilities. The objective of this research is to analyze how ground accelerations within liquefiable soils affect the performance and damage potential of inelastic structures. In order to achieve this goal, physical and numerical modeling of a 3-story, nonlinear, moment-resisting frame is being developed in order to evaluate its behavior on liquefied ground. Geotechnical centrifuge and connection tests of our frame are being conducted to give us a clear understanding of the relationship between ground shaking, liquefaction, building displacements, and building damage. Prior to the complex centrifuge tests of the entire soil structure system, we will conduct scaled component tests of a beam-column connection at 1 g with no centrifuge acceleration. These tests will help ensure that our scaled frame holds similar structural characteristics to those of real buildings, especially in terms of strength, stiffness, degradation, and ductility. We also are developing numerical modeling of our 3-story frame and beam-column connection on SAP2000 and OpenSees in order to have a sufficient amount of

data to compare between our numerical and physical models. Our research will be used in future centrifuge tests of liquefaction impacts on soil and structures in order to further develop mitigation techniques for this important hazard.

### **SAT-933**

#### **SEISMIC RESPONSE OF BASE ISOLATED BUILDINGS WITH RUBBER BUMPERS CONSIDERING POUNDING TO MOAT WALLS**

Carolina Jauregui<sup>1</sup>, John Sanchez<sup>2</sup>, Gilberto Mosqueda<sup>1</sup>.

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Base isolation, also known as seismic isolation, is a simple and effective method used to reduce the damage to buildings and other structures. A base isolation system decouples the superstructure from the ground, which results in a longer period and a reduction in the acceleration transferred to the superstructure during a seismic event. For this decoupling to occur, there needs to be empty space, known as the moat, so that the superstructure can move sideways without hitting the surrounding moat wall. Structural design codes regulate moat wall gap distances so that the building will not hit the moat wall, but despite this there have still been cases of pounding on moat walls during earthquakes. The goal of this project is to verify whether rubber bumpers will serve to reduce the seismic response of a building when pounding occurs. This project builds off of prior research that involved shake table tests using medium rubber, stiff rubber, and no rubber bumpers around a three-story base isolated intermediate moment resistant frame (IMRF) model. The base-isolated IMRF model was chosen due to the simplicity of fabrication and the facility of acquiring the necessary members. This project uses the data from the accelerometers and string potentiometers placed at each story to calculate the acceleration and drift ratio of each story. It is expected that the rubber bumpers will decrease the acceleration and drift ratio.

### **FRI-934**

#### **ASSESSING THE BENEFITS OF RAINWATER HARVESTING ON STORM WATER AND WATER SUPPLY OF AN INSTITUTIONAL WATERSHED IN SAN ANTONIO, TEXAS**

Paul Martinez, Marcio Giacomoni.

*The University of Texas at San Antonio, San Antonio, TX.*

With the ever increasing scarcity of water, it is becoming more urgent to communities all over the world that action be taken to properly manage our water resources. Low impact development is a way to develop as necessary while lessening the impact on the natural hydrology through the use of technologies such as rainwater harvesting systems, which can implement previously unused runoff. The purpose of this study is to determine the potential benefits in harvesting and using rainfall from rooftops in commercial and institutional buildings in San Antonio, Texas, for the purposes of landscape irrigation. The research methodology will be developed through the use of hydrologic simulation modeling. Hydrological simulation modeling represents the physical processes of storm water runoff based on inputs including but not limited to rain intensity, duration, runoff surface properties, and catchment size. Data will also be corroborated with historical rainfall time series and geographical information system

(GIS) data to develop catchment areas, which are then corroborated with other modeling software such as EPA-SWMM, with integrated applications that account for rain water collection. If rainwater harvesting systems are seen to be beneficial and are implemented, it could be a successful showcase to potential investors, architects, and engineers or anybody interested in obtaining the same goal of similar development while efficiently managing our water resources.

#### **FRI-933**

##### **EVALUATING EFFECTS OF DELAYS ON REAL-TIME HYBRID SIMULATION OF SEISMIC RESPONSE OF LARGE CIVIL STRUCTURES**

Jolani Chun-Moy<sup>1</sup>, Jasmine Flores<sup>1</sup>, Tania Martinez<sup>1</sup>, Amado Flores<sup>1</sup>, Cheng Chen<sup>2</sup>.

<sup>1</sup>*Cañada College, Redwood City, CA,* <sup>2</sup>*San Francisco State University, San Francisco, CA.*

Analyzing and evaluating the seismic response of large-scale civil structural specimens can be very costly and difficult. One alternative to testing large-scale specimens is real-time hybrid simulation, which is an experimental method to evaluate structural dynamic behavior by combining physical and analytical models. Therefore, only parts of the structures are experimentally tested. However, time delay, which reduces the accuracy of the experimental results, is inevitable due to the actuator hydraulics. The purpose of this project is to evaluate the effects of delay by comparing delayed and actual responses. MATLAB and Simulink are used to simulate the analytical and the experimental model responses for different cases of degradation. For 100 ground motion records and a maximum considered error, critical delay is calculated and its lognormal distribution parameters are determined. Therefore, knowing the actuator's delay and using a log-normal distribution graph of the critical delay, the probability that experimental error is less than the target error can be determined. This project not only allowed exposure to civil engineering concepts and practices through the perspective of earthquake engineering, but also provided useful teamwork skills. While working on the project, team members developed their time management and teamwork skills by corroborating their individual findings and preparing group reports.

#### **FRI-944**

##### **USING GREEN BUILDING MATERIALS TO FABRICATE SANDWICH PANELS FOR STRUCTURAL USE**

Cristhian Santos, Yeira Barajas, Jin-Lee Kim.

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Important ecosystems are being destroyed because of the high demand for lumber. There is a need to research alternatives that will provide us with options for replacing or drastically reducing the consumption of lumber as one of our primary materials for construction. If a renewable, green panel is achieved, it will significantly reduce the alarming rates of deforestation. The purpose of this study is to construct a wall panel made completely of renewable green resources to reduce carbon footprint and to eliminate the use of precious reserves that will run out in the foreseeable future. Green building materials such as bamboo, burlap, and coconut fiber present a sustainable and ecological method for achieving the use of

composites for structural purposes. An exciting aspect of this study is the use of new and improved green resins which are stronger than resins used in previous works. These previous sandwich panels have proven to have various flaws mainly because the bonding substance is insufficiently strong to hold the panel or core properly. To make this experiment successful, the panel should be comparable to wood panels available today. We will use coconut fiber and a soy protein resin as the core. The facing of the panels will be made of woven bamboo and burlap. The testing results will be presented according to ASTM standards.

#### **FRI-932**

##### **EFFECTS OF RUBBER IMPACT ABSORBERS ON THE RESPONSE OF BASE ISOLATED STRUCTURES IMPACTING SURROUNDING MOAT WALLS**

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Base isolation is a method to protect a structure from seismic activity by installing isolator bearings beneath the structure that help absorb the energy from ground motion. Base isolation is used to protect the structure from failure and damage in high ground accelerations and is mainly used in important structures such as hospitals, city halls, or nuclear power plants. A seismic isolation system is typically installed in the basement level, with moat walls surrounding the building providing a gap to allow movement during seismic activity. In high ground accelerations, this movement can be dangerous as it could impact the moat wall, thereby increasing the building response acceleration, and possibly leading to building collapse. Shake table tests have been done on a moment-resisting frame model with and without rubber dampers on the moat walls. Rubber dampers were placed to absorb energy from moat wall impact and decrease the response acceleration. We analyzed the rubber damper test data and performed modeling using OpenSees to identify correlations.. We compared the results of a ground acceleration including maximum drift, acceleration per floor, and floor response spectra, for the different cases and examined the severity of the damage to the building. After a comparison of the results, we concluded that rubber dampers used in moat walls during seismic activity in base isolated structures were significantly beneficial in reducing accelerations but they tend to increase story drift demands.

#### **COMPUTER/SYSTEMS ENGINEERING**

#### **FRI-938**

##### **PROPAGATION CHARACTERISTICS OF HETEROGENOUS COMPOSITES OF MATERIALS AT 60 GHZ**

Francisco Romero<sup>1</sup>, James Martin<sup>2</sup>, Robert Brodersen<sup>2</sup>, John Wawrzynek<sup>2</sup>.

<sup>1</sup>*University of Southern California, Los Angeles, CA,* <sup>2</sup>*University of California, Berkeley, Berkeley, CA.*

In order to model 60 GHz antenna environments, the reflective properties of building materials need to be understood. This work focuses on understanding millimeter-wave radio frequency

propagations and interactions with several heterogeneous composites of building materials. In particular, we are studying the reflective power as a function of the incident angle. To characterize the materials, we have developed a novel, automated mechanical setup to precisely control the incident angle. The setup also permits us to control the transmitting and receiving units independently or concurrently. The results are presented in graphical and tabular form for analysis and comparison to previous works.

#### **FRI-935**

##### **A MOBILE APP FOR REDUCING PATIENTS' WAITING TIME AT PHYSICIANS' OFFICES**

Katya Borgos, Nestor Rodriguez.

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Prolonged waiting times at physicians' offices have a negative effect on patients. This is a serious problem that may result in physicians losing patients. However, thanks to the advancement of information technologies, this problem can be effectively tackled. Our approach for a solution to this problem is to provide patients timely information about the time to service on the appointment day so that they can decide the proper time to move to the physician's office. The system consists of 3 main components: 1) a web app at the physician's office that continuously calculates an approximate time to service for each patient registered on the day of the appointment; 2) a mobile application that allows patients to make appointments and receive notifications about the time to service on the day of the appointment; and 3) a database that connects the mobile application and the web application. This presentation focuses on the mobile application (2). Through its main interface, the system keeps patients updated on their scheduled appointments. Patients can make appointments with any physician registered in the system and check in on the day of the appointment. On checking in, timely notifications of the time remaining for service would be provided.

#### **FRI-939**

##### **AUTOMATIC PARALLELIZATION OF JAVA PROGRAMS AT THE BYTECODE LEVEL USING TRACES**

Francisco Rodriguez, Vijay Garg.

*University of Texas at Austin, Austin, TX.*

We propose an automatic parallelization approach for Java programs at the bytecode level using traces. With the increase of multi-processor computers, parallel programming has become increasingly popular because a sequential program does not take full advantage of the multiple cores available. But writing a parallel program can be time consuming and difficult considering the numerous issues that arise from concurrent executions. From dependencies to mutual exclusion, issues in parallel programming are difficult to debug because of their irregular execution pattern. In order to liberate the software developer from these burdens, automatic parallelization has gained ground as a possible solution through the use of compilers, a set of programs that translate source code into machine code. Experimenting at the bytecode level presents the primary advantage of not having to examine the source code. The experiment is based on the Jikes Research Virtual Machine and tested on the Java Grande Benchmark suite. Overheads and speedups were compared across platforms and thread count

while relying on run-time information collected during program execution. This information was then used to dynamically recompile the Java bytecode.

#### **SAT-938**

##### **ACCELERATING VLASIATOR SPACE PLASMA SIMULATION CODE FOR MAGNETOSPHERIC INTERACTIONS WITH SOLAR WIND USING OPENACC**

Kevin Marrero, Sebastian Von Alfthan.

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Vlasiator is a parallel-space plasma simulation code that solves Vlasov's equation in order to describe the plasma interaction between solar wind and Earth's magnetosphere by simulating plasma in 6-dimensional space (spatial space and velocity space). The problem is computationally expensive, and Vlasiator relies on high-end HPC resources and cutting-edge techniques to make the simulations feasible. The code was created at the Finnish Meteorological Institute and is targeting full global simulation of the entire magnetosphere to support science as well as space-weather forecasts. In order to improve its performance, the existing core solver will be accelerated using OpenACC programming standard targeting Nvidia K40 GPUs. The main goal is to assess the performance and ease of implementation of this technology. To accomplish this, compiler directives and syntax from the OpenACC Application Program Interface are studied from training resources. Test files are written in C/C++, compiled, and run in a supercomputer with Nvidia K40 GPUs. This approach will be compared, in both programmability and performance, to another existing approach, in which the core solver is ported to CUDA parallel computing platform and programming model. By making this comparison, the research team working with Vlasiator can choose the right method that can be used on supercomputers for their future endeavours. According to sources, CUDA codes perform 10 - 20% faster than OpenACC constructs; however, this difference is starting to get blurred with recent releases of OpenACC compilers.

#### **FRI-936**

##### **DEVELOPMENT OF A DATABASE FOR A SYSTEM THAT REDUCES PATIENTS' WAITING TIME AT PHYSICIANS' OFFICES**

Maria Rivera, Cedro Abajo, Nestor Rodriguez.

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The long waiting time at physicians' offices is an important issue that needs to be addressed because it wastes patients' time. Aware of the importance of this problem, our research team has developed a system that allows patients to use a smart phone application (app) to make appointments and receive notifications on the day of the appointment about the time remaining to be served at the physician's office. The database of the system is maintained through a web service application that allows communication between clients. The service implements a relational database management system that uses PostgreSQL. Four entity tables form the database: physicians, patients, appointments, and registered users. The physicians and patients tables contain all information related to the users of the application. The

registered users table contains a reference to those users, patients, or physicians that have used the online service. The appointment table stores the appointments that link patients and physicians with a specific time slot for a turn. This database system connects a web app at physicians' offices with the smart phone app helping patients to decide when to move to the physicians' office.

#### **SAT-939**

##### **USING DEPTH-MINIMIZATION TO ACHIEVE MINIMUM DELAY AND AREA ON FPGA PHYSICAL UNCLONABLE FUNCTION IMPLEMENTATIONS OF BOOLEAN NETWORKS**

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Physical unclonable functions (PUFs) are used in hardware security to attain secure communication and authentication, as well as prevention of intellectual property theft. An arbiter PUF uses the randomness of circuit delays from the hardware manufacturing process to map a set of challenges to a set of responses. A PUF must quickly generate an almost unpredictable response, destroy itself if an attacker tampers with its internal structure, and stay unaffected by environmental variations. To face the challenges of computing the best PUF implementation of a given Boolean network, we chose to look at an algorithm called FlowMap. FlowMap demonstrates that minimizing the depth (number of edges) on the critical path (longest path) minimizes delay and area in a look-up table (LUT) implementation of a Boolean network. Since an arbiter PUF can be implemented with LUTs in a field-programmable gate array (FPGA), we hypothesize that applying FlowMap's concepts can minimize the delay on the critical path and the area used in an FPGA PUF implementation of a Boolean network. In this project, we create a program using C++ that will receive a Boolean network as input and generate groups of gates that will be implemented as PUFs. To test the program, we will use a Xilinx FPGA to determine if the resulting circuit consists of correct functionality, evaluates at optimal speed, uses minimal area, and prevents side-channel attacks. We predict that developers can use this program to determine, for a given Boolean network, the best PUF implementation in terms of speed and area.

#### **SAT-937**

##### **THIN-CLIENT BASED REMOTE VOLUME VISUALIZATION OVER WIDE-AREA NETWORKS**

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Remote desktop access (RDA) applications are becoming increasingly prevalent in distance learning, telecommunications, and remote computing. RDA applications must have exceptional quality of experience (QoE) to provide end users with the best performance possible. A decision tree model has been developed to provide context awareness through feedback loops by adjusting aspects of the quality of application (QoA) and quality of service (QoS) to improve the overall QoE. It is preferred that the client be adjusted first, the network second, and then the

client third to cause minimal disruption. This project explores encoding schemes and server GPU virtualization as QoE improvements. The encoding involves testing different encodings in a tournament-like competition under different network conditions using a network emulator. The GPU virtualization involves testing the limits of the GPU capacity by putting the server under load until full utilization. These enhancements are implemented on the Remote Interactive Volume Visualization Infrastructure for Researchers (RIVVIR) as a case study. Results show that certain encoding types work best under certain network conditions such as low bandwidth or high latency. GPU virtualization is also shown to be adequate for RDA applications, though in this case it might not be in the most ideal way. In conclusion, encoding selection and GPU virtualization are valid ways to improve the QoE of a RDA application. Future work could be done improving encoding schemes such as algorithms for dynamically selecting the best encoding per network condition. Also, implementing distributed load balancing for better virtualized GPU resource allocation would be beneficial.

#### **FRI-937**

##### **SOFTWARE REFACTORING AND USABILITY ENHANCEMENT FOR GRNMAP, A GENE REGULATORY NETWORK MODELING APPLICATION**

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A gene regulatory network (GRN) consists of genes, transcription factors, and the regulatory connections between them that govern the level of expression of mRNA and proteins from those genes. The dynamics of a GRN is how gene expression in the network changes over time. Over a period of several years, our group has developed a complex MATLAB software package called GRNmap that uses ordinary differential equations to model the dynamics of a 21-transcription factor GRN from budding yeast, *Saccharomyces cerevisiae*. The program estimates production rates, expression thresholds, and regulatory weights for each transcription factor in the network based on DNA microarray data and then performs a forward simulation of the dynamics of the network. The large number of developers and time span of development led to a code base that is difficult to revise and adjust. We therefore refactored the script-based software with global variables into a function-based package that uses an object to carry relevant information from function to function. This modular approach allows for cleaner, less ambiguous code and increased maintainability. Further revisions to the model will also be easier to implement. In addition, we have added a simple user interface, removing the need for users to edit MATLAB code. Finally, after the code was refactored and tested, we used the MATLAB compiler to create an executable file that can be run on any Windows machine without the need of a MATLAB license, increasing the accessibility of our program.



**SAT-936****CANACONDA: AN OPEN-SOURCE SOLUTION FOR VIEWING CAN MESSAGES**

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CANaconda is a small, low-cost, open-source hardware and software suite that allows on-the-fly controller area network (CAN) message filtering and display for use in debugging embedded communications. The CAN communication bus is widely used in automotive and factory automation environments; however, a low-cost, open-source tool for decoding the messages has been missing. CANaconda is used to translate CAN message bit patterns into human readable form with custom filters to exclude or include only certain messages. A graphical interface is provided to aid in configuring these filters and also to visualize the data stream. While some CAN protocols use proprietary data, CANaconda is easily customized from within its Python application to accommodate this. The test case for the CANaconda is the SeaSlug autonomous solar boat, which largely uses CAN messages broadcast on the NMEA2000 standard protocol. The CANaconda is a useful debugging tool to monitor the communications within the SeaSlug vessel in real time, allowing for greater visibility into the operating conditions of the embedded vehicle. The hardware is open source and is used to connect the CAN network to a standard USB port on any computer. The CANaconda software is modular by design and easily extensible from within the Python environment and is able to go beyond the SeaSlug or other NMEA2000 maritime applications.

**SAT-935****SMART PHONES APPLICATION FOR NURSING DOCUMENTATION AT THE POINT OF CARE**

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It is a widely known fact that mobile hardware and software technologies are exponentially evolving. Even though the health industry is taking advantage of these technological advances, very little has been accomplished from a nursing perspective of mHealth electronic patient records documentation applications. In many hospitals, nursing tasks remain mostly documented via rudimentary, inefficient, and time-consuming pen and paper methods. Our research team has developed a solution to this problem with a smart phone app that runs on an Android platform. The app provides access to the record of every patient on a hospital ward. When a patient is selected, the system provides a list of pending medical orders for that patient. At this stage, nurses can acknowledge execution of pending medical orders and view or update documentation modules for vital signs, assessment of pain, assessment of ulcers, patient positioning, administration of medication, general assessment, intake and output of fluids, glucose levels, and progress notes. The usability of the user interfaces has been tested with usability heuristics methods.

**SAT-940****RETRIEVAL OF MAXIMALLY RELEVANT ARTICLE SECTIONS FOR INDEXED DATA**

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The USC Shoah Foundation has collected over 52,000 video testimonies from survivors and other witnesses of the Holocaust. This project is aimed at improving the educational value of this database by incorporating information from external archives. In particular, we will focus on matching video segments collected and indexed by Shoah to a relevant section in an external article (e.g., a Wikipedia article). The challenge then is to formulate both an effective way to search the external archive (formulate a query) and then to compute the relevance of the results to the video segment. To make our search effective, we use query expansion techniques since we are only interested in documents about a specific topic (the Holocaust). We rank the documents based on their relevance using methods from information retrieval, namely latent semantic indexing and probabilistic language modeling. We must adapt these methods to take advantage of the structure of the indexing terms developed by Shoah. Finally, we will investigate how performance is affected by our innovations. We will report results from this work.

**ELECTRICAL/ELECTRONICS/COMMUNICATIONS ENGINEERING****SAT-944****MEASURING ATMOSPHERIC CO<sub>2</sub> USING A TUNABLE DIODE LASER**

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Our research aims to develop a small, field-deployable, laser-based sensor for applications in ecosystem and atmospheric sciences. The sensor should be capable of measuring the concentration of CO<sub>2</sub> in the atmosphere at 10 Hz in order to calculate ecosystem fluxes. This requires a sensor that has fast response, long-term stability, low power requirements, and can withstand natural variations in temperature and humidity. In order to achieve this goal, we are developing laboratory procedures to characterize the lower limit of detection, precision, and accuracy of the sensor as well as a method to relate laser signal to CO<sub>2</sub> concentration. We use a vertical cavity surface-emitting laser (VCSEL). The VCSEL and a gallium arsenide (GaAs) photo detector are mounted in a Fraunhofer multi-pass White cell. We use wave modulation spectroscopy which drives the laser with both an AC and a DC component. The wavelength of peak absorption with pure CO<sub>2</sub> flowing through the White cell is compared to the HITRAN database of gas absorption. We then developed a calibration curve wherein laser signal transmission through the White cell is related to CO<sub>2</sub> concentration. Here, we present our novel approach to achieving a stable signal of CO<sub>2</sub> during extended measurements while using wave modulation spectroscopy to measure fluxes at 10 Hz. The White cell will be implemented into a form factor suitable for field research and drone attachment to measure and monitor the net flux of CO<sub>2</sub> (balance between respiration and photosynthesis) above the tree canopy.

**SAT-941****FAST TIME-FREQUENCY METHODS FOR OPHTHALMIC ECHOGRAPHY APPLICATIONS**

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This work centers on the use of signal processing techniques to analyze linear time-invariant (LTI) systems used as mathematical models for ultrasonic signals for ophthalmic echography applications through wireless communication channels. These channels exhibit a great many distortions due to a diverse number of factors including time delay multipath effects, frequency delay effects, and multipath aggregation effects such as echoes introduced by the 3 main layers of the eye (sclera, choroid, and retina). In many cases, the time and frequency delays occur at the same time, creating a condition known as doubly dispersive time-frequency fading. This causes the channels to behave as time varying channels instead of time invariant systems. For certain periods of time called coherency periods, linear time-varying channels may be approximated by linear time invariant channels which are much easier to model. Our specific work proposes the implementation of time-frequency signal processing algorithms to study mobile communication channels in order to analyze coherency conditions. Also, this work proposes the hardware implementation of time-frequency tools, such as the implementation of discrete cross-ambiguity function algorithms on field programmable gate array (FPGA) computational structures to accelerate the modeling of certain communication channel effects, in order to contribute to the estimation of time-frequency channels under coherency conditions, as well as the use of the computational tool Signal Representation Laboratory (SIRLAB) for near-real-time software implementation of the discrete cross-ambiguity function.

**FRI-942****FABRICATION OF EFFICIENT ALGAN/GAN HIGH ELECTRON MOBILITY TRANSISTOR DEVICES FOR THE PURPOSE OF DNA DETECTION**

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In the fabrication of gallium nitride (GaN) high electron mobility transistor (HEMT) devices, we are addressing the problem of deposition thickness and its effect on HEMT structure. GaN HEMTs have the potential to replace a great number of analytical sensors, and by optimizing their efficiency and performance, we aid in this goal. Aluminum gallium nitride (AlGaN) and GaN are both semiconductors which must be sputtered at low RF powers (no higher than 50 W) to keep from breaking the targets. We are using a magnetron sputtering system to grow the AlGaN and GaN depositions. Our method consists of sputtering, a type of physical vapor deposition (PVD), where we bombard the target material with ionized argon particles to dislodge its atoms and sputter them onto the substrate. We aim to find a certain power and a particular duration that will exhibit the most efficient results. Subsequently, we plan to do AlGaN/GaN depositions on both silicon carbide (SiC) and sapphire substrates for comparison as to which have superior thermal and electric properties. If we are successful in providing

repeatable results, we will then move forward and use the GaN HEMT devices for the purpose of DNA detection.

#### **FRI-943**

##### **USING INTERLAYER DIELECTRICS TO CREATE AN INTERCONNECT SCHEME**

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The Marvell Nanofabrication Laboratory CMOS Baseline process is in need of a multi-level metallization scheme in order to have a platform to build NEM relays, nanoelectromechanical devices that could potentially replace certain kinds of transistors. The scheme consists of 2 interconnecting metal layers and a dielectric material for isolation. When the metal layers cross over one another and isolation is desired, the dielectric material must be between them. This project makes use of a low temperature oxide (LTO)/spin on glass(SOG) thin film stack for isolation. The first LTO film, approximately 1,000 Å, is deposited using the lab's low pressure chemical vapor deposition (LPCVD) reactor (tystar12) and is very conformal to the existing topography on the wafer's surface. SOG is dispensed using a spin coater (svgcoat3) and fills trenches and flows over steps. The final deposited LTO film is approximately 2 µm thick and is planarized using chemical mechanical planarization (CMP). In order to characterize the planarity and quality of the 2 dielectric films, a scanning electron microscope (SEM) will be used to analyze the cross section of the films covering trenches and steps. Additionally, optical measurements will be used to monitor film thickness throughout the fabrication process.

#### **FRI-941**

##### **ROBUST CONTROL OF NONLINEAR SYSTEMS**

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The objective of a control system is to regulate the dynamic behavior of a physical system through feedback. Such regulation should satisfy performance specifications even in the presence of disturbances and perturbations. When a control system performs adequately in the presence of disturbances and perturbations, it is robust. We present a relatively simple approach to the robust control problem of the ball-and-beam system that can be used in basic control systems courses. The ball and beam system exhibits high frequency sensor noise, unmolded high frequency dynamics, disturbances in the process, and parameter variations in the plant. Results of controllers designed through robust control methods are presented and compared with other controllers designed by conventional methods such as the root locus method. We demonstrate that a conscious design using a conventional method can depart from the performance specifications, leading to unsatisfactory performance. To demonstrate this, the real system performance for the controllers using both methods is presented and compared to the simulated performance. The performance of the system designed by the root locus method does not meet the performance specifications, while the performance of the system designed by the robust control method does. These results were obtained from an

undergraduate research project and are currently being applied in an introductory course on control systems.

#### **SAT-942**

##### **CHARACTERIZING THE NORMAL-TO-SUPERCONDUCTING PHASE TRANSITION IN NANOWIRES**

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Superconducting nanowires are used for photon detection, reaching the single photon threshold with high bandwidth of 1 GHz and fast timing jitter of approximately 30 ps. The activation mechanism for the superconducting-to-normal phase transition has shown a crossover from thermal activation to the quantum regime at various width and temperature values. It is essential to establish whether there is a limit to how narrow a superconducting wire can be made while retaining its superconductivity, and, if there is a limit, to determine what sets it. These are interesting, open questions in physics that have a broad technological impact. For instance, understanding the fundamental operating principles of superconducting nanowire single photon detectors (SNSPDs) relies on understanding the superconducting-to-normal transition. Our research focuses on studying the phase transition mechanisms in superconducting nanowires. This transition can be explained by alternative mechanisms. Generally, the competition for the most widely used mechanism is between Cooper-pair and vortex-pair dominancy. We consider Berezinsky-Kosterlitz-Thouless (BKT) transition, phase slips, phase transition in disordered systems, and abrupt Cooper-pair condensation. We attempt to discriminate these specific transition mechanisms experimentally by characterizing the electrical properties of nanowires of different widths as a function of temperature.

#### **SAT-945**

##### **INNOVATIVE LANDFILL PUMP SYSTEMS**

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For centuries, pump systems in landfills operated without the technology of remote monitoring and communication and self-diagnostic capabilities. Several months have been spent innovating the systems to do so. A BeagleBone Black with Debian operating system containing an LCD screen, resistors, sensors, and other miniature technology was programmed to communicate with the pumps. Schematics for a case to house these items were also designed for simplicity and will fit directly on top of the BeagleBone Black. After running the pump for a 2-week period using the research and technology to date, results were promising. Without failure, the system operated successfully, reporting the temperature and voltage readings accordingly, among other outputs. Using this innovative technology, landfill pumps will communicate remotely, and reliability will increase which will lower manufacturing costs and simplify maintenance.

**SAT-943****DIMINISHING PATIENT NON-COMPLIANCE IN PHYSICAL THERAPY USING MOTION CAPTURE TECHNOLOGIES**

Lucia Ramirez, Gustavo Vejarano.

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Undergoing physical therapy can be a long and painful process. But, one of the problems physical therapists face during this process is patient non-compliance. Patient non-compliance occurs when patients do not follow through with performing the exercises assigned by the physical therapist. One cause of patient non-compliance is a lack of positive feedback and lack of confidence when doing these exercises at home. Therefore, we have designed, implemented, and validated a software program using wireless sensor nodes that will help patients perform these exercises with correct alignment and also provide immediate feedback. These sensor nodes, which track human movement, have been programmed using C#, an object-oriented programming language. With the use of 2 sensor nodes on one arm, one above the elbow (humerus) and the other above the wrist (forearm), this system can measure the angle of 5 dimensions made by arm movement. Focusing on the supine-grip bicep curl, one angle is constantly changing while performing the exercise. Therefore, when the user performs a motion that changes any other angle, the program will be able to provide immediate feedback to the patient. Overall, diminishing patient non-compliance will be more cost effective and help patients return more quickly to their daily activities. In future development, the software program will provide more positive feedback by adding videos and/or audio, record the patient's range of motion periodically, and include more exercises geared toward a particular injury.

**ENGINEERING (GENERAL)****SAT-946****BIOMECHANICAL TOLERANCE OF HUMAN TIBIA MODELS UNDER DYNAMIC LATERO-MEDIAL BENDING**

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Research has been conducted for the purpose of testing the tolerance of the lower extremities to high-impact automobile accidents. In order to validate a biomechanical, tibial surrogate in high-impact collisions, dynamic 3-point bending was performed using a custom guided drop-impact apparatus. Two biomechanical surrogates were struck mid-shaft, generating classic butterfly fracture patterns and forces similar to those documented in post-mortem, human-subject testing. With additional validation, the tibial surrogate may be used as a forensic tool to investigate trauma-inducing leg impacts for the purpose of determining loading conditions from fracture patterns.

**FRI-945****PV CLEANER ROBOT**

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One of the problems with solar panels is efficiency degradation as a function of time. This is due to air particles that coalesce on the panel's surface, which lowers the power output for the photovoltaic (PV) panels by blocking incident light. Regular cleaning of the panels is required to keep efficiency levels at maximum. This group is part of a long-term project to develop a PV cleaner robot. Last year, a robot was designed and constructed. An h-bridge circuit was designed and built to allow 4-wheel drive on the robot. The purpose of this year's project is to test different types of wheels in order to objectively determine the best wheel set. In order to complete this project, the first step is to develop a code to enable the robot to traverse a specific path along the solar panels. Furthermore, a test bench will be designed and built to tilt a solar panel to test the performance of wheels at different tilt angles.

**ENGINEERING SCIENCES/MECHANICS/PHYSICS****FRI-947****RESOLVING RESOLUTION USING ADAPTIVE OPTICS AND STRUCTURED ILLUMINATION**

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Obtaining a high resolution image of objects that are small and difficult to see with a standard microscope is a challenge in modern science. Coupled with classical diffraction limitations, however, the challenge becomes much more difficult than usual with the presence of aberrations that distort image quality. Much of the knowledge biologists have about our world is based on information gathered by observing microscopy images. If those images are distorted in any way, that severely limits what scientists can learn. A possible solution to this problem is using adaptive optics (AO) and structured illumination (SI). By using AO and SI, we could extract super resolution images of samples that would otherwise be distorted by aberrations. Using light from a laser and a digital light processor (DLP) to direct several patterns into the object, we could collect images, mathematically rearrange data extracted from them, and rebuild them again to form a higher resolution image. A wavefront sensor (WFS) and deformable mirrors (DM) would be used to correct for any aberrations that appear in the raw image. We will present our findings on samples using the method described.

**FRI-946****SUPER RESOLUTION THROUGH STRUCTURED ILLUMINATION**

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In biology, substantial amounts of information are gathered through microscopy, and our scope of understanding is limited by the observable plane. Standard microscopes are governed by the classical diffraction limit, restricting the resolution of its images to about 250 nm. In recent years, several methods have been developed in an effort to exceed this limit and achieve super-

resolution, roughly doubling the previous amount of resolution achieved. One such method is with the use of structured illumination (SI). We illuminate the sample with a grating pattern set using a digital light processor (DLP) and take several images at different phases. In this process, variations in the tissue being observed introduce aberrations, reducing the actual resolution obtained. These aberrations increase as we look deeper. We measure the aberrations with a wavefront sensor (WFS), a form of adaptive optics (AO), and make corrections to the light to compensate for the aberrations that occur as light travels through the sample using deformable mirrors (DM). Given the specific patterns, multiple images are taken at specific offsets or shifts as calculated mathematically. Using mathematical inverse analysis, the images collected are then reconstructed creating a final image with approximately twice the resolution as compared to the previous classical limit. In this project, we will present our findings using 2 different SI patterns and discuss the results of the final images reconstructed.

#### **SAT-947**

##### **DISTINGUISHING BETWEEN NEUTRON AND GAMMA INTERACTIONS IN $^6\text{Li}$ -CONTAINING CRYSTALS**

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The need for radiation detectors for neutron science and homeland security over the past decade have led to great interest in materials for neutron detection. This project aims to study different radiation interactions in  $^6\text{LiInSe}_2$ , a promising semiconducting crystal for neutron detection. In order to minimize unwanted neutron capture reactions with  $^{115}\text{In}$  and improve the overall detection efficiency, a series of  $^6\text{Li}$ -containing crystals were fabricated whereby the indium component was systematically replaced by gallium— $^6\text{LiInSe}_2$ ,  $^6\text{LiIn}_{0.8}\text{Ga}_{0.2}\text{Se}_2$ ,  $^6\text{LiIn}_{0.6}\text{Ga}_{0.4}\text{Se}_2$ ,  $^6\text{LiIn}_{0.5}\text{Ga}_{0.5}\text{Se}_2$ ,  $^6\text{LiIn}_{0.4}\text{Ga}_{0.6}\text{Se}_2$ ,  $^6\text{LiIn}_{0.2}\text{Ga}_{0.8}\text{Se}_2$ , and  $^6\text{LiGaSe}_2$ . The generated samples were characterized by differential scanning calorimetry (DSC), I-V, UV-VIS, and infrared spectroscopy to determine phase transition points, electrical resistivity, and light transmission. Radiation measurements were performed with a  $^{137}\text{Cs}$  gamma ray source and a moderated  $^{252}\text{Cf}$  thermal neutron source. Crystals were fabricated such that they could either operate as a semiconductor, whereby the  $^6\text{Li}$  (n, $\alpha$ ) reaction results in current generation, or as a scintillator, where the nuclear reaction generates photons. The results will be presented.

#### **ENVIRONMENTAL ENGINEERING**

#### **FRI-948**

##### **SIZES OF INSECT BIOTA PRESERVED IN AMBER FOSSILS**

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Polymerization is the process by which amber, a tree resin, hardens. Amber's sticky and viscous nature allows entrapment and preservation of a variety of insect species, but taphonomic biases may be present, particularly regarding the size of entrapped specimens. Biasing factors influencing preservation of insect fauna include climate, insect size and wingspan, and



geographical setting. The majority of insect taxa trapped in amber are smaller than those preserved in sedimentary rock. We used the Paleobiology Database to enter papers that included measurements of wing and body size of specimens in both amber and rock. We analyzed the data, allowing us to compare between insect sizes in amber fossils to insect sizes in rocks. The majority of insects found trapped in amber had wing sizes less than 5 mm, so we assumed that insect taxa with wings less than 5 mm had a higher risk of getting trapped in resin. We needed to understand the reason why smaller insects are more vulnerable so conducted an experiment to fully understand the forces that cause an insect to get trapped. This experiment revealed that resin position is another factor that influences what is trapped inside the resin. It is generally known that biota in amber are mostly small insect taxa, but this paper will explain and explore the possible reasons why, with supporting evidence. Rarely do we find anything but insects in amber, making insect inclusions in amber crucial in reconstructing the insect fossil record.

#### **SAT-949**

##### **DRUG TRENDS USING WASTEWATER EPIDEMIOLOG**

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The current Utah Drug Control Update has revealed that Utah is ranked fourth in abuse of opiates and highest in drug-related deaths within the United States as of 2007. Through various studies, we have come to understand the essential drug use in a specific area. Although these surveys have potential, they are limited due to migrating populations and wavering factual evidence from participating subjects. Studies in Oregon and Ireland have utilized this form of research. One study in Ireland revealed a higher use of cocaine on weekends and in larger cities by analyzing the local wastewaters. In Oregon, results also revealed a higher use of methamphetamine, cocaine, and MDMA in urban cities rather than rural areas. In our research, the Neogen drug assay kits were used to determine the drugs in use in Salt Lake City. The test kit screens drugs in a convenient bioassay, and responds to drugs and their metabolites. Divided into 8 regions, Salt Lake City's sewer lines gave access to investigate the drugs being abused in each populated region. Evidex columns were used to extract 5 drug classes to reveal drug quantities. To conduct this study, methamphetamine, THC, opiates, oxycodone, and cocaine were measured in wastewater samples to reveal concentration of drug occurrences. In addition, standards and recovery samples were used to determine accuracy. Within these findings, we have determined that Neogen bioassay drug kits are able to detect abuse trends within a city via water samplings, with a minimal error margin.

#### **SAT-948**

##### **COMPATIBILITY OF DUAL-DISINFECTION IN A DISTRIBUTION SYSTEM**

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The City of Sarasota currently treats and produces its own drinking water, disinfecting using free chlorine. However, in emergency situations, it may become necessary to use water from

neighboring chloraminated systems through the use of existing interconnects. One concern in using the potable water from neighboring systems is the compatibility of the two different disinfectants in the distribution systems. This research was conducted to identify and report the effects of mixing free chlorine with chloramines in the City of Sarasota's distribution system. The concentrations of free ammonia, monochloramine, free chlorine, and total chlorine were monitored to assess the compatibility of blending the water systems. Breakpoint chlorination curves were developed for multiple interconnections to determine the chlorine demand to reach breakpoint at each location. Data showed that a chlorine demand of 4 mg/L was required before breakpoint occurs. To adhere to the regulatory limit of 4 mg/L on chlorine injection, it was recommended that the interconnections be modified with chlorine and ammonia injection systems, and if an emergency situation should occur, the city should temporarily convert to a chloramine system in the interconnect service area.

#### **SAT-956**

##### **OPTIMIZING NITROGEN RECOVERY FROM SOURCE-SEPARATED URINE**

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To reduce the eutrophication of aquatic environments that stem from the excess nitrogen not removed at waste water treatments plants, ion exchange cartridges are being developed to incorporate into source-separating toilets for the recovery of nitrogen from urine. Comprising 1% of waste water volume, urine contains the majority of excreted nutrients such as nitrogen, potassium, and phosphorous. The nitrogen that may be recovered by these cartridges is in the form of ammonium, resulting from the hydrolysis of urea from fresh urine. Resins of interest for the design of the ion exchange cartridge include clinoptilolite and faujasite (natural occurring minerals) and Dowex 50 and Dowex Mac 3 (synthetic materials). To determine the efficiency of each resin to adsorb ammonium, 24-hour batch experiments with an ammonium chloride solution were performed to generate equilibrium adsorption isotherms. Preliminary results demonstrate that Dowex Mac 3 adsorbed larger quantities of ammonium as nitrogen than the other resins. This may indicate that Dowex Mac 3 may be the ideal resin to include in the ion exchange cartridge design. However, further studies involving synthetic urine and actual urine must be conducted to confirm this. The effective design of these ion exchange cartridges will lead to the alternative production of ammonium-based fertilizers from the recovered nitrogen in the form of ammonium from urine.

#### **INDUSTRIAL/MANUFACTURING ENGINEERING**

#### **FRI-950**

##### **COMPARISON OF SERVICE RELIABILITY METRICS ON VULNERABLE STOCHASTIC NETWORKS**

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This study introduces a new service reliability metric based on service survivability when network components are vulnerable to disruptions. The network service reliability, i.e., its

capability of providing service when requested, could be affected by intentional or natural disasters such as earthquakes, storms, or terrorist attacks, etc. The proposed metric, termed mean network survivability, is an improvement over the existing reliability efficiency metric because it takes into consideration that nodes may have different service demands and edges may have different operational probabilities. Additionally, to calculate mean network survivability, the authors propose the use of an approximation to the real value of two-terminal reliability that is more accurate than other approximations that use either the most reliable route or lower bounds based on minimal paths, especially when edge operational probabilities are different. The proposed metric is important in characterizing the performance of a network and allows comparison among different topologies. Examples that illustrate the use of the proposed metric and compare it with other service reliability metrics will be presented.

#### **SAT-951**

##### **ERGONOMIC ASSESSMENT OF A HIGH-DENSITY METROPOLIS MOBILITY DEVICE**

Mauricio Garcia, Javier Garcia-Mendoza, Delia Valles.

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The purpose of this study is to propose a novel approach for the assessment of ergonomics in the design of mobility devices targeted toward a specific percentage of the population habituating a high-density metropolis. The method ensures that optimal ergonomic specifications that eliminate injury risk, provide comfort, and reduce fatigue of users operating a mobility device are considered while the device is in the design process. This has been achieved by establishing the appropriate collection of ergonomic measurements and ranges that suit the Brazilian population within the 5<sup>th</sup> and 95<sup>th</sup> percentiles in size dimensions. These ranges and measurements have undergone a feasibility assessment with the use of Tecnomatix Jack software and are used in the building of a prototype. Moreover, external road factors affecting the user, such as vibration, are considered in the ergonomic model. The ergonomic design characteristics have been analyzed with a quality function deployment (QFD) matrix to evaluate their impact in the overall device's design. Preliminary results confirm that the array of ergonomic measurements and ranges meet the desired expectations in comfort, feasibility, fatigue, and injury risk. In conclusion, the approach has been proven effective in the design stage of the mobility device, thus reducing the possibility of future changes. Further research includes the use of the theory of inventive problem solving (TRIZ) to generate solutions when the QFD matrix indicates an unfeasible impact in the mobility design by the ergonomic measurements and ranges.

#### **SAT-950**

##### **EXPERIMENTAL DESIGN-BASED MULTIPLE CRITERIA OPTIMIZATION ALGORITHM TO AID MANUFACTURING DESIGN AND PROCESS ADJUSTMENT**

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The aim in a multiple criteria optimization problem is to find the values of the decision variables that result in the best possible balances among all criteria in the presence of conflict. These

best balances are called Pareto-efficient solutions for the most efficient result of the problem. Often times, the functions that relate the decision variables to the criteria of interest are not well established or completely known. An experimental design, which helps to build empirical approximations based on systematic sampling, is then a helpful tool in these cases. In this work, experimental design is used along with an iterative strategy to approximate the efficient frontier of the multiple criteria optimization problem. Optimality conditions are sequentially used to make this algorithm effective and precise in reaching the efficient frontier. The development of this algorithm will be carried out using injection-molding simulations where multiple criteria are considered simultaneously to effectively decide design features as well as processing conditions. At this first stage of the work, the method is presented and demonstrated through a simple-to-verify problem.

## **MATERIALS ENGINEERING (INCLUD. CERAMICS/TEXTILES)**

### **FRI-951**

#### **SUPPORTED LIPID BILAYERS TO CREATE MULTICOMPONENT BIOLOGICAL STRUCTURAL MIMICS**

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Cell membranes are complex, multi-component systems that contain dynamic elements such as lipid rafts and protein rich domains. Lipid bilayer assemblies (LBAs) can be used as model membrane systems for investigating interactions and responses to different stimuli, but producing a lipid bilayer of biological complexity is challenging. By introducing lipopolysaccharide (LPS), a component of the outer membrane of Gram-negative bacteria, to the LBA, a new level of complexity is obtained. In a process that is both thermodynamically and kinetically driven, we showed that LPS causes formation of stable holes in LBAs, allowing us to manipulate membranes. Depending on the incubation period, concentration, and temperature, we can control the hole size and distribution. These holes can be backfilled with different components such as protein, polymer, and different phase lipids. Hierarchical domain arrangements can be formed by addition of multiple cycles of LPS. Through micro-contact printing we can transfer geometric patterns of hydrophobic chemistry to surfaces, which lead to alternating lipid monolayers and lipid bilayers. The monolayers provide a thermodynamically unfavorable boundary for LPS, causing the molecules to aggregate, creating holes in a geometrically-ordered fashion. This technique provides a soft, lithographic, multicomponent organized system that is symmetrical over several hundred microns. These new findings and proposed techniques can now be used to better understand LPS-membrane interactions, lead to new approaches for potential biosensor design, and provide a new material to study biological interaction. One example would be the display of pathogenic proteins or their receptors in membrane-based arrays for interaction testing.

**SAT-953****MEASURING CELLULAR ADHESION FORCES ALONG A NANOPARTICLE GRADIENT**

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<sup>1</sup>*University of California, Santa Barbara, Santa Barbara, CA,* <sup>2</sup>*Chalmers University of Technology, Gothenburg, SE.*

Successful integration of surgical implants is dependent on the properties of the used biomaterial. It has been found that not only are the chemical composition and implant's design important, but the nanotopography of the implant plays a critical role in cellular interaction to establish successful integration. In order to study the differences in cellular interaction between different nanotopographies, we employ a novel technique to create a nanoparticle concentration gradient along a surface. We hypothesize that when cellular interaction is measured along the surface of the gradient, there is a correlation between the nanoparticle density and the level of cellular adhesion to the surface. To study this hypothesis, we will form silicon dioxide nanoparticle gradients on glass surfaces and characterize the change in nanoparticle density using scanning electron microscopy (SEM) and contact angle measurements. We will then use a modified atomic force microscope (AFM) and attach single cells to the cantilever and measure the interaction of the cell along the surface. The force required for removing the cell off the surface correlates to the binding force. Parameters such as cell/surface interaction time, chemical functionalization of the surface, and cell type will be varied. We predict there is an optimum distance required between the particles to form successful cellular adhesion. Since the topography of an implant plays such a key role in integration, our results in determining the optimum density of nanoparticles along a surface can be used to tailor specific topographies for implants based on cell type.

**FRI-954****SYNTHESIS AND BREAKDOWN STUDY OF POLYPROPYLENE COPOLYMERS CONTAINING HINDERED PHENOL FUNCTIONAL GROUPS**

Omar Padilla<sup>1</sup>, T.C. Mike Chung<sup>2</sup>.

<sup>1</sup>*University of Puerto Rico at Cayey, Cayey, PR,* <sup>2</sup>*Pennsylvania State University, State College, PA.*

The oxidation of polymer, thin-film capacitors at high temperatures leads to material degradation, thereby inhibiting energy storage capabilities. Current commercial polypropylene (PP) products are mixed with hindered phenol antioxidants to avoid polymer chain scission by interacting with the free radicals produced by oxidative conditions. However, the unbound antioxidant molecules in the polymer film can cause serious dielectric loss due to free charges under high-field operation conditions. In this study, a series of polypropylene polymers were chemically modified to integrate a hindered phenol group in the polymer chain. This polar functional group incorporation with homogeneous distribution in each polymer chain will improve stability at high temperatures and provide higher polarization that can increase the dielectric properties of the material. A  $\text{rac-Me}_2\text{Si}[2\text{-Me-4-Ph(Ind)}]_2\text{ZrCl}_2$  metallocene catalyst was used for the copolymerization of high molecular weight and narrow composition distribution polymers. The resulting propylene and 10-undecenol copolymers (PP-OH) were further modified and the esterification of a hindered phenol to the co-monomer OH group was

achieved. Polymers were subjected to high temperature NMR analysis and were found to contain up to 6 mol % of co-monomer functional groups. After mechanically compressing the polymers into approximately 30  $\mu\text{m}$  thin films, dielectric properties studies reveal an increase in the dielectric constant ( $\epsilon$ ) of these materials without having a significant increase in energy loss. A final thermogravimetric (TGA) analysis concluded PP-Phenol polymers had higher degradation temperatures as compared to commercial PP products.

#### **SAT-952**

##### **COMPARISON OF MECHANICAL COMPLIANCE AND SOLAR CELL EFFICIENCY BETWEEN SMALL MOLECULES AND POLYMERS**

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This project will look at mechanical properties of organic solar cells made from small molecules and polymers. We will test the hypothesis that small-molecule, solution-processed, semiconducting films have a greater tensile modulus than that of films processed from conjugated polymers. We will test the photovoltaic (PV) performance of the small molecules and polymers by spin coating the active layer, producing a smooth semiconducting film. We measure its performance by exposing it to a sun simulator and then use software to analyze the current and voltage produced. Mechanical compliance is tested by transferring the film onto a pre-stretched polydimethylsiloxane (PDMS) stamp. Upon releasing the PDMS stamp, the film is exposed to a strain, producing visible buckles whose wavelength can be used to obtain the elastic modulus. So far, we have tested the photovoltaic properties of several high-performing polymers and small molecules. The results indicate that, on average, they both perform equally well although there were some small molecule cells that outperformed all the polymer cells. We are now beginning tests on the mechanical compliance of the different films. The goal of this project is to determine if one material is superior. This information will support the solar cell community in determining the material with which they choose to work.

#### **FRI-955**

##### **GROWING AND CHARACTERIZING 2D SILICA BILAYERS ON GRAPHENE EPITAXIALLY GROWN ON RUTHENIUM(0001)/SAPPHIRE**

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<sup>1</sup>*California State University Dominguez Hills, Carson, CA,* <sup>2</sup>*Yale University, New Haven, CT.*

Two-dimensional silica ( $\text{SiO}_2$ ) glass bilayers are a new form of  $\text{SiO}_2$  that is exactly 2 atoms thick with no dangling bonds. Since 2D silica bilayers have no dangling bonds, it is expected to be a van der Waals material with no detectable covalent bonding. Two-dimensional silica can have many applications in layered graphene electronics and dielectric layers in atomically thin transistors, along with applications as membranes that allow only molecules smaller than a specific size to fit through and where the atomic thickness promises unprecedented throughput. The goal of this research is to determine the optimal conditions for growing a 2D silica bilayer on a uniform graphene monolayer and to also study its characteristics and intrinsic properties when removed from all substrates. The first step is to determine the optimal growth

conditions for growing a uniform graphene monolayer on epitaxial ruthenium (0001) on c-plane sapphire. The next step is to determine the optimal growth conditions of 2D silica bilayers on graphene. The 2D silica will then be isolated from the substrate so that its characteristics and intrinsic properties can be studied using Raman spectroscopy, transmission electron microscopy, scanning transmission electron microscopy, and electron energy loss and X-ray emission spectroscopy.

#### **SAT-955**

##### **EFFECT OF BACTERIAL CONTAMINATION ON SURFACE PROPERTIES OF POLYMER COLLOIDS**

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Bacterial contamination is a serious problem encountered by experimentalists working with polymeric colloids, or latex particles. Our preliminary data suggests that it is the cause of some unexplained adhesion or instability. In order to understand the surface effect of an unknown or incidental bacterial contamination, we study the zeta potential and surface adhesion of sulfated polystyrene latex particles in the presence of live or lysed *E. coli* [BL21(DE3)] cells. We also use a novel technique, video microscopy rotational electrophoresis (VMRE), to measure the charge non-uniformity on the particle surface. We found that particles in the presence of lysed bacterial cells had a different zeta potential than that of the controls in a range of pH, the greatest difference being at pH 3 where the contaminated sample had a zeta of +58 mV as opposed to -82 mV for the control. The contaminated particles exhibited 70% adhesion to a glass surface in 1 hour, much higher than the control, which was 2%. Using VMRE we found that in 4 days, bacteria caused significant charge non-uniformity to develop on particles that started out as uniformly charged on day 1. Interestingly, we found that particles stored under usual, non-sterile conditions, devoid of purposeful contamination also developed charge non-uniformity, and increased adhesion in a few days. This latter finding shows that incidental contamination is quite common and can unfavorably affect the surface charge and stability of polymeric particles. Thus, sterile techniques are important in the storage and handling of particles.

#### **FRI-963**

##### **ANALYSIS OF MMNC USING RVE MODELS**

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Development of nanocomposites is one of the rapidly evolving areas of composite materials research. Metal matrix nanocomposites (MMNC) are attractive because they produce balanced mechanical properties between nano- and microstructured materials. These materials display enhancements which are believed to be due to the addition of nanosized reinforcement particles into the matrix and include enhanced hardness, Young's modulus, 0.2%; yield strength; and ultimate tensile strength and ductility. In this work, we developed geometric and analytical representative volume element based models to analyze these composites using 3D finite element analysis. MgZn-SiC metal matrix nanocomposites are analyzed by capturing

process conditions from scanning electron microscope images and the geometry of experimental samples. The results are being identified by the stress-strain behavior of their metal matrix nanocomposites and compared to experimental values. The models can be used to evaluate parameters to perform quick, what-if analyses for cost effective manufacturing.

#### **FRI-953**

##### **SELF-ASSEMBLY OF "SMART" DNA-BASED MOLECULARLY RESPONSIVE SOFT BIOMATERIALS: A COMPUTATIONAL AND EXPERIMENTAL APPROACH**

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Significant research efforts have focused on the development of stimuli-responsive biomaterials that undergo physiochemical changes in reaction to external factors; however, there has been a great urgency for the development of biomaterials that can provide higher specificity, including target-dependent control. Our research focuses on the development of macro-, micro-, and nano-scaled polymeric hydrogels that use strands of deoxyribonucleic acid (DNA) as a cross-linking component. These DNA-containing hydrogels are being developed as molecularly responsive materials by incorporating DNA aptamers that have specificity to certain biomolecular targets, e.g., secreted growth factors associated with disease. As the DNA cross-linking component interacts with high concentrations of a secreted biomolecule, the hydrogel dissociates allowing, for example, the release of a specific drug to a designated area or cell replication-controlled degradation of polymeric scaffolds. Current work includes both computational and experimental approaches. Computationally, we are modeling the self-assembly process of specially-designed strands of DNA. Molecular dynamics simulations are being used to understand the formation of the hydrogels and their ability to release drugs at a specific biological target. Simulations provide molecular level insight into the dynamic behavior of hydrogels which cannot be seen experimentally, and can be used as a tool to guide continued experimental research. While we have made significant computational progress, DNA association in simulation is not yet optimized. Experimentally, we have successfully demonstrated the formation of the DNA aptamer complex via fluorescence resonance energy transfer as well as the functionalization of hydrogel precursors via spectroscopic methods and hydrogel formation via viscosity analysis.

#### **FRI-952**

##### **CARBON NANOTUBE DISPERSION BY AMPHILIC LINEAR COORDINATION POLYMERS**

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The inherent properties of carbon nanotubes (CNTs) make them an exceptional component for electronic devices and composite materials. For example, CNTs exhibit strong photoabsorption across the solar spectrum, from infrared to ultraviolet, while maintaining high carrier mobility and reduced carrier transport scattering, leading to their enormous potential in solar cell applications. The issue that plagues this particular carbon allotrope is its tendency to aggregate



into amorphous insoluble solids in common solvents. This hinders manufacturing techniques, which keeps CNTs from achieving their full potential. Current chemical approaches to nanotube dispersion use covalent or non-covalent interactions. Solubilization has been achieved via covalent functionalization of the CNTs, but this compromises their desirable physical properties. Herein we present a novel way to disperse CNTs in various solvents while also organizing them within nanostructures. This was achieved through the use of coordination polymers containing long hydrocarbon groups designed to interact with CNTs and direct their folding into defined nanostructures. The synthesis of novel Zn(II) and Cu(II) coordination polymers will be presented as well as the microscopy data from TEM (transmission electron microscopy) and AFM (atomic force microscopy) showing evidence for the new CNT composites.

#### **SAT-954**

##### **SILICON-COATED CNFS FOR RENEWABLE ENERGY APPLICATIONS**

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Carbon nanofiber- (CNF) based materials have been widely explored as conduits for transporting electrons in energy storage (batteries and supercapacitors), energy conversion (photoelectrochemical solar cells, fuel cells), and biosensing. In addition to their high electrical conductivity, CNFs can be used as a scaffold to host functional silicon-containing polymers, which are hypothesized to render CNFs with electrocatalytic and electrochemical activities. CNFs are directly grown on stainless steel substrates (SS) by catalyst-assisted chemical vapor deposition (CVD). Systematic studies indicate that polymers can be electropolymerized conformly on CNFs. We have shown that mildly treated CNFs have good storage capacity and exhibit oxygen reduction capability. This investigation focuses on establishing a process to fabricate silicon-containing polymers on CNFs and pyrolysis via examination of energy storage and conversion properties. This hybrid has shown larger capacitance and enhanced ORR (oxygen reduction reaction) capabilities, making it a new, promising material in renewable energy applications.

#### **MECHANICAL ENGINEERING**

#### **FRI-961**

##### **DESIGNING A ROBOT WITH SHAPE METAL ALLOY (SMA) AS ACTUATOR AND CONTROLLING IT WITH ARDUINO**

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*California State University Fresno, Fresno, CA.*

The purpose of using shape-memory alloy (SMA) wire to replace electric motors is to reduce the cost and weight of a product. The objectives of this research are to prove that SMA wire can be used to replace electric motors and show the efficiency versus conventional counterparts. A mini-robot was designed with 4 legs and 1 arm, using only SMA wires to move each component. SMA is a smart metal that remembers its original shape. If the SMA is deformed through force or other means, it will return to its pre-deformed shape when heated. The SMA in this

experiment was heated by passing electricity through each wire. Torsion springs were also used to deform the SMA and helped move the components back to their original position. The robot was then programmed to control the level of electricity being inputted to each SMA wire using the microcontroller Arduino. The degree of inputted electricity directly relates to the output of heat to the SMA wire. Standard equations of motion for SMA were also derived and used to model, in Simulation and Model-Based Design (Simulink), how the SMA would move in relation to the inputted electricity. With the combination of Arduino and Simulink, the robot was controlled via controller and we demonstrated that SMA can be used in place of electric motors. Though the adaptation of using SMA wire greatly reduces the efficiency of the robot, it proves that alternative methods can be used to replace electric motors.

#### **SAT-960**

##### **USING SCHLIEREN TECHNIQUES TO VISUALIZE AND QUANTIFY THE VELOCITIES IN A THERMAL PLUME OF A NON-PREMIXED FLAME WHEN AN ELECTRIC FIELD IS APPLIED**

Alejandro Sherman, Jesse Tinajero, Derek Dunn-Rankin.

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The objective of this project is to obtain the velocity of a thermal plume of a non-premixed flame when an electric field is applied. Electric fields can influence a flame because of ions produced in the chemical-to-thermal energy conversion process. Schlieren techniques are used to visualize the reaction of the thermal plume to the electric field. The captured images are processed to display intensity values on a grayscale across horizontal lines throughout the entire plume. The diameter of the thermal plume as the plume fluctuates is recorded on graphs with respect to the height of the plume using MATLAB. Multiple graphs will be created over time from the time of introduction of the electric field to the time the thermal plume stabilizes. Research will continue over the next 8 weeks, and the results will give a better understanding of the forces and influences electric fields have on flames and thermal plumes.

#### **SAT-961**

##### **CHARACTERIZING THE HEAT TRANSFER PROPERTIES OF FLAT, MICRO-HEAT PIPES**

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Heat pipes are reliable thermal management devices that can be used in various forms for applications in aerospace and computer systems. Thermal ground plane (TGP) is a flat heat pipe being developed at the University of Colorado which can be used to cool electronic systems that have little room to accommodate larger heat transfer devices. It is important to properly prepare the TGP before use or testing. A key step in manufacturing TGPs is to charge a micro-fabricated TGP with a precise amount of cooling liquid. A charging station was developed to evacuate the flat heat pipe and accurately fill it with degassed water. Typical charging stations accomplish accurate evacuation and filling of the TGP but do not allow for re-use once it is charged. The charging station used in this project can pull water out of an already-filled TGP allowing for re-use, leading to more accurate and consistent data. A heat transfer testing station was also assembled to accurately measure the effective thermal conductivity of TGP

with different form factors. The testing station uses a maximum power input of 1,000 W/cm<sup>2</sup>, which heats one end of the TGP while a condenser extracts the heat at the other end of the TGP. Using LabView, data is gathered from thermocouples positioned at various points allowing for the effective thermal conductivity to be calculated during testing. This system makes it possible to determine the effective thermal conductivity of a TGP with various parameters such as length, width, micro-channel size, and heat addition, etc.

#### **FRI-957**

##### **DEVELOPMENT OF IMPROVED ASSAYS FOR CELL ADHESION THROUGH LOCAL APPLICATION OF FORCES TO CELLS**

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In this project, we are developing new methods to investigate if and how cell adhesion strength changes in diseased cells. In neurons, cell adhesion is particularly important, as cell-to-cell contacts at the synapse are required for electrical signal transmission. In Alzheimer's and other neurological diseases, neuron signaling networks fail by cell retraction, but it is not known if retraction arises from loss of adhesion or by another pathway. To test this, we are developing improved methods to apply forces directly to cells using optical traps or magnetic tweezers, custom-built tools that manipulate small dielectric or magnetic particles that are coupled to the cell surface. In our preliminary work, we are using both a synthetic system of engineered hydrogels as well as living cells to test adhesion strength of known cellular proteins and to optimize our binding and pulling protocols. For our cellular work, we will start with a non-neuronal cell line (Cos 7 cells), which has the advantage of fast proliferation, ease of transfection with proteins of interest, and ease of imaging with microscopy. By applying forces directly to the cells, we can measure detachment forces and, in the future, will also visualize cell deformation under loading. In addition to investigating the role of adhesion in neurological disease, the ability to apply forces to neurons would also allow us to investigate the effects of blunt force trauma, which has importance in understanding traumatic brain injury.

#### **FRI-958**

##### **DEVELOPING STABILITY ATTACHMENTS TO IMPROVE THE EFFICACY OF A MOBILE STANDING DEVICE**

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Assistive technology encompasses a range of devices used to help persons with disabilities with everyday tasks. This project aims to develop a portable, lightweight attachment to the MOBI-S, a mobile device that attaches to any sturdy desk or table and assists the user in maintaining a standing position. The MOBI-S was developed as an assistive technology tool for children suffering from irregular motor development due to a condition affecting the central nervous system. The MOBI-S attaches to the side of the desk or table using 2 adjustable clamps. The user is held upright with the help of a belt positioned around the torso and several support

pads located bilaterally and posteriorly. Upon further investigation of the MOBI-S prototype being used by a child, potential hazards such as shifting or tipping the table were noted, which warranted further assessment of the device. Observations of the child in classroom and physical therapy settings gave us the necessary information to narrow down the important forces and axes of rotation to include in the force diagrams. These force diagrams were used, along with corresponding static equations, to assess the magnitude of forces that lead to tipping or shifting the table. These results were then incorporated into the design of the stability attachments, which were adjusted to properly counter the tipping and shifting forces. The next stage will be implementing the results from the force evaluations in the design of the stability attachments so production can commence.

#### **FRI-960**

##### **FLOW DIAGNOSTICS OF SWIRL STABILIZED COMBUSTION WITH AND WITHOUT POROUS INERT MEDIA**

Carolina Vega Recalde, Ajay Agrawal.

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Due to regulations, the industry and the scientific community have become interested in combustion noise and thermo-acoustic instabilities, especially those produced under lean-premixed (LPM) conditions. Instabilities are self-excited and arise when energy from combustion is added to the system faster than energy is dissipated by heat transfer. Since porous, inert media (PIM) has been shown to mitigate combustion noise and thermo-acoustic instabilities in lean direct injection (LDI) using kerosene fuel, the present study will study the flow fields produced with and without PIM. By using a time-resolved particle image velocimetry (PIV) technique, the non-reacting and reacting flow fields will be studied to determine the underlying mechanisms. The purpose of this experiment is to gain more understanding of how this PIM material works. Since it has been shown it can reduce these instabilities, modifications to combustors can be made to make them more efficient and safe for the environment.

#### **FRI-959**

##### **DESIGN AND TEST OF A COPPER-BASED, MINI-CHANNEL SOLAR WATER-HEATING SYSTEM**

Keith Saechao, Van Duong, Gerardo Diaz.

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The process of heating water accounts for a significant portion of energy consumption in the world. Scientists and researchers have developed solar water heaters that are slowly being adopted in residential as well as commercial sectors. The main issue with these current solar water heaters relates to the efficiency of transferring the heat from the sun to the working fluid. The objective of our project is to further the advancement of solar water heaters through the addition of copper-based, mini-channel collectors. Prior to our project, there has been a prototype design of an aluminum-based, mini-channel collector. Although the results obtained for this aluminum collector showed improvements with respect to standard flat-plate collector designs, operation at higher temperatures requires other materials such as copper. The overall system to be implemented will include the collector, pump, piping, and sensors. A control logic

will be implemented that will consist of input signals using temperatures at the inlets, outlets, and within the water storage tank. The collector will be tested in single-phase operating mode and also in steam generation mode. Computational models are being developed to compare with test data to allow for system optimization. We hope our invention will increase the efficiency of solar collectors by minimizing the thermal resistance.

#### **SAT-958**

##### **DATA COLLECTION AND ANALYSIS FROM THE SENSORS EMBEDDED IN A PROSTHETIC SOCKET**

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A growing demand in the United States and all over the world is the use of prosthetics to improve the mobility of amputees. One of the most prominent locations requiring prosthetics is the lower extremities of the body. Lower limbs typically are more susceptible to injury in traumatic events, wars, and diseases and may need to be amputated. The goal of our research is to construct a prosthetic socket with embedded sensors, create a system that can collect pressure data in real time at the prosthetic socket-limb interface wirelessly, and analyze the collected data to extract useful features. The embedded sensor will be able to communicate with LabView, an engineering virtual workbench, where the parameters of the pressure applied will be quantified. Currently, a LabView program has been created that transmits a signal that creates a graph in real time. To differentiate between noise and the signal, the signal was substantially magnified. Further research will distinguish particular characteristics of the embedded pressure sensors to extract useful features for the future construction of the prosthetic socket. By successfully implementing these sensors, doctors will be able to study their patients' prosthetic sockets through an online database and monitor the pressure exerted on the socket in real time, ultimately improving amputees' quality of life.

#### **SAT-957**

##### **CHARACTERIZING THE EFFECTS OF SHADING ON THE PERFORMANCE OF A MOBILE PHOTOVOLTAIC ARRAY**

Quentin Samuels, Carl Lyles.

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With advances in technology, photovoltaics (PV) are becoming ever more feasible as a power source for electrified passenger vehicles. These mobile PV arrays, however, will experience operating conditions different than those of traditional PV arrays. For instance, shade caused by trees, buildings, dust, etc. may limit the performance of a mobile PV array. The goal of this research is to characterize the effects of shading on the performance of a mobile PV array designed for an electrified passenger vehicle. An electrified passenger vehicle with a roof-mounted PV array was placed under a series of characterization tests. These tests included shade tests to determine the effects of various levels of shading on the performance of the PV array. The shade testing was separated into two parts, which included fully covering and partially covering one of three adjacent PV panels in the roof-mounted array with materials of a known transparency. In doing so, the actual shade level on the PV array could be controlled.

During the tests, current and voltage loggers were used to record data from each of the three PV panels. In these controlled tests, the findings indicated a 15% greater reduction in power than anticipated from the shade level alone. The additional loss in power is attributable to mismatch losses in the PV array. For a mobile PV array, non-uniform and varying shade levels are likely to occur; therefore, further testing will be required to understand such effects on a mobile PV array.

#### **FRI-956**

##### **THE DEVELOPMENT OF A LOW COST SEMI-AUTONOMOUS, FIXED-WING AIRCRAFT WITH REAL-TIME VIDEO FEED**

Cody Torno, Luis Rodolfo Garcia Carrillo.

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As technological advancements in the fields of integrated circuits and battery polymers make electric propulsion systems more accessible, the development and understanding of unmanned aircraft systems (UAS) has begun to grow exponentially. Applications first used for military purposes are quickly being adapted to fit the needs of civil and governmental purposes. However, there are very few developed UASs that can exploit these technological advancements within a reasonable price range. This manuscript focuses on the development and testing of a low cost, high-versatility, fixed-wing platform for live video transmission. Platform choice was determined based on the requirements for high flight range and endurance while maintaining low operational footprint. The proposed UAS uses low-level autopilot capabilities for stabilized flight, with a minimum flight time of 60 m and 60 K distance. Additionally, a 3-axis gimbal-stabilized camera system was designed and implemented to produce a steady video stream to a ground control station.

#### **SAT-959**

##### **SOFT EXOSUIT FOR HIP ASSISTANCE**

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Over past decades, exoskeletons have been developed to augment movement of the body's biological joints, reducing strain put on the musculature. For the lower extremity, devices assist with long-distance walking, aid in heavy load carriage, and provide assistance and rehabilitation for those with disabilities. Recently introduced soft exosuits show benefits over previous robotic prototypes. Wearable materials make the devices light, efficient, and versatile in application, not limiting the body's natural range of motion. The lack of rigid links reduces the risk of misalignment of the devices with the biological limbs. A proof-of-concept prototype of a soft exosuit for hip assistance has recently been built and successfully tested for level-ground walking. The system was shown to apply up to 30% of the nominal forces needed in hip extension. The goal of this research is to redesign the current prototype to create a small, lightweight system that reduces the body's overall energy consumption during walking and remains fast and able to apply high forces at the correct time in the gait cycle. Ideally, the final design will pay for itself metabolically and further enhance human performance. The exosuit will be tested using a force-feedback-controller to demonstrate its ability to transfer forces to

the wearer. Its efficiency will be evaluated in a motion capture lab through electromyography and the monitoring of oxygen consumption in volunteers walking on a treadmill.

## **OTHER ENGINEERING**

### **FRI-962**

#### **COMPARISON OF ELASTODYNAMIC ANALYTICAL AND MESH-FREE NUMERICAL SOLUTIONS OF STEEL BEAMS SUBJECTED TO BLAST LOADING**

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Numerical methods have been in development for some time now and have been a principal source of modeling structures undergoing blast loads. Recent developments have led to more advanced numerical methods called meshfree methods where the structures are modeled by discrete points without structured mesh. Meshfree methods are shown to be particularly effective for problems involving large deformation and fractures, such as in modeling structures undergoing blast loads. The aim of this work is to compare analytical solutions of steel beam deflections to those predicted by meshfree numerical methods and thereby verifying the accuracy of these methods for beams undergoing blast-loading conditions. Analytical solutions for beam deflections are derived using blast equations and elastodynamics based on Euler-Bernoulli beam theory, and the radial blast waves are treated as planar. In meshfree modeling, elastodynamic solutions will be obtained for comparison with the analytical solution. In conclusion, this would ascertain that the meshfree methods used in this comparison are well suited for the analysis of bomb-threatened structures. Future work will be to consider the meshfree analysis of non-linear elastoplastic-damage behavior to understand the inelastic response of beams subjected to blast events.

### **SAT-962**

#### **ARTIFICIAL ENZYME-POWERED MICROMOTORS FOR WATER-QUALITY TESTING**

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We present a novel micromotor-based strategy for water-quality testing based on changes in the propulsion behavior of artificial biocatalytic microswimmers in the presence of aquatic pollutants. The new micromotor toxicity testing concept mimics live-fish water testing and relies on the toxin-induced inhibition of the enzyme catalase responsible for the biocatalytic bubble propulsion of tubular microengines. The locomotion and survival of the artificial microfish are thus impaired by exposure to a broad range of contaminants that lead to distinct time-dependent irreversible losses in the catalase activity, and hence the propulsion behavior. Such use of enzyme-powered biocompatible polymeric (PEDOT)/Au-catalase tubular microengine offers highly sensitive direct optical visualization of changes in the swimming behavior in the presence of common contaminants and to a direct real-time assessment of the water quality. Quantitative data on the adverse effects of the various toxins upon the swimming behavior of the enzyme-powered artificial swimmer are obtained by estimating common ecotoxicological parameters, including the EC50 (exposure concentration causing 50%

attenuation of the microfish locomotion) and the swimmer survival time (lifetime expectancy). Such novel use of artificial microfish addresses major standardization and reproducibility problems as well as ethical concerns associated with live-fish toxicity assays and offers an attractive alternative to the common use of aquatic organisms for water-quality testing.

#### **SAT-963**

##### **GANGLIOSIDE-COATED POLYMERIC NANOPARTICLES FOR TARGETED DRUG DELIVERY TO ANTIBIOTIC-RESISTANT BACTERIA**

Kate Newcomer, Ronnie Fang, Liangfang Zhang.

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With the threat of superbugs ever increasing, the use of nanoparticle technology has the potential to more effectively combat these antibiotic resistant bacteria. We are developing a biomimetic strategy for targeting nanoparticles to bacteria that takes advantage of the affinity that bacteria have for specific glycolipids. Nanoparticles made from the FDA-approved polymer poly(lactic-co-glycolid acid) (PLGA) will be coated with naturally derived gangliosides. The resulting lipid-polymer hybrid nanoparticle should exhibit specificity toward many types of bacteria including strains of *E. coli* and *H. pylori*. As a proof-of-concept, ampicillin will be used as a model drug and loaded into the nanoparticles using a double emulsion process during the particle synthesis procedure. The nanoparticles will be thoroughly characterized in terms of both their physicochemical properties as well as their stability in physiological buffer. We will examine the bacteria-targeting capability of our formulation as well as evaluate its efficacy compared to free ampicillin. Ultimately, we hope to demonstrate that ganglioside functionalization can be used as an effective strategy for developing bacteria-targeted nanoparticles, thus introducing a new strategy for addressing a pressing medical need.

#### **HEALTH**

##### **AUDIO/SPEECH PATHOLOGY**

#### **FRI-201**

##### **THE DEVELOPMENT OF ENGLISH WORD-FORMATION RULES IN ENGLISH-SPEAKING, MONOLINGUAL CHILDREN**

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*The University of Texas at Austin, Austin, TX.*

The knowledge and ability to use word-formation rules is highly correlated to other important aspects of language development such as vocabulary development and reading comprehension. However, most recent findings on the developmental trajectory of different rules are disjointed and variable. A firm understanding of the development of word-formation rules in typically developing children would improve clinicians' and educators' diagnostic accuracy of language use and knowledge in children with possible language disorders or delays. This study examines how certain compound and derivational rules develop in preschool- and early school-aged children with varying ages and vocabulary sizes. Forty English-speaking monolingual children between 4 and 7 years old will be called upon to produce real and novel



words using 3 types of word-formation rules: noun-noun compounding (e.g., snowman), derivational-er ending (e.g., driver), and derivational-y ending (e.g., spotty). We anticipate all participants to perform better on the compounding and derivational-er ending tasks in relation to the derivational-y ending assessment, as the 2 former rules have linguistic properties which may facilitate semantic transparency and, thus, early acquisition of the given rules. Additionally, we predict children with larger vocabulary stores to perform better on all 3 tests in comparison to children with smaller vocabulary sizes. Results would offer more insight on the developmental timeframe of different rules, as well as how linguistic structure of word-formation rules, age, and vocabulary knowledge might influence a child's understanding of certain language rules.

## **MEDICINE (E.G., DENTISTRY SURGERY OPTOMETRY VETERINARY)**

### **SAT-203**

#### **SUDDEN CARDIAC ARREST IN LATINO/HISPANIC POPULATIONS**

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Cardiovascular disease is one of the leading causes of death within the Latino/Hispanic population. Often the disease goes unnoticed until it manifests in the form of sudden cardiac arrest (SCA). Whereas the incidence and survival due to cardiac arrest and bystander response has been well documented and compared in the African American and Caucasian populations, there is a paucity of data in the Latino/Hispanic population. Variation in survival closely follows rates of bystander cardiopulmonary resuscitation (CPR) and automated external defibrillator (AED) use. It has been putatively accepted that African Americans have lower bystander CPR rates, but higher incidence of SCA, which is the opposite of Caucasians. The paucity of data on cardiac arrest incidence, bystander response, and subsequent survival among Latino/Hispanics may include absence of cardiac arrest registries in these neighborhoods, lower reporting due to fear of deportation or legal repercussions, and mis-categorization since existing registries do not consistently record race/ethnicity data. We suggest that a viable way to approach closing the gap is doing research within predominately Latin/Hispanic neighborhoods and encouraging major registries, such as the Cardiac Arrest Registry to Enhance Survival (CARES), to collect more granular race/ethnicity data, and including in larger cardiovascular disease longitudinal studies, such as the Multiethnic Study of Atherosclerosis (MESA) and the Study of Latinos (SOL) to include measurements on sudden cardiac arrest and knowledge of bystander CPR and AED use among Latino/Hispanics. We hypothesize that rates of SCA and bystander CPR and AED use in the Latino/Hispanic population will mirror that of the African American population.

**FRI-203****RETINOID METABOLISM IN MODULATION OF VASCULAR CALCIFICATION**

Diana Aponte-Colón<sup>1</sup>, Jorge Plutzky<sup>2</sup>, Shriram Nallamshetty<sup>2</sup>, Hong Wang<sup>2</sup>, Jiaohua Chen<sup>2</sup>, So Hun Kim<sup>2</sup>.

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Retinoids, the active metabolites of Vitamin A, exert important transcriptional effects that control a broad range of fundamental biological processes such as cell differentiation, proliferation, and apoptosis. Recent data from our group indicate that all trans retinaldehyde (Rald), the precursor of all trans retinoic acid (ATRA), increases bone density and protects mice against age-related bone loss. Furthermore, Rald induces bone morphogenetic protein 2 (BMP2) expression in both marrow-derived mesenchymal stem cells and whole bone. Given a growing body of evidence establishing important similarities between skeletal mineralization and vascular calcification (VC), we hypothesized that retinoids modulate VC. To investigate the effects of retinoids on mineralization in vascular cells, we employed inorganic phosphate (Pi)-induced VC in human coronary artery smooth muscle cells (HCASMCs), a well-established cellular model of VC. Our preliminary data indicate that both Rald and ATRA enhance Pi-mediated calcification in HCASMCs as demonstrated by alizarin red staining at day 7. We hypothesize that retinoids accentuate VC through induction of BMP-2. Retinoids may also modulate key VC inhibitors such as Fetuin-A, MGP, OPG, OPN, and BMP-7. The results of our studies may hold important therapeutic implications for targeting dysregulated mineralization in the vessel wall in patients at a high risk for VC, including individuals with diabetes mellitus, kidney failure, and osteoporosis.

(Supported in part by SHURP award R25 HL121029 and an award from the Biogen-IDEA Foundation.)

**SAT-202****CHARACTERIZING THE SAFETY AND EFFICACY OF FLUORIDE DENTAL VARNISH WITH APPLICATIONS FOR STANDARDS DEVELOPMENT AND CLINICAL RELEVANCE**

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Fluoride dental varnishes were analyzed to validate a standard method for measuring the total fluoride content of fluoride-releasing varnishes. The purpose of the varnish is to stop cavities from continual growth or to completely reverse formation. There are wide varieties of fluoride-releasing compounds in a dental varnish. They may contain sodium fluoride (NaF), sodium monofluorophosphate (MPF), amine fluoride (NH<sub>3</sub>-F), stannous fluoride (SnF<sub>2</sub>), or any combination of these fluoride compounds; therefore, the evaluation method must be capable of analyzing any fluoride present. This validation method is part of a multi-lab International Standards Organization (ISO) standard drafting process. The ISO method needs to accurately determine the quantity of total fluoride in any fluoride varnish as dispensed from a commercial container in an accurate and preferably simple manner. Fluoride measurements were

performed by ion selective electrode (ISE) properly diluted within total ionic strength adjustment buffer II (TISAB II). Fluoride ISEs are constructed from single-crystal sections of rare earth fluorides and respond to fluoride ion activity over 5 orders of magnitude while showing a high selectivity for fluoride over other common anions. Results from the study show that the digestion and measurement techniques proposed are repeatable and suitable for ISO method adoption. The methods were also adapted for the measurement of fluoride varnish release and fluoride uptake into a hydroxyapatite disk, the mineral form of dental enamel.

## **FRI-202**

### **SODIUM BICARBONATE MAY SLOW CKD PROGRESSION IN PEOPLE WITH NORMAL SERUM BICARBONATE CONCENTRATIONS**

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An estimated 16.2 million Americans with chronic kidney disease (CKD) are at risk for end-stage renal disease (ESRD) which is associated with significant morbidity, mortality, and economic burden. Sodium bicarbonate treatment in CKD patients with metabolic acidosis appears to slow the progression of CKD, presumably by reducing renal fibrosis. However, preliminary data suggest that an increase in renal ammoniogenesis, a normal physiologic response that prevents metabolic acidosis, will still promote renal fibrosis by activating the complement system within the kidney. Therefore, sodium bicarbonate therapy, which lowers renal ammoniogenesis, in people with CKD and normal acid levels may also reduce the rate of CKD progression. We hypothesize that sodium bicarbonate therapy in people with CKD and normal acid levels reduces renal fibrosis by reducing renal ammoniogenesis and intrarenal complement activation. To test this hypothesis, we are performing a randomized, placebo-controlled, double-blinded study with 74 participants with diabetes, normal acid levels, and CKD. Half will receive sodium bicarbonate and the other half will receive placebo for 6 months. The change in urinary transforming growth factor beta-1 (TGF- $\beta$ 1), a mediator of renal fibrosis, will be measured as the primary outcome; the changes in urinary complement and ammonia excretion (a marker of renal ammoniogenesis) will be secondary outcomes. We hypothesize that sodium bicarbonate will reduce urinary TGF- $\beta$ 1, complement, and ammonia excretion. If true, these results would support the hypothesis that sodium bicarbonate treatment is an effective and inexpensive strategy to prevent ESRD in patients with diabetic renal disease even if they have normal acid levels.

## NURSING

### FRI-204

#### **BREASTFEEDING INTENTION AND INITIATION WITHIN A DIVERSE POPULATION OF WOMEN IN GROUP AND INDIVIDUAL CARE**

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Compared to the Healthy People 2020 national target for breastfeeding initiation of >81.9%, breastfeeding initiation rates in Illinois were 70.2% in 2007 with substantial racial disparities: African American women having a 52% breastfeeding initiation rate compared to 64% and 85% in Caucasians and Hispanics, respectively. CenteringPregnancy (CP), an innovative model of group prenatal care, has the potential to improve breastfeeding across ethnicities. The objective of this prospective quasi-experimental study is to examine differences in breastfeeding intention and initiation between women in group and traditional individual care (IC) and across racial groups. A prospective, quasi-experimental study compared low-income ethnically diverse women (N = 1040) in CP and IC attending clinics across Illinois. Data were collected using interviews with women < 21 weeks gestation and 1-week postpartum. Analysis included generalized mixed models controlling for covariates. Results indicated that breastfeeding initiation rates were higher among women in group (86.8%) compared to women in individual care (83.8%), but the differences were not statistically significant ( $p = .19$ ). Racial disparities were found for intention and initiation. For intention to breastfeed, Hispanic women had the highest breastfeeding initiation rate (93.8%) followed by Caucasian (90.7%) and then African American (71.6%) women ( $p = .000$ ). Regarding breastfeeding initiation, Hispanic women had the highest breastfeeding initiation rate (89.3%) followed by Caucasian (84.5%) and then African American (67.0%) women ( $p = .000$ ). Breastfeeding initiation rates were similar in group and individual prenatal care. Racial disparities indicate that providers need to assess potential barriers to breastfeeding, especially among African American and Hispanic women, and work with them to develop strategies to reduce these barriers.

### SAT-204

#### **IMPROVING THE ATTITUDES TOWARD BREASTFEEDING IN LATINAS THROUGH A BREASTFEEDING PEER COUNSELING PROGRAM**

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Breastfeeding initiation rates and duration are lower in low-income women such as Latinas. This is important because many Latinas may not be educated concerning the benefits and importance of maintaining breastfeeding for at least a year. The purpose of this project is to measure the attitudes of Latinas toward breastfeeding peer counseling, comparing those with contact with peer counselors (PC) to those without contact. English-speaking Latinas from greater Elgin, Illinois, participated in the study by answering a questionnaire. Latina responses were then compared to non-Latina responses on questions concerning demographics and attitudes toward breastfeeding. Nurses at Sherman Hospital distributed the questionnaire to

appropriate participants. We expected attitudes toward breastfeeding to improve following contact with PC, thus increasing the initiation and duration of breastfeeding. The results demonstrated that, out of 96 participants, 76.2% of Hispanics were more likely to breastfeed and/or maintain a longer duration than non-Hispanics. There were also low numbers for contact with a PC in the Hispanic group, so there is not a clear answer if there was an impact by the PC in the Hispanic population. The next step would be to have a cultural and language-appropriate PC address the needs of this under-served population.

## **OTHER HEALTH/MEDICAL SCIENCES**

### **SAT-205**

#### **CAUSES AND COSTS FOR ED VISITS AFTER ADENOTONSILLECTOMY IN CHILDREN**

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Identifying strategies to reduce emergency department (ED) visits after pediatric adenotonsillectomy (T&A) could improve outcomes and reduce costs. To accomplish this, we reviewed the reasons, timing, management, and costs for children presenting at the ED after T&A. A standardized, activity-based hospital accounting system was used to create an observational cohort of children from an academic, pediatric otolaryngology practice who presented at the ED after T&A from 2011 to 2012. The reason for presentation, number of days after surgery, and facility costs for each visit were recorded. The study cohort included 176 patients. Five of the patients had visits unrelated to the operation. Of the remaining patients, 21% presented for post-tonsillectomy hemorrhage, 54% for dehydration, 13% for poorly controlled pain, and 12% for miscellaneous reasons. The mean post-operative day at the time of ED presentation was  $3.7 \pm 3.4$  days. The mean hospital facility cost when the patient was discharged from the ED was \$153 per visit. This increased to \$1,634 per encounter when the patient was admitted or observed overnight, and the cost per return to the OR for bleeding was \$1,392 per episode. A relatively significant portion of children presented to the ED after T&A for dehydration, poorly controlled pain, or hemorrhage. The costs from these visits are not insignificant. Developing strategies to reduce these visits may improve outcomes and reduce costs.

### **SAT-207**

#### **EFFECT OF INTRAUTERINE GROWTH RESTRICTION ON RETINAL VASCULAR DEVELOPMENT IN RATS**

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Retinopathy of prematurity (ROP) is a leading cause of childhood blindness. Risk factors include low birth weight, young gestational age, and poor postnatal weight gain. Intrauterine growth restriction (IUGR) causes low birth weight, but its effects on ROP remain incompletely

understood. We sought to study the role of IUGR in ROP using models representative of human disease. IUGR in rat pups was created by a well-established protocol in which pregnant rat dams underwent prenatal, bilateral, uterine-artery ligation 3 days before pup birth. Newborn IUGR pups or anesthesia controls were placed in a model of ROP, in which oxygen levels fluctuated between 50% and 10% every 24 hours. Controls were IUGR pups placed into room air (RA). Retinas were prepared as flat mounts, stained with lectin, and analyzed for areas of abnormal intravitreal neovascularization (IVNV) and peripheral avascular retina (AVA) to total retinal area, reported as percentages. Pup birth weights were no different among the three groups. At postnatal day (p)18, weights were greater in the IUGR+RA group than in the IUGR+ROP group. The differences in weight gain between birth and p18 were  $31.6 \pm 0.2$  g in IUGR+RA and  $14.5 \pm 0.6$  g in IUGR+ROP ( $p < 0.0001$ ). There was no AVA in the IUGR+RA group and  $22.8 \pm 3\%$  in the IUGR+ROP group ( $p < 0.0001$ ). There was no IVNV in the IUGR+RA group and  $3.8 \pm 1\%$  in the IUGR+ROP group ( $p = \text{NS}$ ). In this experiment, fluctuations in oxygen in the ROP model were associated with reduced body weight gain in IUGR pups and with increased AVA.

#### **FRI-206**

##### **VITAMIN D STUDY IN HEALTHY ADULTS**

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Vitamin D is a fat-soluble steroid hormone that has an important role in musculoskeletal health. It is mostly synthesized in the skin after solar exposure, and little is acquired from the diet. Vitamin D deficiency in older adults has been linked with determinants of disability, including falls and fractures. Vitamin D deficiency has received much attention as a risk factor for falls because of its effect on musculoskeletal health. Until now, there has been little study that investigates the association of vitamin D status and its determinants, like sun exposure and vitamin D intake, with age related changes in physical functioning, flexibility, physical activity, and depression. The purpose of this study is to cross-sectionally investigate the relationship between vitamin D status in 130 healthy adults over the age of 55. Vitamin D status was measured by serum 25-hydroxyvitamin D and vitamin D intake. Vitamin D intake was determined by a vitamin D and calcium food frequency questionnaire and sun exposure. The sun exposure was assessed by the sun exposure recall questionnaire and reflectance colorimetry using the IMS SmartProbe 400. Another purpose of this study was to investigate the relationship between vitamin D status and physical functioning, flexibility, food security, physical activity, and depression. Physical functioning was measured by the Established Population for Epidemiologic Studies of the Elderly physical performance battery. Flexibility was assessed by the Sit and Reach Test. Food security was evaluated by a 6-item U.S. Household Food Security Survey Module. Physical activity was measured by the International Physical Activity Questionnaire (IPAQ). Depression was evaluated by the Beck Depression Inventory.

**SAT-206****USING TECHNOLOGY TO ASSIST RURAL AND SPANISH SPEAKING FAMILIES OF PEDIATRIC ONCOLOGY PATIENTS**

Elena Fredericks, Mark Fluchel.

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The successful treatment of childhood cancers depends on the parents' ability to provide care and communicate with healthcare providers. Childhood cancers require treatment at specialized care centers, typically located in urban areas. As a result, pediatric oncology centers will often treat patients that come from rural communities and great distances. This poses unique challenges for both providers and caretakers. In addition to remote patients, Spanish-speaking immigrants make up a large percentage of pediatric oncology patients. Studies have shown that patients from both of these populations experience disparities in health care and may have poorer compliance, poorer understanding of medical treatment, decreased satisfaction, and increased complications. We designed a study to use tablet computers to facilitate medical treatment for patients from underserved communities. In order to assess the feasibility of such a study and allow for input from parents, we administered a brief exploratory survey to caretakers of childhood cancer patients. Of 21 participants, 71% of caretakers had experience with tablet computers, 86% had access to internet service, and 81% had WiFi access. Ninety percent of Spanish-speaking caretakers have had difficulty communicating with healthcare providers. Over 95% felt that tablet computers would help manage treatment. We concluded tablet computers may help parents manage their child's treatment and improve communication with providers. With input from potential participants, we have developed a study to evaluate the utility of video-conferencing, appointment calendars, electronic medication reminders, digital protocol information, and audio recordings in the pediatric oncology setting.

**SAT-208****ANALYSIS OF HEART RATE VARIABILITY AND CORTISOL DIURNAL PROFILES IN PSYCHOGENIC MOVEMENT DISORDER PATIENTS**

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We are interested in measurements of stress biomarkers in psychogenic movement disorder (PMD) patients given the hypothesis that abnormal movements seen in PMD patients are the result of converted psychological stress. Cortisol, a major stress hormone in the hypothalamic pituitary adrenal (HPA) axis is a stress biomarker. Its secretion is not understood in PMD patients. Heart rate variability (HRV) measurements provide quantitative assessment of autonomic activity. While reduced HRV has been seen in an assortment of anxiety disorders, it has not been well studied in the PMD population. As a result, we sought to determine cortisol diurnal profiles and heart rate variability in patients with PMD compared to healthy subjects. PMD patients and age-and-gender-matched healthy control subjects were hospitalized overnight for electrocardiogram (ECG) recording. The ECG data was analyzed using Impresario

software, artifacts removed, and ECG data was imported into Matlab for calculation of HRV parameters including standard deviation of the N-N intervals (SDNN), number of adjacent N-N intervals differing by more than 50 milliseconds (NN50). During hospitalization, saliva samples were collected at 5 different times and later analyzed by a commercial laboratory. Thirty-six PMD patients and 34 healthy controls were assessed in an ongoing investigation. Although not reaching statistical significance, cortisol levels were higher in PMD patients as compared to the healthy controls at 2 of the 5 times collected. Subjects with shorter symptom duration were found to have greater cortisol values on average.

#### **FRI-208**

##### **EVALUATING INTERVENTIONS FOR LATINAS AT RISK OF CARDIOVASCULAR DISEASE TO IDENTIFY CULTURALLY TAILORED PREVENTATIVE MEASURES**

Jacqueline Guzman, David Marquez.

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Cardiovascular disease (CVD), also known as heart disease, is a health problem that affects thousands of people in the United States. As the fastest growing minority group in the U.S., Latinos have the highest prevalence of risk factors for CVD such as diabetes and obesity. CVD is the leading cause of death in women, and Latinas are at higher risk. The major risk factors that contribute to CVD among Latinas include low levels of physical activity, excess weight or obesity, diabetes, and high cholesterol, among others. The goal of this literature review is to evaluate previous interventions targeted for Latinas in order to reduce risk factors and CVD. This review will also make recommendations for future culturally tailored interventions in order to increase physical activity in Latinas as a preventive measure against CVD. A review of the literature that examines interventions concerning CVD knowledge and its risk factors within the Latina population was conducted. CINAHL and PubMed databases were used to find articles. Many studies focused on awareness and knowledge of CVD by measuring how much women knew about CVD and its risk factors, but few focused on reducing them. Studies have shown positive outcomes for interventions focusing on promotion of group support. Spanish and/or bilingual interventions have better outcomes in Latinas for reducing CVD risk factors. Future interventions should focus on culturally tailored preventive measures that incorporate social support, mental and emotional health, and socially acceptable exercises, as these methods have shown to help reduce CVD and its risk factors among Latinas.

#### **FRI-207**

##### **PREVALENCE OF OBESITY IN LATINO YOUTH: IDENTIFYING EFFECTIVE TREATMENT AND PREVENTION**

Samuel Castro, David Marquez.

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Over the past three decades, the prevalence of childhood excess weight and obesity has increased substantially to epidemic proportions. Although prevalence has increased among youth of all ages of racial and ethnic groups, studies and data have continuously shown that Latino children and adolescents have been disproportionately affected. Researchers have found



that disparities exist by preschool age, suggesting that obesity originates during infancy. The purpose of this literature review is to determine long-term, effective methods of treatment and prevention that will benefit the health of Latino youth. A review of the literature that examines the current trends of obesity in Latino children with emphasis on intervention or prevention will be conducted. Databases such as PubMed were used to find articles. The cause of obesity is complex and influences racial/ethnic groups differently. Despite diligent investigations and different attempts at managing obesity, no single treatment option has been deemed generally effective. Excess weight and obesity rates appear to have plateaued in certain subgroups, such as non-Hispanic whites and those of higher socioeconomic status. Yet overall rates remain high, and racial/ethnic disparities continue to widen. Parents significantly impact the development of dietary and physical activity habits in children as they generally spend considerable amounts of time with them. Parents should be considered key figures in future studies as they are major influences on the behavioral plasticity of children. Addressing risk factors of adult health may lead to treatment and prevention of child and adolescent obesity prevalence.

### **PHYSICAL THERAPY/REHABILITATION/THERAPEUTIC SERVICES**

#### **SAT-209**

#### **THE EFFECTS OF AN AEROBIC AND COGNITIVE TRAINING INTERVENTION ON COGNITIVE FUNCTION IN CANCER SURVIVORS: A PILOT STUDY**

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There are more than 100 clinically distinct types of cancer, each having their own symptoms and requiring a different method of cancer treatment. Despite current advances, the positive effects from treatment are often matched and outweighed by negative effects. Chemotherapy-related cognitive impairment (CRCI) has been reported to negatively affect memory, concentration, reaction time, attention, cognition, organizational skills, linguistic abilities, executive function, and daily living activities. We examined the effects of 12-weeks of aerobic and cognitive training on cognitive function in cancer survivors who have undergone or are currently undergoing adjuvant treatment for cancer. A total of 13 cancer survivors and 2 non-cancer controls were broken into 4 groups based on the type of training they received. These 4 groups were cancer - aerobic (n = 2), cancer - cognitive (n = 2), cancer-aerobic and cognitive (n = 2), and non-cancer controls (n = 2). Each subject completed an initial comprehensive physical assessment, cognitive assessment, Quality of Life (QOL) assessment, Piper fatigue inventory, and Beck depression inventory. Following these assessments, a 12-week computer-based aerobic training, cognitive training, or flexibility training intervention was completed for every subject based on the subject's group. On completion, all of the variables were reassessed. Friedman's 2-way non-parametric ANOVA revealed significant ( $p < 0.05$ ) differences in QOL, depression, Piper fatigue subtest-B, the plank test, and the Weschler Memory Scale LMII. However, follow-up dependent measures t-tests only confirmed significant decreases in fatigue in the cancer-cognitive group. This data suggest that both cancer survivors and non-cancer controls respond favorably toward aerobic and/or cognitive training and that cognitive training alone may be specifically beneficial for cancer survivors suffering from CRCI.

**FRI-209****THE ASSOCIATION BETWEEN EXERCISE BARRIERS AND MOTIVES TO EXERCISE**

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Physical inactivity is a major problem that has been associated with chronic diseases such as obesity, diabetes, and cancer. Research suggests that physical inactivity leads to greater risks of heart attack or stroke to occur than smoking, obesity, hypertension, or high cholesterol. The majority of Americans do not meet current exercise guidelines: 150 minutes of moderate physical activity/week and 2 days of strengthening exercise. Studies have reported different barriers to being physically active range from lack of time and motivation, to other priorities and being too tired. Additional studies have investigated motives for exercise, including health, fitness, stress reduction, enjoyment/pleasure, attractiveness, and mood. However, there is little information on the associations between barriers to exercise and motivations for exercise. This information is needed to inform and develop health promotion interventions to promote physical activity targeting specific exercise motives and their associated barriers. The goal of this study was to explore the degree to which barriers to exercise vary with exercise motivations. Ultimately, our goal is to lower health risks by promoting physical activity in a targeted manner.

**SAT-210****A COMBINED THERAPEUTIC REGIMEN OF ENVIRONMENTAL ENRICHMENT AND AMANTADINE**

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Traumatic brain injury (TBI) affects 1.7 million people in the United States each year, making it a significant health care issue with limited treatment options. One therapeutic strategy that has been investigated is environmental enrichment (EE), which consists of a complex living space, novel stimuli, and increased social interaction that collectively confers cognitive and motor recovery when provided after TBI vs. standard (STD) housing. Furthermore, amantadine (AMT) is a pharmacotherapy with dopamine receptor agonist activity that has also been shown to improve cognition after TBI or concussion. Hence, the goal of this study is to test the hypothesis that combining EE and AMT would lead to greater motor and cognitive performance after TBI than either therapy alone. Anesthetized adult male rats received a controlled cortical impact or sham injury and then were randomly assigned to enriched or standard (STD) housing where AMT (10 mg/kg) or vehicle (VEH; 1.0 mL/kg) was administered intraperitoneally 15 minutes before testing every day for 19 days. Motor function (beam-balance/beam-walk) and spatial learning/memory (Morris water maze) were assessed on post-operative days 1 to 5 and 14 to 19, respectively. The data showed that the combination treatment group (TBI+EE+AMT) performed significantly better than the non-treated group (TBI+STD+VEH) in both the motor [ $p = 0.0038$ ] and cognitive [ $p = 0.0036$ ] tasks, which supports the hypothesis. Ongoing studies are evaluating potential mechanisms for the observed findings.

## **PUBLIC HEALTH (INCLUD. ENV. HEALTH/EPIDEMIOLOGY)**

### **SAT-213**

#### **SUDDEN CARDIAC ARREST IN LATINO NEIGHBORHOODS**

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Sudden cardiac arrest is one of the top leading causes of death, accounting for approximately 450,000 fatalities each year. Survival is contingent upon the execution of the chain of survival: 1) activation of EMS, 2) bystander CPR, and 3) use of an AED. Previous studies have discovered that majority Black neighborhoods have a high incidence of cardiac arrest and low performance of bystander CPR. In contrast, majority non-Hispanic White neighborhoods have lower incidence of cardiac arrest and higher performance of bystander CPR. Some of the barriers to learning CPR quoted by previous studies include financial factors, informational factors, and motivational factors. While multiple studies have demonstrated marked disparities in cardiac arrest treatment and survival in Black vs. non-Hispanic White neighborhoods, there is limited data comparing cardiac arrest in Latinos with other ethnic groups. The specific aims of this study are to determine the incidence of sudden cardiac arrest and rates of bystander CPR and AED use in Latino neighborhoods. By associating census tract data with cardiac arrest registry databases, cardiac arrest incidence and bystander CPR rates in majority Latino neighborhoods can be estimated. We hypothesize that incidence in Latinos will mirror incidence of other cardiovascular diseases and that given the language, financial, and legal barriers there will be lower performance of bystander CPR compared to White neighborhoods. The results of this study will help to better understand how the Latino population is affected by cardiac arrest and will lead to better targeting of CPR and AED training programs and cardiac arrest prevention.

### **FRI-212**

#### **ADENOSINE 5' MONOPHOSPHATE KINASE (AMPK) REGULATES MACROPHAGE ACTIVATION AND IMMUNITY AGAINST HELMINTHS**

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Parasitic helminth infections affect approximately 2 to 3 billion people worldwide. Helminth infections cause malnourishment, anemia, cognitive disabilities, and impaired vaccine efficacy against influenza and measles viruses. Helminth infections are generally chronic, lasting for decades and often associated with dampened immune responses. Given that many helminth-infected individuals experience malnutrition, the concept that host metabolic state regulates immune cell function is considerably important to address. In this study, we investigate whether adenosine 5' monophosphate kinase (AMPK) controls the balance between inflammatory and immunosuppressive pathways. Studies in bone marrow-derived macrophages (BMDM) stimulated with various toll-like receptor (TLR) ligands and cytokines demonstrate that

AMPK gene deficiency promotes a pro-inflammatory phenotype, characteristic of classically activated macrophages, as determined by high levels of TNF- $\alpha$ . In contrast, overexpression of AMPK in macrophages promotes immunosuppression characterized by high levels of IL-10 and TGF- $\beta$ 1. Furthermore, inoculation of mice that specifically lack AMPK expression results in enhanced susceptibility to the murine hookworm parasite *Nippostrongylus brasiliensis*, characterized by high levels of adult worms within the gastrointestinal tract. Therefore, our studies demonstrate that metabolic enzymes such as AMPK serve a key role in shaping the balance between M1 vs. M2 pathways and host resistance to parasitic worm infection. It may be possible that pharmacologic agonists of AMPK activity could be used to limit chronic worm infections.

#### **SAT-218**

##### **THE EFFECTS OF MATERNAL EXPOSURE TO THE ENVIRONMENTAL POLLUTANT POLYBROMINATED DIPHENYL ETHERS ON EPIGENETIC REPROGRAMMING OF METABOLISM-RELATED GENES OF THE OFFSPRING**

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Fetal development is a significant period in which great plasticity occurs and any dysregulation of epigenetic processes can potentially be associated with disease development such as obesity, heart disease, and various cancers. Several epigenetic studies have associated developmental reprogramming and methylation changes *in utero* from the maternal exposure to endocrine-disrupting chemicals (EDC) such as polybrominated diphenyl ethers (PBDE). Environmental exposure to PBDE is a major public health issue because it bioaccumulates and is transferable in breast milk. That transfer may cause toxic effects to the offspring, as well as alter developmental programming *in utero*. However, there is limited literature describing how maternal exposure to PBDE alters epigenetic changes on the offspring. We hypothesized maternal exposure to PBDEs induces DNA methylation of insulin (INS) and insulin-like growth factor 2 (IGF2) in offspring and results in higher susceptibility to metabolic disease development. We used DNA isolated human peripheral blood mononucleated cells (PBMCs) and the cord blood DNA from the Boston Birth Cohort. First, we determined the direct relationship between PBDE47 exposure and INS and IGF2 promoter methylation in PBMCs. We demonstrated PBDE47 alters the INS and IGF2 promoter methylation in PBMCs by methylation specific PCR. Second, we examined the gene-specific DNA methylation (INS and IGF2) of the cord blood and its association with the maternal PBDE levels. Knowledge of *in utero* epigenetic reprogramming changes to INS and IGF2 caused from PBDEs can potentially illustrate the association between maternal exposure effects on fetal reprogramming and potential metabolic disease development in their offspring.

**SAT-220****IS MATERNAL IRON STATUS ASSOCIATED WITH FETAL ALCOHOL SPECTRUM DISORDER GROWTH ABNORMALITIES**

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Fetal alcohol spectrum disorder (FASD) encompasses a group of adverse neurodevelopmental and physical abnormalities associated with prenatal alcohol exposure. Optimal maternal nutritional status may play a role in attenuating the teratogenic effects of alcohol on the growing fetus. This study explored the relationship between maternal iron status and FASD-related growth abnormalities. This study included 250 pregnant, Ukrainian women (alcohol-exposed, n = 135; non-exposed, n = 115) from the Collaborative Initiative on Fetal Alcohol Spectrum Disorders (CIFASD). At enrollment, information on demographics, pregnancy history, use of vitamin/mineral supplements, pre-pregnancy BMI, gestational age, and alcohol consumption were collected. Blood samples were drawn for measurement of iron status (serum iron, serum ferritin, and transferrin receptor). Linear regression analysis was used to test the association of iron measures on infant-related growth abnormalities. Women who consumed alcohol during pregnancy were less educated, had lower socio-economic status, higher parity, lower use of multivitamins, and lower serum iron compared to their non-exposed counterparts. Using simple linear regression, lower serum iron was significantly associated with lower birth weight, shorter birth length, and smaller head circumference. Lower serum transferrin receptor levels were significantly associated with higher birth weight, longer birth length, and larger head circumference only among those consuming alcohol. No associations were found in non-drinkers or with serum ferritin. Altered maternal iron status as a result of alcohol consumption may explain at least part of the FASD-related growth abnormalities. Improved maternal iron intake may improve growth outcomes related to FASD.

**FRI-223****A COHORT STUDY OF LOW BACK PAIN**

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Low back pain (LBP) is an epidemic that affects 1 in every 3 adults worldwide and 20% of all workers compensation claims in the United States. Most of our knowledge comes from cross-sectional studies. To further our understanding in etiology, disease course, pain treatment, and effects on daily living including work life, we conducted a multi-center, 8-year prospective cohort study. We evaluated potential risk factors for low back pain including demographics, job task analysis, physical activities, and psychosocial factors. We enrolled 828 workers from 27 employers within 34 diverse facilities located in 4 states. We found for LBP prevalence: lifetime prevalence of 63.4%, a 1-month period prevalence of 44.0%, and a point prevalence of 20.8%, respectively. In lifetime prevalence of LBP workers we found that men were twice as likely as women to report LBP, the average age was 39.4 years old, and they were more likely to have chronic health problems like diabetes and hypertension than people who never had LBP. We found an increased risk of LBP among workers in manufacturing companies like food, garage

door, office chair, salt products manufacturing, and warehouses. In addition, we found that the average worst pain score was 6.9 in a 0 to 10 scale, 98% of participants missed work due to LBP, 57% of LBP was work-related, and 13% had used opioids to treat their pain. We find that LBP is a more complex problem affecting all aspects of daily living for American workers and an extensive financial cost for their employers.

#### **FRI-224**

##### **IMMUNIZATION PROTECTION IN CHILDCARE**

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Childcare programs have often been recognized as a potential source of increased risk for outbreaks of vaccine-preventable diseases. The overall goal of the Immunization Protection in Child Care (IPiCC) project is to examine and identify barriers that need to be addressed to improve immunization coverage for children attending childcare programs. After recruiting and enrolling Utah childcare programs, IPiCC randomly assigned participating childcare programs to a control or intervention group. The childcare programs assigned to intervention groups received either a low or a high intensive intervention. After interventions have been implemented for 2 years, focus groups will be conducted specific to the intervention the childcare centers received. The aim of these focus groups is to receive feedback on the feasibility and effectiveness of the IPiCC interventions. Another aim is to describe whether childcare providers' knowledge, attitudes, and strategies concerning immunizations changed as a result of the interventions. Childcare program directors were invited to attend a focus group meeting specific to the intervention received. During this meeting, they were interviewed about their experience and opinions on the intervention. The interview questions and responses were recorded according to IRB standards. Focus groups are still ongoing, so a definitive conclusion has yet to be reached. After focus groups are completed, a complete analysis of the feedback will be conducted. Study outcomes will guide future immunization strategies for children enrolled in childcare programs.

#### **SAT-229**

##### **COMPLEXITY OF SCHOOL-AGE CHILDREN'S RESPONSES DURING HEALTH MAINTENANCE VISITS**

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Middle-childhood health maintenance visits target emerging emotional and behavioral issues of life-long importance, but little is known about the processes that lead children to form trusting relationships with doctors and verbally disclose sensitive personal information. Because of communication barriers and the fast-paced nature of health maintenance visits, we believe children are not answering questions to their fullest language capacity. In order to test this, health maintenance visits of 29 children ages 7 to 11 years (mean 9.5) and their post-visit

interviews were recorded and transcribed. Transcripts of children's' answers to open ended questions were analyzed for grammatical complexity by measuring mean length of utterances (MLU), the amount of vocabulary diversity (token-type ration), and the use of conjunctions. In the post-visit interviews, the average MLU, token type ration, and number of conjunctions used were 7.99 (SD = 3.17), 3.57 (SD = .98), and 29.15 (SD = 24.3) respectively. We hypothesize that children will have decreased MLU and token-type ratio and use less conjunctions in health maintenance visit when compared to the post-visit interview. These decreases in MLU and grammatical complexity may be attributed to factors relating to the doctor's behaviors – grammatical complexity of questions and explanations, rate and tone of speech, and non-verbal behaviors relating to warmth and kindness. In order to maximize the effectiveness of health maintenance, children must become verbally engaged partners in their own health care. To achieve this goal, doctors' communicative behaviors may need to be altered to eliminate communicative barriers between doctor and children.

#### **FRI-217**

##### **MOBILE MAMMOGRAPHY: FROM A LATINA'S PERSPECTIVE**

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Mobile mammography services are an increasingly used strategy to promote screening among Latinas. However, little is known about Latina patients' perceptions, experiences, and preferences. Data are needed to explore preferences for traditional clinic settings versus mobile services and the impact of perceptions and experiences with mobile services on preferences. We hypothesize that a high proportion of Latinas will prefer traditional clinic settings, preferences for traditional clinic settings may be due to Latinas' negative views of mobile services, and Latinas who have used mobile services in the past will be more likely to prefer mobile services. This current study used baseline survey data from a larger study for Latinas in western Washington State (n = 645). Only 15% of Latinas had previously obtained a mammogram with mobile services. Approximately 48% preferred traditional clinic settings, 2% preferred mobile services, and 50% had no preferences. Women explained these preferences were due to perceptions of greater quality, privacy, and safety. Women who had never obtained a mammogram with mobile services were more likely to prefer traditional clinic settings compared to women who had experienced a mammogram from mobile services: 48% versus 28%,  $\chi^2 = 20.92$ ,  $p < .0001$ . Latina women preferred traditional clinic settings, potentially due to a lack of experience with and misperceptions about mobile services. Educational advertisements and programs promoting mobile mammography for Latinas may help to raise awareness of the high quality, privacy, and safety found on mobile mammography services.

**FRI-219****EXPLORING THE POTENTIAL HEALTH BENEFITS OF ZONING POLICIES TO REDUCE ALCOHOL OUTLET DENSITY**

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Maryland law mandates a maximum of one alcohol retail outlet license per 1,000 people. Baltimore, Maryland has twice that number: 1,330 outlets for a population of 622,104. Numerous studies have demonstrated a positive association between alcohol outlet density and alcohol-related harms, such as increased violence, vandalism, and public nuisance. The city's health commissioner has called for a 15% reduction in alcohol outlets in the city by 2015. The revision to Baltimore City's zoning code currently under way will influence alcohol outlet density. This paper focuses on the provisions affecting "BD-7" tavern license types. These establishments will have to prove their tavern status by showing that 50% of sales receipts are from food sales and 50% of floor space is for on-site consumption. Researchers at the Johns Hopkins Bloomberg School of Public Health developed an assessment tool to evaluate whether BD-7-licensed taverns are operating according to the requirements, as well as to assess their interior and exterior marketing and enforcement of drinking laws. More than half of the taverns are anticipated to be in violation of the requirements. Preliminary visual and numerical data will be presented. Zoning can provide unique opportunities for influencing alcohol outlet density and service and marketing practices. Data collected in this project will inform the ongoing debates among Baltimore City policy makers about how to use the current zoning revision process to influence the city's overconcentration of outlets.

**SAT-224****CHARACTERISTICS THAT LEAD TO ATTRITION IN A FAITH-BASED WEIGHT LOSS PROGRAM FOR AFRICAN AMERICANS**

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Research has shown community and social support to be key components in crafting and implementing a successful weight-loss program for African American communities. Attrition, the reduction in participation or the weakening effect of dropouts, is a major problem in obesity treatment programs. We aim to deal with the obesity epidemic within the African American community through a faith-based weight loss study. This project focuses on examining the factors and characteristics that affect the success and retention of our program participants within 3 churches that have chosen to participate in this faith-based weight loss intervention. Through close monitoring and analysis of process evaluation forms, demographics, and stressors, we hope to find correlations and trends to ultimately find solutions to the effects of attrition.



**FRI-222****ANALYZING THE EFFECTS OF AIR POLLUTION ON COGNITION AND BEHAVIOR IN ELEMENTARY-SCHOOL-AGED CHILDREN RESIDING IN EAST LOS ANGELES**

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The effects of air pollution on the respiratory and cardiovascular systems are well documented, yet its effects on the brain are still not as well understood. A growing body of evidence points to air pollution as being much more toxic than previously thought, linking chronic exposure to high levels to accelerated cognitive decline, increased risk of neurodegenerative diseases such as Alzheimer's, and lower IQ scores in children. This study pilot tested a 43-item questionnaire designed to further probe possible risk factors identified in previous research. Questions included the proximity of a child's home and school from a busy road or freeway, the child's diet, physical activity, tobacco exposure, the child's behavior at home and school, as well as socioeconomic status and education of parents. The goal is 10 - 20 participants with parents answering for their child. Parents with children between ages 6 - 12 years residing in East Los Angeles are the target population. We expect preliminary results to yield a possible negative relationship between levels of air pollution and behavior and cognition. Despite the small sample size, this study will provide a way to test the effectiveness of the questionnaire in measuring the intended variables. Children remain one of the populations most vulnerable to air pollution as they are still undergoing brain development. With Los Angeles continuously ranking at the top of the worst cities in the United States in terms of air quality, it is clear that a significant number of children are being exposed to damaging levels of pollution.

**SAT-211****PRETRANSPLANT DIABETES MELLITUS, NEW-ONSET DIABETES AFTER TRANSPLANT, AND ACUTE REJECTION ASSOCIATIONS WITH ADULT HEART TRANSPLANT OUTCOMES**

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Acute rejection contributes significantly to mortality in adult heart transplant recipients. Immunosuppressive drugs reduce the number of acute rejection cases, but also increase the risk of diabetes after transplant. This study tested the associations of pretransplant diabetes (PDM), new-onset diabetes after transplant (NODAT), and acute rejection (AR) with heart transplant outcomes in adult recipients. A total of 9,674 recipients (age ≥ 18 years; 2004 - 2010) surviving with a functioning graft after 1 year were identified in the Organ Procurement and Transplant Network/United Network for Organ Sharing (OPTN/UNOS) database as of March 15, 2013. Recipients were stratified into 6 mutually exclusive groups according to diabetes and AR status at 1 year: group 1, neither (reference, n = 3,975); group 2, NODAT alone (n = 858); group 3, PDM alone (n = 1,592); group 4, AR alone (n = 1,861); group 5, NODAT and AR (n = 557); and group 6, PDM and AR (n = 831). Analyses were adjusted for confounding factors. Groups 4 to 6 were associated with a significantly higher risk of graft failure. Groups 2 and 3 were relatively similar; whereas, group 6 was associated with a significantly greater risk of graft failure than

group 5. In adult heart transplant recipients with a functioning graft after at least 1 year, AR during the first year was a major predictor of graft failure. PDM and NODAT were not associated with any significant difference in transplant outcomes. In contrast, those with both AR and PDM had a higher rate of graft failure during the follow-up period.

#### **SAT-219**

##### **THE WNT INHIBITOR APCDD1 CONTROLS PRUNING AND MATURATION OF THE RETINAL VASCULATURE BY MODULATING $\beta$ -CATENIN SIGNALING**

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In the central nervous system (CNS) endothelium, the blood-brain barrier (BBB), restricts paracellular diffusion of molecules into the brain by forming high-resistance, tight junctions between endothelial cells. Here, we report that *Apccdd1*, a downstream effector of *Wnt*/ $\beta$ -catenin signaling, is highly expressed in brain and retina endothelial cells during angiogenesis when endothelial cells acquire barrier properties. Moreover, *Apccdd1* is selectively expressed in CNS, but not in peripheral endothelial cells, and it can interact with both *Wnt* ligands (e.g., *Wnt7a*) that induce barrier properties in endothelial cells as well as non-canonical *Wnt* ligands (e.g., *Wnt5a*). In order to test if *Apccdd1* is necessary for various aspects of angiogenesis and barrier properties, we have generated *Apccdd1* knockout mice using gene targeting and have examined vascular density in the brain and retina at various developmental stages. By E16.5 of embryonic development, *Apccdd1*<sup>-/-</sup> mice have normal brain vascular density similar to wild-type littermates, whereas by postnatal day P5, the mutants have increased brain vascularization. Similarly, while the initial stages of retinal angiogenesis are normal, the *Apccdd1*-deficient mice have an increased vascularization by P10 - P12 when vascular pruning occurs in the retina. Furthermore, *Apccdd1*<sup>-/-</sup> mice show no increase in endothelial cell proliferation, but they have deficits in vascular pruning, suggesting that *Apccdd1* plays an essential role in pruning and maturation of the CNS vasculature. We are currently analyzing whether *Apccdd1* mice have deficits in BBB formation.

#### **SAT-222**

##### **THE EFFECTS OF AIR POLLUTION ON PATIENTS WITH IDIOPATHIC PULMONARY FIBROSIS**

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Idiopathic pulmonary fibrosis (IPF) is a chronic, progressive, interstitial lung disease characterized by irreversible lung destruction that is universally fatal. The disease has no clear etiology, and there are no effective therapies. Individuals with IPF experience acute exacerbations or rapid clinical decline. Exacerbations may result in worsened lung function, respiratory failure, and even death. Epidemiologic studies suggest an association between environmental exposures and IPF development, particularly between IPF exacerbations and ozone air pollution. In pulmonary diseases, symptoms, lung function, and exacerbations are influenced by air pollution. Studies in Salt Lake County have demonstrated that particulate

pollution is associated with increased respiratory symptoms and decreased lung functions in individuals with chronic obstructive pulmonary disease. Our study initiates research investigating the impact of air pollution on IPF. We will measure daily respiratory symptoms, conduct a weekly assessment of lung function and quality of life, and investigate biomarkers in serum and exhaled breath condensate. We hypothesize that increased short-term levels of outdoor air pollution will be associated with increased respiratory symptoms, decreased quality of life, and decreased lung function in patients with IPF. Our study may determine pollutants that should be avoided and represents one of the most effective interventions for IPF, slowing down the progression rate of IPF. Our study will also provide good data for future studies investigating the effects of air pollution on a variety of lung diseases.

#### **SAT-216**

##### **OBESITY, CHRONIC DISEASE, AND PHYSICAL ACTIVITY IN THE RURAL SOUTHWEST**

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Obesity is a serious health issue and is a primary risk factor for a myriad of chronic diseases. Obesity is rooted in sociocultural, economic, and political factors, and thus apparent disparities exist in the obesity disease burden. In the United States, poorer and rural populations as well as Hispanic and American Indian populations suffer elevated obesity rates. Because obesity is situated in the psychosocial context, prevention programs should be tailored to meet the needs of individual communities. However, most prevention efforts have been designed for urban, non-Hispanic, and non-Native populations, and more research is needed in order to design successful prevention programs for rural and minority communities. This study focuses on Cuba, New Mexico – a rural, under resourced, and primarily Hispanic and American Indian community that suffers a severe obesity and chronic disease burden. The study evaluates the reach and effectiveness of the University of New Mexico Prevention Research Center's Step Into Cuba campaign, a physical-activity focused prevention program. A regression analysis of data from a multi-year cross-sectional Step Into Cuba survey will be performed using R software and will attempt to identify a least-reached demographic in terms of both exposure to, and behavioral changes in response to, the program. For sociocultural and economic reasons, older men are expected to be the least-reached and least-influenced demographic. Obtaining a more nuanced understanding of Step Into Cuba's influence is important in order to improve the program, and also in order to design more effective rural and minority obesity prevention strategies.

**SAT-223****HEALTH DISPARITIES WITHIN LESBIAN, GAY, BISEXUAL, AND TRANSGENDER COMMUNITIES IN NEW MEXICO**

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Unequal access to health care is an issue that many lesbian, gay, bisexual, and transgender (LGBT) individuals face in New Mexico. Unequal access is exacerbated by conditions of rural isolation, poverty, realities of ethnic/cultural minority status, and other social determinants of health. These conditions discourage some LGBT patients from visiting professional health clinics due to fear of discrimination. This leads to disparate health treatment for LGBT individuals, preventing gay men and transgender persons from seeking tests for HIV/AIDS, or screening for breast and cervical cancers in lesbian women. The project asks what can be done to increase feelings of safety and overall health care delivery for LGBT individuals in primary care settings. To answer these questions, our research team will conduct a series of town hall meetings to record the major issues that affect health care for LGBT persons in 5 rural communities across the state. Identified themes will be used to develop future research projects, but will be used immediately to provide direction for a one-day health summit to discuss LGBT health at a statewide level. In the summit, we will ask participants what resources currently exist for LGBT health and health care, what needs to be done to address unattended health concerns, and what it means to have a healthy LGBT community. Social media, a website, surveys, and emailing a “call for presentations” are the techniques we are using to recruit for town halls and the summit.

**FRI-210****INTERACTION OF VITAMIN B12 AND ANCESTRAL GENETIC BACKGROUND WITH ADIPOSITY IN CHILDREN**

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Obesity is a complex disease that affects children and adults. Differences in obesity prevalence have been documented among racial/ethnic groups within the United States. These differences may respond to the interaction of micronutrients with individuals’ ancestral genetic background (ADM). We attempt to determine if the interaction (INT) of Vitamin B12 (B12) consumption and ADM influence levels of body fat among children from a multi-ethnic sample. B12 consumption was obtained from dietary recalls in a sample of 322 children from the Birmingham metropolitan area. Body fat was obtained through dual-energy X-ray absorptiometry, and ADM was calculated from ancestral genetic markers. Multiple regression models were used to determine the contributions of INT to levels of body fat after adjusting for relevant covariates. Levels of B12 did not differ among racial/ethnic groups. In a model evaluating the contributions of ADM, B12, and INT, B12 and INT significantly contributed to levels of body fat ( $p = 0.0008$  and  $p = 0.0036$ , respectively). An individual’s genetic background may interact with micronutrient consumption to impact levels of body fat and may partially explain observed

racial/ethnic differences in obesity-related measurements. Understanding how individuals' ancestral background and nutrient consumption contributes to adiposity levels may be of importance when identifying pediatric obesity prevention strategies.

#### **FRI-220**

##### **ADOLESCENT EVALUATION OF ACCELEROMETER-LINKED MOTIVATIONAL WEBSITES**

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Adolescent obesity is a significant problem in New Mexico. Nearly 30% of high school students in New Mexico are overweight or obese, and these students are disproportionately likely to be Hispanic or Native American. Because adolescent obesity is a strong predictor of obesity in adulthood, it is important that at-risk youth participate regularly in moderate to vigorous physical activity (MVPA). Technology, such as accelerometer-linked motivational websites (ALMWs), has the potential to play a role in motivating adolescents to engage in regular MVPA. Unfortunately, little research has been done on the efficacy of ALMWs for adolescent populations. In our study, 30 adolescents were separated into 3 cohorts and given a fitness tracker (Fitbit Flex, Polar Loop, or Zamzee) to wear continuously for 4 weeks. Participants indicated their demographics and completed a physical activity questionnaire prior to the study. Adolescents within the same cohort wore the same accelerometer and completed weekly surveys about the perceived benefits and value of the ALMW, continuity and difficulty of use, and inclination toward long-term, habitual use. Also, the number of online features that each adolescent used and their level of physical activity were recorded daily. We expect that descriptive data on the positive and negative aspects of each ALMW and objective data on the time spent in MVPA will allow the feasibility and approval of these ALMWs to be assessed. Further evaluation of the efficacy of ALMWs and other technology in preventing and treating adolescent obesity is warranted.

#### **FRI-221**

##### **RURAL HEALTH PROVIDERS' PROFESSIONAL LICENSURE AND THEIR MANAGEMENT OF CHRONIC NONCANCER PAIN (CNCP) PATIENTS USING PRESCRIPTION OPIOIDS**

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Prescription opioid misuse disproportionately affects rural areas in New Mexico. Studies have shown that providers in rural areas struggle with treating chronic noncancer pain (CNCP) patients with prescription opioids because they are concerned with oversight, regulations, and negative health outcomes. Our hypothesis is that years of experience for providers in rural areas correlates with how comfortable they feel about managing CNCP patients. The purpose of our project is to analyze baseline survey data from providers in rural areas to examine beliefs, attitudes, and norms around opioid prescribing and the management of CNCP; and to correlate these beliefs with years of practice. This will be accomplished by analyzing the surveys and workshop evaluations. The surveys (n = 38) were sent to the providers before the workshop. The evaluations (n = 57) were completed by the providers who attended the CNCP management workshop. The surveys and workshop evaluations collected general demographic information as well as information regarding the beliefs, attitudes, and norms of the providers toward the management of CNCP. These data have been entered into REDCap, a data collection

program, and exported into STATA, a statistical software program, to calculate the mean, mode, and median. Basic analysis on the correlation between years of experience will be run in relation to demographic information to identify any other correlations. Based on the preliminary data, there is a correlation between years of experience and opioid prescribing habits. However, this correlation is not causal. Further studies are needed to examine this correlation and other factors associated with physician prescribing behavior.

#### **FRI-218**

##### **UNDERSTANDING THE PERCEPTIONS OF AMERICAN INDIANS IN OKLAHOMA**

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Numerous studies can be found to better understand disproportional morbidity and mortality rates among American Indians and Alaska Natives (AI/AN). Research suggests multiple sources are used for these rates; however, few investigations can be found seeking the perceptions of this special population. In this study, sponsored by the Oklahoma Area Tribal Epidemiology Center and AARP, a Tribal Community survey was conducted to better understand the beliefs of AI/AN residing in Oklahoma. The 313 participants of the survey were AI/AN community members aged 40 years or older. This comprehensive assessment provided information on the challenges and priorities in life, monthly expenses and discounts, demographics, and consumer related issues. Interviews were conducted face-to-face at various tribal community meetings, luncheons, health fairs, and powwows. One result of this assessment indicated seeing grandchildren happy or being a part of their lives ranked the highest priority of those interviewed. Another result suggested personal health problems/staying healthy was the single most important problem facing those who are mid-life and older. Additional results from the survey will be further analyzed so prevention and education programs can be developed to cater to the specific desires and needs of the AI/AN population in Oklahoma.

#### **SAT-221**

##### **UNDERSTANDING THE RELATIONSHIP OF TRAILS, SOCIAL CAPITAL, AND HEALTH IN CUBA, NEW MEXICO TO INFORM A HEALTH IMPACT ASSESSMENTS**

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Health impact assessments (HIA) have been conducted throughout the United States, but few have been conducted in rural communities, specifically on the development of trails. This study will explore the relationship between trails, social capital, quality of life, and health to determine if trail building in the small, rural, multi-ethnic community of Cuba, New Mexico is associated with increased social capital and thereby increased health. First, a literature review of the benefits of social capital on health and in relation to trails will be done addressing the importance of social capital for a community. Second, STEP-HIA survey data will be analyzed

using descriptive statistics for percentages of people indicating if they walk with family/friends and gain both social and health benefits from the trails. Third, interview data from Cuba residents will be explored looking at the relationship between physical activity, access to trails and social support. This analysis will be done using the qualitative data analysis software, NVivo. Overall, we expect these results will support the development of trails in Cuba, New Mexico, based on social capital and health. This information will be highlighted in the HIA to influence decision makers regarding the location of new trails in and around Cuba. These findings can then be used as evidence to plan the development of trails in other communities, particularly in rural areas surrounded by federal lands.

## **SAT-212**

### **ASSESSMENT OF COMMUNITY CAPACITY FOR URBAN GARDENING IN EAST LOS ANGELES USING GOOGLE EARTH AND GROUND-TRUTHING STREET INTERVIEWS**

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Urban agriculture is a practical approach to increasing low-income population consumption of fruits and vegetables, thereby possibly decreasing the population prevalence of obesity-related chronic diseases. The hypothesis is that urban gardening, or the growing of vegetables in residential areas, has the potential to significantly increase local availability of fresh produce. Google Earth Pro aerial maps were used to identify potential plots for starting a home garden. Using this information, a sample of 12 residences within a 0.25 mile buffer around each of 30 randomly selected stores will be surveyed for ground-truthing, providing a maximum of 360 residences overall. Preliminary results showed 1.1% of residences have neither a frontyard nor a backyard. Another 4.2% had both a frontyard and backyard that were functionally unavailable for gardening either because there were large trees preventing seeds from sprouting in the yard or because they were paved over or had some concrete structure covering the soil. This left 94.7% of residences with some capacity to host a garden. Forty-four percent (44%) of backyards were irrigated enough to include a garden; another 6% had enough soil to sustain a garden but were not irrigated. Eighty-four (84.2%) percent of frontyards were irrigated enough to include a garden; another 2% had sufficient soil to support a garden but were not irrigated. In short, most East Los Angeles residences not only have the capacity to support a garden plot but are sufficiently irrigating the soil that green vegetation is discernible from aerial reconnaissance.

**FRI-211****MATERNAL ANTHROPOMETRIC MEASURES, AND THEIR ASSOCIATIONS WITH ANTEPARTUM DEPRESSIVE SYMPTOMS: FINDINGS FROM POUCH STUDY**

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The aim of this research is to study antepartum depressive symptoms in relation to maternal anthropometrics in both pre-pregnancy and 7 to 15 years post-pregnancy. This analysis used data from The Pregnancy Outcomes and Community Health (POUCH) Study that included 3,019 women from 5 clinics in 52 different Michigan communities. At enrollment (16 to 27 weeks gestation) depressive symptoms were measured using the CES-D (Center for Epidemiologic Studies Depression Scale) and women reported their height and weight prior to gravidity. Pre-pregnancy BMI was calculated accordingly. CES-D data was categorized using a standard cutoff of high ( $\geq 16$ ) and not high ( $< 16$ ). The 3,019 women were examined for the maternal follow-up study 7 to 15 years post-pregnancy and direct measures were obtained for their height and weight. High CES-D ( $\geq 16$ ) was associated with pre-pregnancy BMI categories of underweight ( $< 18.5$ ) aOR = 1.9 (95% CI 1.2, 2.9) and obese ( $\geq 30$ ) aOR = 1.3 (95% CI 1, 1.6) in White/other women, but not in African American women. At maternal follow-up, high CES-D in pregnancy ( $\geq 16$ ) was related to high BMI in both White and African American women. It is important to identify risk factors for antepartum depressive symptoms. Physicians should make it a priority to screen for depressive symptoms during gravidity. By noting this association, health care providers have a better understanding of the relationship between maternal anthropometrics and depressive symptoms during pregnancy. Recognizing a woman at high-risk for antepartum depression could prevent negative outcomes in the infant and mother.

**SAT-214****MATERNAL EXPOSURE TO HOUSE DUST MITES MODULATES AIRWAY HYPERRESPONSIVENESS IN MICE AND ASSOCIATES WITH EPIGENETIC CHANGES IN THEIR LUNGS**

Isabel Jimenez-Bush<sup>1</sup>, Tyna Dao<sup>2</sup>, Nathachit Limjunyawong<sup>2</sup>, Wayne Mitzner<sup>2</sup>, Wan-Yee Tang<sup>2</sup>.

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Asthma is the most common chronic childhood disease and its risk may be strongly influenced by prenatal events. However, existing knowledge does not provide a full understanding of this, prompting us to explore the underlying mechanisms in asthma pathogenesis in order to prevent childhood asthma. We hypothesize epigenetic changes *in utero* will account for the changes in the airway hyperresponsive phenotypes in the offspring. The present study aims to determine the effect of maternal exposure to a house allergen (house dust mite, HDM) on the lung function of their offspring and how this associates with DNA methylation changes. The first part of the study uses an experimental asthma model and investigates lung function of the offspring by measuring airway hyperresponsiveness (AHR) and examining the differential immune cell profile from bronchoalveolar lavage cells. The second part of the study examines the global and gene-specific DNA methylation of mice tracheas by using methylation specific



polymerase chain reaction. Our preliminary results demonstrated maternal HDM exposure protects the HDM-induced AHR in the offspring and associates with the increase of LINE1-methylation. It suggests maternal exposure did alter the methylome of the offspring globally. Further experiments will be needed to identify gene-specific methylation changes in the offspring and investigate the epigenetic effects on the lung function. This project is important for public health in that it raises awareness of environmental exposures for pregnant women. It may improve education and curb the incidence of childhood asthma.

#### **SAT-217**

##### **THE EFFECTS OF HETEROGENEITY ON MEASLES OUTBREAKS WITH FRANCE AS A CASE STUDY**

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The rubeola virus, commonly known as measles, is one of the major causes of vaccine-preventable deaths among children worldwide. This is the case despite the fact that an effective vaccine is widely available. Even in developed countries, elimination efforts have fallen short, as seen by recent outbreaks in Europe which had over 30,000 cases reported in 2010. The string of measles outbreaks in France from 2008 to 2011 is of particular interest due to the documented disparity in regional vaccination coverage. The impact of heterogeneous vaccine coverage on disease transmission is a broad interest and is at the heart of this preliminary study. A susceptible-exposed-infectious-recovered (SEIR) multi-patch epidemiological model capturing the regional differences in vaccination rates and mixing is introduced. The mathematical analysis of a simple two-patch system is carried out to help our understanding of the dynamics of multi-patch systems. Numerical simulations are generated using a multi-patch system motivated by our desire to connect theory to applications. We are particularly interested in connecting the model to the outbreak data from France, a step that would help explore the role of regional adherence to intervention policies in increasing or decreasing measles prevalence.

#### **FRI-216**

##### **UNDERSTANDING THE RELATIONSHIP BETWEEN DEMOGRAPHIC CHANGES IN SOUTHERN CALIFORNIA AND LOCALIZED ENVIRONMENTAL HEALTH RISKS**

Francisco Rios Casas, Juan De Lara.

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Prior examinations of the natural and built environment have clarified some of the exposure risks that individuals may face in Southern California. While additional research has also shown that many potential dangers are not equally distributed, patterns of environmental and public health inequities, including pollution and lack of access to social services, may correspond to an individual's race, ethnicity, or socioeconomic status. Currently, it is unclear how these patterns may change given the transformations that are occurring in the region's demographic and spatial organization. In order to understand what the effect of demographic change might mean for the quality of life in the region, an examination of changes at the local level were considered along with changes in data on different environmental factors. Demographic and

environmental health hazard data from the years 2000 through 2010 were obtained from federal, state, and local public agencies and analyzed together using geographic information system (GIS) software to track proximities and change over time. Preliminary analyses have shown there are very distinct changes which have taken place in various parts of Southern California and these often correspond to some of the areas with above average levels of pollution. Given the relative abruptness of these changes, it is unclear whether relevant parties or the region as a whole are prepared to take the necessary steps to ensure former patterns of environmental injustices are not repeated. These findings could also have implications for understanding how communities change and how urbanization can contribute to overall quality of life.

#### **SAT-215**

##### **PREDICTIVE FACTORS OF INITIATING TOBACCO CESSATION AMONG FEMALE SMOKERS IN DRUG ABUSE TREATMENT**

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The aim of this pilot study is to identify which factors among female current smokers in residential drug abuse treatment programs serve as predictors of voluntarily attending a tobacco cessation program after participation in a 3-week, group-based readiness intervention. The readiness intervention uses the Prochange Expert Systems intervention to assess stage of change in readiness to quit and provides strategies to support progression through the stages toward cessation. Preliminary analysis includes 41 female smokers for whom we have complete data. Measures were obtained using an electronic questionnaire that included the smoking knowledge, attitudes, and services (S-KAS) survey and items pertaining to demographic information, smoking behavior, risk perception, and advertising receptivity. Statistical hypothesis tests suggest that smokers are more likely to attend smoking cessation groups if they have never tried nicotine replacement therapy (NRT), have higher risk perception, and attend more readiness groups. Non-Hispanics are also more likely than Hispanics to attend the smoking cessation program. A logistic regression model further supports the correlation between higher risk perception and smoking cessation initiation. Follow up data collected after the readiness intervention shows a statistically significant decrease in cigarettes per day, increase in past year quit attempts, increase in NRT use, and increase in risk perception. These findings support the implementation of readiness interventions that communicate smoking risks in order to motivate drug abuse treatment populations to initiate smoking cessation.

## HUMANITIES

### HISTORY (EXCEPT HISTORY OF SCIENCE)

#### FRI-105

##### THE POLITICS OF SELF-PROGRESSION: FROM SLAVE TO BLACK LEADER DURING THE ENLIGHTENMENT PERIOD

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After America won its independence in 1776, citizens established a national ideology. Not long after, however, Americans began to long for expressing individuality and slaves began to write on the attainment of a new identity. This study examines the effect of social barriers on slaves' achievements of their idealistic selves. Slave narratives from the 18<sup>th</sup> century and early 19<sup>th</sup> centuries, periodicals from the 18<sup>th</sup> century, and autobiographies will be analyzed alongside Jerrold Siegel's "Idea of the Self" and Michal Sobel's "Teach Me Dreams". The findings will take us on a journey which shows how slaves like Oladuah Equiano progressed from slave to Black leader.

### LETTERS (EXCEPT LINGUISTICS)

#### SAT-105

##### PAPERS AND LEGITIMACY: AN ANALYSIS OF LEGAL DOCUMENTATION AND MIGRANT SALVADORANS' PERCEPTIONS OF BEING AMERICAN

Beatriz Maldonado<sup>1</sup>, Josue David Cisneros<sup>2</sup>.

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This research highlights Salvadoran migrants' identities within the United States since their departure from El Salvador during its Civil War. The purpose of this research is to provide a historical context of the Salvadoran Civil War and an analysis of citizenship documentation transitions upon arriving to the United States. In doing so, we demonstrate how documentation builds an influential and detrimental power over the Salvadoran migrants' participation within the community. It is important to mention the Civil War because of two reasons: 1) for its introduction to various stages of enduring violence, and 2) for its impact on policy migration laws toward Salvadoran refugees. This research not only portrays the various shifts of violence, but it also distinguishes documentation as a form of classism. More importantly, the findings reveal a correlation between the dynamics of violent documentation and the Salvadorans' distorted, misguided, and inconclusive perceptions that they hold about the concepts of belonging and identity.

## OTHER HUMANITIES

**FRI-106**

### **POLICING BLACKNESS: RECURRING STATE VIOLENCE AND POLICE MISCONDUCT IN AUSTIN, TX, 1998 to 2013**

Taylor Carr, Eric Tang.

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This study investigates police misconduct and tense police-community relations in Austin, Texas, using data gathered by a quantitative media content analysis of the Austin Chronicle and Austin American Statesman. Using specific keywords such as "police misconduct", the Austin Chronicle and Austin American Statesman were searched for descriptions of incidents of police misconduct against citizens and tense police community relations that appeared from January 1, 1998, to December 31, 2013. Relevant articles were analyzed based on the race and gender of the officers and victims, as well as issues of socioeconomic class. Developing findings and results are currently in progress.

## MATHEMATICS & STATISTICS

### APPLIED MATHEMATICS

**SAT-802**

### **SEGMENTING IMAGES THROUGH REPRESENTATION AS A CONTENT-RICH NETWORK**

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Image segmentation is the process consisting of partitioning digital images into multiple sections with the goal of detecting objects within the image. In this work, we represent an image as a graph, where each pixel is a node in the graph and an edge is present between 2 nodes if they are close spatially within the image. In particular, we treat the image as a content-rich graph, where each node is associated with a vector of different features of the image, such as RGB and HSV (hue saturation value) color representations and textures. We consider graph cut and clustering methods to partition the nodes, resulting in a segmented image. We use the information theoretic approach, the content map equation, which minimizes the description length of the network by compressing the graph into distinct modules of nodes giving the partitioning of the image. We compare this method to existing graph-cut methods, such as normalized cut, on a variety of images. Implementation of the content map equation on a simple black and white image provides promising results which encourage further investigation on more complex images.

**FRI-805****A MODEL FOR STRIPE RUST GROWTH WITH TWO FUNGICIDAL EFFECTS**

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Stripe rust, also known as yellow rust, is a pathogen caused by the *Puccinia striiformis* fungus that affects host crops, primarily barley and wheat. It is the most prevalent strain of wheat rust within North America and can account for a significant amount of yield loss within a harvest. Two fungicidal effects, anti-sporulant and preventive, are considered to inhibit further spread of the infection and reduce susceptibility, respectively. In order to estimate the dynamic yield loss of a wheat crop infected by stripe rust undergoing fungicide application, a single-host, single-pathogen compartmental model is introduced using a system of nonlinear ordinary differential equations. We identify the stability conditions associated with the disease-free and endemic equilibria. Numerical simulations are then used to examine the time-dependent behavior of fungicide efficacy and approximate yield loss. Furthermore, sensitivity indices are calculated to study the impact of fungicide efficacy and retention relative to plant growth.

**FRI-815****UNCOVERING CARDIAC DYNAMICS USING A MODEL INDEPENDENT TECHNIQUE FOR EIGENVALUE ESTIMATION**

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Cardiac alternans, a beat-to-beat alternation in action potential duration in cardiac cells, is a harbinger of ventricular fibrillation. Ventricular fibrillation is a fatal arrhythmia and leads to sudden cardiac arrest which takes the lives of about 300,000 Americans each year. Alternans is characterized by an eigenvalue of the Jacobian approaching -1. Unfortunately, specifying a model to fully describe cardiac dynamics may be impossible. Furthermore, the full state space may not be physically measured. Petrie and Zhao developed statistical data-driven statistical techniques to estimate dominant eigenvalues and their standard errors by measuring action potential duration values. This work expands the previous technique by introducing random disturbances to the pacing rate. The added disturbance proves to improve the robustness of the technique, rendering it more suitable for experimental analyses, where noises and measurement errors impose challenges to data analysis.

**SAT-811****ATHEROSCLEROSIS EFFECT ON BLOOD FLOW IN A CATHETERIZED ARTERY**

Jorge Cisneros, Daniel N. Riahi, Ranadhir Roy.

*The University of Texas-Pan American, Edinburg, TX.*

We investigate the characteristic of blood flow in a catheterized artery in the presence of atherosclerosis, a condition in which the artery wall thickens as a result of fatty-material buildup, such as cholesterol. Atherosclerosis can result in heart attacks and strokes that largely occur when the flow of oxygen-rich blood to the heart ceases due to blockage or breakage in the arteries, and the heart cannot receive oxygen. The use of a catheter is of immense importance as a standard tool for diagnosis and treatment in a patient whose artery is affected adversely by the presence of atherosclerosis. The blood flow in the arterial tube is represented by a two-phase model composing a suspension of erythrocytes, like red blood cells, in plasma. In this study, the differential equations for both fluid and particles are solved theoretically and are subjected to reasonable modeling and approximations based on the available experimental data. The important quantities such as plasma speed, velocity of red blood cells, blood pressure force, impedance or blood flow resistance, and wall shear stress are computed for different catheter cross-sectional radii, axial locations of atherosclerosis, and hematocrit values of red blood cells to plasma mixture in the blood flow system. These variables and conclusions are of major significance to the medical sciences, specifically cardiology.

**SAT-805****CANCER LINEAGES AND RADIOTHERAPY**

Geena Ildefonso<sup>1</sup>, John Lowengrub<sup>2</sup>.

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The traditional view of cancer states that the unregulated division and growth of cells is the cause of tumor formation and growth. In recent years, studies have shown that only small subpopulations of tumor cells are responsible for the relentless growth of tumors. These cells are called cancer stem cells (CSC), and this new point of view is known as the CSC hypothesis. Here, we propose to investigate the use of radiotherapy in cancer treatment of heterogeneous tumors containing stem and non-stem cells. A feature of our approach is that we incorporate feedback processes that regulate cell behavior. In addition, we account for radiation-induced reprogramming of differentiated cells into stem cells which has been observed experimentally. We develop a mathematical model of the cell dynamics using differential equations and the linear-quadratic model to estimate the survival of cells to radiation exposure. To simulate spatial effects, we also plan to use the cellular Potts model in which individual cells are represented as a collection of pixels and the dynamics are governed through a probabilistic algorithm which takes into account adhesion, motility, and cell stiffness. To parameterize the models, we will use data from brain tumors provided by the laboratory of F. Pajonk. The goal is to develop tumor-specific therapy schedules and dosages to optimize response of tumors to radiation treatment. This is an important step toward developing individualized therapy protocols where therapy is designed to optimize response for patient-specific tumor cells.

**FRI-804****TRACKING THE SPREAD OF SCHISTOSOMIASIS THROUGHOUT SÉNÉGAL USING TELECOMMUNICATIONS**

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<sup>1</sup>Howard University, Washington, DC, <sup>2</sup>University of California, San Diego, La Jolla, CA.

Linking information systems across a variety of sectors can vastly improve our understanding of disease epidemiology for the benefit of public health. Currently, there is an opportunity to integrate telecommunication and epidemiological data from Sénégal to track the spread of the potentially fatal parasitic disease schistosomiasis. Here, we use a Senegalese cell phone company's telecommunications data, including incoming and outgoing calls and text messages, to correlate people's movements with information on schistosomiasis outbreak cases from the Center for Disease Control (CDC) and the World Health Organization (WHO). This approach helps us understand why this disease is more prevalent in certain areas and/or within certain ethnic groups. We expect that poverty-stricken areas closest to potentially contaminated bodies of water will have the highest amount of schistosomiasis outbreaks given that the disease is transmitted from infected snails. Such results would emphasize the need to invest in access to clean water within these areas instead of solely focusing on the eradication of snails. From this comprehensive analysis, the extent of the schistosomiasis problem in Sénégal will be quantified, and public health recommendations influencing governmental policies to contain or eradicate this disease will be made.

**FRI-814****AN AGENT-BASED APPROACH TO MODELING POLICE PATROL STRATEGIES AND THEIR EFFECTS ON CRIME**

Alejandro Camacho, Hye Rin Lee, Laura Smith, Carlos Zambrano.

*California State University Fullerton, Fullerton, CA.*

In many urban communities, crime is an unfortunate reality for its inhabitants. High levels of crime require law enforcement agencies to optimize their resources to address criminal behaviors. The goal of this project is to extend an agent-based model for crime pattern formation to incorporate police. This approach allows us to simulate criminal and police behaviors. Through these simulations, we can provide a means to test hypothetical policing strategies without costly and unethical experiments. The theories we test incorporate realistic patrolling scenarios and the effect it has on both criminal behavior and the total crime in a region. We compare our results with existing agent-based approaches, such as random patrols and hotspot policing. Using more realistic models, we can test theories to help law enforcement mitigate crime.

**FRI-806****COMPUTATIONAL AND PROBABILISTIC PREDICTION OF ENHANCER-GENE INTERACTIONS**

Christopher Castro<sup>1</sup>, Joseph Azofeifa<sup>2</sup>.

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Regulation of cellular transcription coordinates ensures proper synthesis of proteins. In order to achieve optimal transcription regulation, regulatory elements are needed. Often, mutations in these regulatory elements arise, causing genes to be expressed improperly, leading to phenotypic abnormalities such as tumorigenesis. We focus our study on enhancers: regions of DNA that directly control the level of transcription of a target gene subset. Here, we provide a computational framework for making fast and accurate gene-enhancer prediction pairs. Our method relies on a key finding that enhancers are transcribed at the same level as their target gene pair. Although this correlation has been observed through previous studies, a way to predict links between specific enhancer regions and specific target genes has not been developed yet. Here, we measure transcription via global nuclear run-on sequencing (GRO-seq), which provides a direct read-out of nascent RNA transcripts, and we identify these transcripts using a new algorithm, Fast Read Stitcher (FStitch). Put simply, we compare regions of transcription with similar levels of expression and provide a list of putative enhancer-gene relationships.

**SAT-807****MATHEMATICALLY MODELING THE INNER MEMBRANE OF A MITOCHONDRIA**

Alejandro Sanchez Jr.<sup>1</sup>, Michael Miksis<sup>2</sup>.

<sup>1</sup>*Northeastern Illinois University, Chicago, IL*, <sup>2</sup>*Northwestern University, Evanston, IL*.

The goal of this research project is to develop a mathematical model to understand the morphology of a mitochondrion. Mitochondria are small bodies within the cytoplasm of the cell. They are enclosed by a double-layer membrane and produce most of the ATP that powers the cell's activities. The inner membrane has a large surface area when compared to the outer and has many folds, known as cristae, which are narrow fingers protruding into the center of the mitochondrion. This project aims to better understand the shape of the inner membrane and, in particular, the cristae by developing a mathematical model which accounts for the elastic properties of the membrane. Our model consists of an elastic membrane confined between 2 parallel, rigid walls. As the length of the membrane is increased, it deforms into a complex series of shapes that depend on the elastic properties of the membrane and the amount of fluid it bounds. Using our mathematical model, we will present results showing the physical parameter regimes on which it is possible to have the observed cristae-like shapes. The mathematical model consists of a fourth-order differential equation with parameters for tension,  $\sigma$ ; pressure,  $P$ ; and a parameter  $A$  that measures the magnitude of the intermolecular forces between the membrane and the parallel walls. There are 2 integral conditions: one for the total arc length  $S$ , and the second for the volume enclosed by the membrane  $V$ . The solutions are found analytically and also numerically using MatLab.



**SAT-812****VALIDATING SIGNS OF REGULATORY INTERACTIONS IN GENE NETWORKS**

Jessica Otah, Rachel Crusius, Brandilyn Stigler.

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Tissue development in *C. elegans* has been a source of much research. Recently a literature-derived embryonal model in *C. elegans* was proposed that contained regulatory modules for both ectoderm and mesoderm development. While the model was built using results from multiple laboratories, the interactions in the model were not classified as being either activating (positive) or inhibiting (negative). In this project, we extend this model by classifying the interactions in the existing model. Experimental results from the literature are used to derive signs of the interactions. This comprehensive model can be used as a gold-standard network for inference methods. We also provide a network-theoretic analysis of the new model and compare it to known gene network motifs.

**SAT-813****THE FLOUR BEETLE: A DISCRETE MATHEMATICAL MODEL**

Matthew Buhr, José Flores.

*University of South Dakota, Vermillion, SD.*

Some recent experimental studies of flour beetles (*Tribolium Castaneum*) have indicated a possibility of behavior in the laboratory that appears to be chaotic. We describe and attempt to analyze a model for such behavior, taking note of the properties of the life cycle of the flour beetle. The life cycle consists of larval and pupal stages, each lasting approximately 2 weeks, followed by an adult stage. Both larvae and adults are cannibalistic, consuming eggs and thus reducing larval recruitment. In addition, there is adult cannibalism of pupae. We will take 2 weeks as the unit of time and formulate a discrete mathematical model describing the larval population, pupal population, and adult population at 2-week intervals. We can begin with a linear model as if there were no cannibalism, then we can modify the model to assume that cannibalistic acts occur randomly as the organisms move through the container of flour that forms their environment. This suggests a metered model with cannibalism rates proportional to the original size of the group being cannibalized. Finding the equilibria of this basic model, we can find solutions corresponding to the extinction and also a solution corresponding to survival for some sets of additional parameter values. We can then manipulate parameter values to determine if the dynamics are sensitive to any changes in the cannibalism rate. Then we can determine any possible chaotic behavior, which is crucial for a variety of real-life applications.

**FRI-809****EXPLORING SPATIO-TEMPORAL MODELS OF MRNA DEGRADATION IN PROKARYOTES**

Bruno Beltran<sup>1</sup>, Christine Jacobs-Wagner<sup>2</sup>, Sangjin Kim<sup>2</sup>.

<sup>1</sup>*Louisiana State University, Baton Rouge, LA,* <sup>2</sup>*Yale University, New Haven, CT.*

Bacteria are very successful at proliferating in an ever-changing environment because of their ability to dynamically regulate transcription and translation of their genome. Previous

theoretical and experimental studies of gene regulation have focused on the effect of transcription factor binding near the promoter, regulating initiation of RNA polymerases. However, we have found by experiment that dynamic gene regulation is further promoted by heretofore unreported spatio-temporal coordination between mRNA synthesis and degradation. We constructed models of mRNA decay kinetics at various levels of mechanistic, spatial, and temporal resolution to explain this phenomenon. By augmenting NFsim, an existing agent-based, network-free simulator, we are able to compare our models quantitatively to the experimental data. Our results highlight potential sources of error when measuring molecular half-life, reproduce all available data when using experiment-based parameters, and include explicit, time-dependent solutions to the chemical circuits central to mRNA synthesis and decay. These results are important for biologists wishing to measure or modify time-dependent gene regulatory networks in engineering applications.

#### **SAT-808**

##### **THE VELOCITY OF A JACKSON CHAMELEON'S TONGUE**

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Jackson chameleons (*Trioceros jacksonii*) have the ability to capture their prey from a distance of about one and a half times the length of their body with the use of their tongue at a speed the human eye cannot naturally observe. The purpose of this study was to determine, with the use of mathematics, the magnitude of the velocity of a Jackson chameleon's tongue while capturing prey. Data was collected using a ruler attached to a feeding jar, and a video recording was taken at a rate of 30 frames per second. Video software QuickTime Player was used to record and capture the projection and retraction of the tongue. A computer algebra system (CAS), Mathematica, was then used to plot the data points. The tongue movement was broken into 3 stages: projection, acceleration, and retraction. Each stage was calculated separately and a best-fit line was generated. CAS was also used to plot the derivatives of the best-fit lines to determine the rate of change. We hypothesize the fastest rate of change of a chameleon's tongue while capturing prey will be during the acceleration stage. Preliminary results suggest the acceleration stage has the fastest rate of change of approximately 139.6 cm/s.

#### **SAT-810**

##### **SAFEGUARD FAIR VOTING: MATHEMATICALLY DIAGNOSING GERRYMANDERS**

Eric Shehadi, Thomas Wakefield.

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Mathematical measures of gerrymandering across political units such as congressional districts and city wards will be discussed. Gerrymandering is the act of shaping political units to offer an unfair advantage to a population. Concepts of compactness and convexity and their effectiveness at ensuring "one person, one vote" will be examined. These current measures of gerrymandering focus heavily on the geometric shape of a political unit. In contrast, the concept of population compactness of political units as a measure of gerrymandering will be

elaborated. Examples of population compactness and the benefits of its use over geometric compactness will be presented.

#### **FRI-807**

##### **TRADE-OFF OF GLIAL CELL ACTIONS IN RESPONSE TO ISCHEMIC HYPOXIA IN THE BRAIN**

Tiffany Reyes<sup>1</sup>, Matthew Buhr<sup>2</sup>, Hasan Sumdani<sup>3</sup>, Oscar Garcia<sup>4</sup>, Benjamin Morin<sup>5</sup>, Adrian Smith<sup>6</sup>.

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We introduce a model that explores the dual role of glial cells in the formation of scar tissue and in neural repair following hypoxic ischemia in the brain. We consider the fact that scar tissue helps protect the brain during the acute phase of injury by limiting the spread of secondary damage caused by the ischemia but limits recovery by inhibiting both the formation of connections between cells and the repair of damaged neurons. We also take into account that repaired neurons offer better functional recovery but do nothing to halt the spread of ischemic injury. A stochastic, spatially explicit cellular automaton model is used as our *in silico* version of the brain's biology. Mathematical analysis is carried out via mean field (MFA) and pair approximation (OPA) models. We show that the MFA, which neglects all spatial autocorrelation, leads to brain death or a brain composed of only damaged and scarred neurons. The OPA demonstrates that explicitly modeling spatial adjacency gives outcomes that include the possibility of scar tissue surrounding damaged cells, preventing further secondary death. Our results show how the trade-off between scar tissue formation and neural repair impacts future brain health, thus supporting the use of mixed-treatment regimes.

#### **FRI-811**

##### **LAX PAIRS FOR INTEGRABLE EVOLUTION EQUATIONS**

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Certain nonlinear partial differential equations, known as integrable evolution equations, can be derived by using 2 linear ordinary differential operators. One of these linear operators describes the evolution of an associated linear system in the spatial coordinate, and it is related to an ordinary differential equation with a spectral parameter. The other describes the evolution in time of the same linear system, and it is related to a linear partial differential equation without a spectral parameter. This method of derivation of integrable evolution equations is due to Peter Lax, and the corresponding pair of linear operators is known as a Lax pair. We derive Lax pairs for various integrable evolution equations and analyze their properties. We also derive and analyze Lax pairs for various integrable evolution equations when the spatial independent variable is no longer a continuous variable, but is a discrete variable.

**FRI-808****A STUDY OF ENTANGLEMENT IN PROTEINS**

Leticia Torres, Kenneth Millett, Eleni Panagiotou.

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Proteins are large molecules composed of one or more chains of amino acids in a specific order determined by the base sequence of nucleotides in the DNA coding for the protein. They are required for the structure, function, and regulation of the body's cells, tissues, and organs. It has been shown that the conformational characteristics of proteins, such as entanglement, are related to their function. Simplifying the representation of proteins, we can imagine them as mathematical simple (closed or open) curves in space. A knot is a closed curve in space that does not intersect itself anywhere. Thus, we can use tools from knot theory to study their entanglement complexity. A method to study the local and global knotting of a protein sequence is its knotting fingerprint, a matrix representation that encodes the knotting of the protein and all of its sub-chains in a matrix image and provides a visual means to inspect the knots formed by all sub-chains. A simple measure of entanglement between two open or closed curves is the Gauss linking integral. In this study, we employ the Gauss linking integral in order to study the local and global entanglement in proteins. More precisely, we estimate the linking integral between different portions of the chains. In analogy to the knotting fingerprint, we introduce the linking matrix of proteins and study its mathematical structure.

**FRI-813****DIPOLE - DIPOLE ENERGY OF TWO STABLE, NON-LINEAR AGGLOMERATES OF MAGNETIC PARTICLES IN FERROFLUID**

Richard Mata, Hector Cenicerros.

*University of California, Santa Barbara, Santa Barbara, CA.*

Magnetic fluids, or ferrofluids, are technologically important suspensions of nano-sized magnetic particles in a liquid carrier. As such, the flow properties of ferrofluids are strongly influenced by the presence of a magnetic field. Likewise, the formations of magnetic particle clusters are due mainly to an external magnetic field and dipole-dipole interaction. The interaction of these structures within the fluids is largely responsible for the spectacular flow properties observed. It is often the case that magnetic particles will form linear chains due to the fact that it takes less energy to do so. However, there are cases of magnetic particles in ferrofluids coming together to form non-linear clusters. This project seeks to obtain the dipole-dipole energy for two specific, stable clusters: a triangular one and a centered hexagonal one. By finding the global and local minima of the dipole-dipole energy for these structures, we can identify the most energetically favorable, magnetic moment configuration of these two specific clusters of magnetic particles. By using the dipole-dipole energy equation, we can produce an equation that describes the dipole-dipole energies of both the triangular cluster and centered hexagonal cluster. Thus, by identifying the magnetic moment configuration of the triangular and centered hexagonal clusters, we can determine how these two particular clusters may influence the flow properties of the ferrofluid compared to linear chains of magnetic particles.

**SAT-809****THE EFFECTS OF A TIME-DEPENDENT GENETIC MUTATION RATE ON CANCEROUS GROWTH**

Krista Kernodle, Frederic Wan.

*University of California, Irvine, Irvine, CA.*

One of the principal effects of genetic instability is an increase in the probability for a cell to experience a strong malignant mutation resulting in a much faster proliferation rate. Since genetic instability plays a very important role in carcinogenesis, we are interested in finding the optimal malignant mutation rate. We are developing algorithms to determine the optimal mutation rate for a mathematical model of the growth of cancer cell populations when an oncogene is activated. Previously, we were able to find the optimal control by solving an initial value problem. For the current case, we are using the Richardson extrapolation with Runge-Kutta 4 to solve a boundary value problem in order to obtain a numerical solution. Knowledge of the most efficient way cells acquire a malignant mutation would provide insight and information on clinical intervention and a lower bound for the time available for clinical intervention.

**SAT-806****THE EFFECT OF RURAL/URBAN MOVEMENT ON DENGUE TRANSMISSION DYNAMICS**

Jasmine Jackson<sup>1</sup>, Olivia Justynski<sup>2</sup>, Danielle Williams<sup>3</sup>, Yessica Gaitan<sup>4</sup>, Fabio Sanchez<sup>5</sup>, Omayra Ortega<sup>5</sup>, Komi Messan<sup>5</sup>, I Made Eka Dwipayana<sup>5</sup>.

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Four serotypes of dengue (DENV1 - DENV4), a vector-borne disease transmitted by 2 species of mosquitoes, *Aedes aegypti* and *Aedes albopictus*, are prevalent in various tropical and subtropical regions of the world, with dengue fever posing a serious health threat to humans. Dengue is no longer restricted to tropical regions due to increasing levels of mobility via travel, migration, or displacement due to conflict. We use a simple framework, a system of nonlinear differential equations, to explore the effect of rural/urban movement on dengue transmission dynamics and control. The model incorporates movement between rural and urban regions. These populations are subdivided into susceptible, exposed, infected, and recovered classes. Vectors, assumed to remain in a single region, are divided into rural (*Ae. albopictus*) and urban (*Ae. aegypti*) populations. The vector populations are subdivided into susceptible, exposed, and infected classes. We compute the basic reproductive number ( $R_0$ ) for the system with and without movement and use this key dimensionless parameter to study the effects of rural/urban host movement on dengue dynamics and control.

**FRI-812****CONSTRUCTION OF A DYNAMIC MODEL OF IRON METABOLISM FROM EXPERIMENTAL DATA**

Naarai Garcia, Anael Verdugo.

*California State University Fullerton, Fullerton, CA.*

Iron regulation is an important set of chemical reactions that controls iron concentration in the body. Understanding this iron network is important for understanding diseases of iron overload and iron deficiency. Our goal is to create a mathematical model consisting of differential equations in order to identify key regulators in the iron metabolism network. This was accomplished by quantifying experimental data (western blots) in an image-processing program known as ImageJ. We then used our quantification plots to construct a system of differential equations which we numerically analyzed in a computing program known as Matlab. We were then able to fit our quantification results by changing parameters in our model. This enabled us to study the response of our iron network to different iron concentrations, which allowed us to gain a deeper understanding of the dynamics of our iron network.

**SAT-803****POPULATION DYNAMICS OF WOLVES AND COYOTES AT YELLOWSTONE NATIONAL PARK: MODELING INTERFERENCE COMPETITION WITH AN INFECTIOUS DISEASE**

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<sup>1</sup>*Boston University, Boston, MA*, <sup>2</sup>*Arizona State University, Tempe, AZ.*

Gray wolves were reintroduced to Yellowstone National Park (YNP) in 1995. The population initially flourished but, since 2003, the population has experienced significant reductions due to factors that include disease-induced mortality, illegal hunting, park control programs, vehicle-induced deaths, and intra-species aggression. Despite facing similar conditions and interference competition with the wolves, the coyote population at YNP has persisted. In this study, we introduce an epidemiological framework that incorporates natural, human-caused, and disease-induced mortality as well as interference competition between 2 species of predators. The outcomes generated by this theoretical framework are used to explore the impact of competition and death-induced mechanisms on predators' coexistence. Deterministic and stochastic versions of the framework are analyzed. Data is used from YNP to draw conclusions on the causes that may limit the ability of the dominant species to be outcompeted, and a sensitivity analysis is performed to study the robustness of the results. It is the hope that these results on the competitive dynamics of carnivores in YNP will provide park management insights that result in policies that keep the reintroduction of wolves successful.

**FRI-803****AN EPIDEMIOLOGICAL MODEL OF BOVINE RESPIRATORY SYNCYTIAL VIRUS INFECTION DYNAMICS**

Taylor Kuramoto<sup>1</sup>, Vivian Anyaeche<sup>2</sup>, Shi Chen<sup>3</sup>, Tashika James<sup>4</sup>, Christina Lanzas<sup>2</sup>, Suzanne Lenhart<sup>4</sup>, Taylor Nelsen<sup>4</sup>.

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Bovine respiratory syncytial virus (BRSV) is one etiological agent in the larger bovine respiratory disease (BRD) complex that causes damage to the respiratory tract, facilitates bacterial growth, and compromises the immune system. Negative effects of BRSV include costs stemming from death, reduced performance, poor growth, and the administration of vaccines and treatments. Understanding the effect of cattle contact networks on the transmission of the pathogens causing BRD will help reduce unnecessary treatments, costs, and public health concerns of growing drug-resistance. A stochastic agent-based epidemiological model has been developed to predict the outcome of infection under different circumstances. The model simulates the spread of BRSV using a spatially implicit contact network generated by a real time location system and visualized in NetLogo. It takes a top-down approach to understanding the complex relations between the key transmission components. The underlying theory relies on basic susceptible-infected-recovered (SIR) compartmental principles. Simulations were completed under varying initial conditions and compared susceptibility, incidence proportion, maximum prevalence, and cumulative centrality to see how disease dynamics and emergence differ under given initial conditions. Qualitative observations from the model interface and preliminary quantitative analysis indicate that cows' social behavior and interactions affect how the virus spreads through a population. The interaction between the network structure and the disease status drives the disease dynamics. These findings indicate that decreasing the number of cows in a herd will not decrease the transmission rate but, if the network density and sociality of the cows can be controlled, so can the transmission.

**SAT-801****BEAM-PATTERN OF TRI- AND BI-AXIAL VELOCITY-SENSORS WITH NON-ORTHOGONAL AXES**

Hye Rin Lee, Charles Lee.

*California State University Fullerton, Fullerton, CA.*

An acoustic vector sensor (AVS) is used to measure acoustic particle velocity and pressure to localize and detect sound sources in various media such as in air, water, and solid. Its applications range from detecting gunshots to moving vehicles and vessels, and it has been useful in the field of urban security, border patrol, and the military. AVS is composed of 2 or 3 collocated and orthogonal velocity-component sensors with an optional collocated pressure sensor. However, the velocity sensors are often manufactured with imperfect orientations and, thus, the axes are no longer orthogonal. This misorientation results in a distortion of the beam response pattern. Our research focuses on characterizing the impact of the misorientation of the tri- and bi-axial velocity components of AVS on the beam response. Particularly, we derive

the formulations for the beam response pattern of the imperfect system with the least number of misoriented parameters and quantify the impacts and distortions with various degrees of misorientations. Even with much simpler formulations, the explicit beam response patterns for the spatial matched filter, the filter of AVS that maximizes signal-to-noise ratio, are quite complex and lengthy. As a result, we also derive the approximations of the beam response pattern and verify that the approximations produce highly accurate estimates with small imperfections.

#### **SAT-804**

##### **IMPACT OF NEEDLE EXCHANGE PROGRAM ON THE DYNAMICS OF ADDICTION-TREATMENT DYNAMICS**

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A mathematical model of the dynamics of a population of drug users that incorporates a needle exchange program is formulated. Model analysis is conducted to determine the impact of needle exchange programs on the drive of intravenous drug users to seek treatment for addiction. The basic addiction reproduction number is defined and computed, and its role on the prevalence and control of drug addiction is explored. Specifically, the local stability of the addiction-infection free equilibrium and endemic equilibrium are determined when relapse from treatment is not considered. Sensitivity analysis is conducted to determine the impact of perturbations of key parameters on the basic reproduction number and endemic levels of a population seeking treatment.

#### **SAT-814**

##### **LINEAR LONG WAVE PROPAGATION**

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The dynamics of an isolated long wave passing over underwater obstacles were investigated. Areas of practical application include coastal defense against tsunami inundation, harbor protection, and erosion prevention with submerged breakwaters. Three sea-floor configurations were considered: an underwater shelf, a single obstacle, and a series of obstacles. A piecewise continuous coefficient was used to model the various sea-floor topographies. A simple and easily implementable numerical scheme using explicit finite difference methods was developed to solve the discontinuous partial differential equations. The numerical solutions were verified with the exact analytical solution of linear wave propagation over an underwater shelf and experimental data. The efficacy of approximating more complicated continuous underwater topographies by piecewise linear distributions was determined. As an application, a series of underwater obstacles were modeled and



reflection/transmission coefficients determined. It was found that as the amount of obstacles increase, a tsunami's impact was reduced.

#### **SAT-828**

##### **A MATHEMATICAL MODEL FOR SETTING CRIME REDUCTION TARGETS**

Anthony Gusman<sup>1</sup>, Erik Bates<sup>2</sup>, Stephanie Sanchez<sup>3</sup>, Sarah Verros<sup>4</sup>, Yoon-Sik Cho<sup>5</sup>.

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Traditionally, the Los Angeles Police Department (LAPD) sets crime reduction goals for each division according to a linear model of 5% reduction from the previous year's levels. Such an approach may not account for seasonal patterns, random environmental fluctuations, limiting threshold conditions, nor the unique spatial context of each policing area. These limitations may result in potentially inaccurate performance assessments. We seek to develop a generalizable approach for setting reasonable crime reduction goals that accounts for each of these factors. The primary challenges are noise in the data that makes the extraction of patterns more difficult and the inherent uncertainty of forecasting crime rates over long-term time scales (months to years). The LAPD has agreed to supply appropriate data. Data smoothing over mid- and long-term windows will be used to explore general behavior and to identify potential seasonal trends, which will then be extrapolated via pattern-detection forecasting methods. To test our forecasting procedure, half of the data will be used as a training set, and accuracy will be quantified using standard goodness-of-fit tests. Furthermore, we will measure the variance due to environmental noise by modeling crime levels as the intensity of a Gaussian Cox process. These techniques will guide the setting of crime reduction goals for policing areas. When compared to the traditional method of setting crime reduction targets, we anticipate that our method will yield more realistic and accurate crime reduction goals. Moreover, we expect that our approach could be extended to other agencies, offering a data-informed alternative to arbitrary crime reduction target setting.

#### **FRI-801**

##### **ON THE CAUCHY INITIAL VALUE PROBLEM FOR GENERAL LINEAR DIFFUSION AND SCHRÖDINGER TYPE EQUATIONS**

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The bioheat equation models heat transfer between nanoparticles and cancer tumor cells. This sort of modeling is important to determine whether a cancer treatment would be viable or not. Using a method based on solving nonlinear ordinary differential systems, a correct closed solution can be found for the equation that models this phenomenon. Further, in this poster, the same method is used to solve the Cauchy initial value problem for general linear diffusion and Schrödinger type equations with time dependent coefficients. With known solutions of Riccati type nonlinear differential equations it is possible to construct general closed-form

solutions that can be used to solve classical examples presented in any standard partial differential equations (PDE) class. Some of the aforementioned closed-form solutions would probably be impossible to obtain by any of the standard methods taught in a PDE class.

## **MATHEMATICS (GENERAL)**

### **SAT-818**

#### **THE ABELIAN SANDPILE GROUP OF A TYPE OF SERIES PARALLEL GRAPHS: A SUBFAMILY OF THICK CYCLE GRAPHS**

Vincent Longo<sup>1</sup>, Bianca Mastache<sup>2</sup>, Angel Castillo<sup>3</sup>, Luis Garcia-Puente<sup>2</sup>.

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<sup>3</sup>*Texas A&M University, College Station, TX*.

In 1987, Bak, Tang, and Wiesenfeld introduced the abelian sandpile model, which was the first dynamical system displaying self-organized criticality. The abelian sandpile model falls at the intersection of group theory and graph theory in that each graph has an associated group called the abelian sandpile group. Researchers have studied the abelian sandpile groups of various families of simple graphs such as cycle graphs. The abelian sandpile group of the simple cycle graph on  $n$  vertices is the cyclic group of order  $n$ . We give a precise description of the sandpile groups of these simple cycle graphs when multiedges are added between adjacent vertices. These graphs are known as thick cycle graphs. We further extend what is known for series-parallel graphs.

### **SAT-825**

#### **P-ADIC VALUATIONS OF THE FRANEL NUMBERS**

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The Franel numbers are the sum of cubes of binomial coefficients. This particular sequence is of great interest. For instance, the primes that divide them do not seem to be known. By examining the  $p$ -adic values of the Franel numbers, patterns among these valuations have been observed. Using Mathematica, graphs of the  $p$ -adic values are generated to observe relations among the different valuations. Roughly half of the  $p$ -adic graphs follow the same pattern, and the regular sequences are displayed as automata. Branches corresponding to the  $p$ -adic values for the Franel numbers cycle back to  $G(n)$ , where  $G(n)$  is the  $p$ -adic value of the  $n$ th Franel number. However, one branch in the form of  $(p-1)/2 \pmod{p}$  has the value of  $G(n)+1$ . A second type of primes do not follow this pattern. One of the goals of this project is to classify these types.

**SAT-823****CONSTRUCTING THE CHARACTER TABLE OF  $SL_3(F_q)$** 

Aura Salazar<sup>1</sup>, Renee Bell<sup>2</sup>, Ju-Lee Kim<sup>2</sup>.

<sup>1</sup>*University of Texas at Brownsville, Brownsville, TX*, <sup>2</sup>*Massachusetts Institute of Technology, Cambridge, MA*.

Characters of group representations are fundamental tools for performing calculations in representation theory. The character table of a group  $G$  is a  $k \times k$  matrix with  $k$  being the number of conjugacy classes and irreducible characters of  $G$ . The entries of the character table of  $G$  are the values of each irreducible character on the conjugacy classes of  $G$ . From the character table of a group we can obtain important group theoretical information about it. Most notably we can deduce all the irreducible representations of this group. Our goal is to write the character table of the group  $SL_3(F_q)$  over a finite field  $F_q$  in order to obtain the regular representations of this group in terms of characters.

**SAT-820****OMEGA-PRIMALITY IN NUMERICAL MONOIDS GENERATED BY ARITHMETIC SEQUENCES**

Jonathon Spaw<sup>1</sup>, Roberto Pelayo<sup>2</sup>, Ashley Mailloux<sup>3</sup>, Meghan Malachi<sup>4</sup>.

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The  $\omega$ -primality invariant has been defined to quantify “how prime” an element is in numerical monoids, which are co-finite subadditive monoids in the natural numbers. We used computed examples of numerical monoids to motivate our results regarding certain factorization invariants. For numerical monoids generated by an arithmetic sequence, we present well-supported conjectures that expand on previous results by providing a closed form for the  $\omega$ -primality of the generators and for all elements greater than the dissonance point. Additionally, we show potential closed forms for the dissonance points of numerical monoids with embedding dimension 3 and 4.

**FRI-818****P-ADIC LIMITS OF COMBINATORIAL SEQUENCES**

Alexandra Michel<sup>1</sup>, Joseph Rennie<sup>2</sup>, Andrew Miller<sup>3</sup>, Victor Moll<sup>4</sup>.

<sup>1</sup>*Mills College, Oakland, CA*, <sup>2</sup>*Reed College, Portland, OR*, <sup>3</sup>*Amherst College, Amherst, MA*, <sup>4</sup>*Tulane University, New Orleans, LA*.

The  $p$ -adic field is an alternative to the real numbers as a completion of the rational numbers under a different metric for every prime  $p$ . The definition of a  $p$ -adically Cauchy convergent sequence can be equivalently stated in terms of congruences of elements of that sequence modulo arbitrarily large powers of  $p$ : a sequence is  $p$ -adically Cauchy convergent if and only if it is eventually constant modulo integer powers of  $p$ . Using results of previous studies on factorials modulo powers of primes, we identify a class of  $p$ -adically convergent subsequences of Catalan numbers in terms of the  $p$ -ary expansion of the sequence elements. An extension of

our results to a more general class of sequences involving factorials and binomial coefficients is also considered.

#### **FRI-819**

##### **COMPUTING A-DISCRIMINANT CHAMBERS AND FASTER HOMOTOPY ALGORITHMS**

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*University of Hawaii at Hilo, Hilo, HI, <sup>2</sup>Texas A&M University, College Station, TX.*

The A-discriminant variety is the unique irreducible algebraic hypersurface containing all polynomials (with exponent set contained in A) having singular zero set. While the defining polynomial for the A-discriminant variety is difficult to calculate, it is central in numerous applications, including homotopy algorithms for approximating the real solutions of polynomial systems. We are developing a software package and related quantitative estimates to fully understand the A-discriminant variety for A contained in  $\mathbb{Z}^n$  of cardinality  $n + 4$ . Our main goal is to quickly compute which discriminant chamber contains a given polynomial system in order to find homotopies preserving the number of real roots. Understanding the real solutions of polynomial equations will provide applications in numerous disciplines such as robotics and analyzing chemical reactions. (This research was conducted as a part of the 2014 Algorithmic Algebraic Geometry REU at Texas A&M University sponsored by the National Science Foundation.)

#### **SAT-821**

##### **A CLOSER LOOK AT $x_0$ IN LEAMER MONOIDS: TWO GENERATOR CASE**

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A numerical monoid  $\Gamma$  generated by an arithmetic sequence with step size identical to the distance between the generators is called an arithmetical Leamer monoid. Much is known about the factorization theory for arithmetical Leamer monoids. For every numerical monoid of embedding dimension 2, it is generated by the arithmetic sequence  $\{a, a+d\}$ . However, much is still unknown about Leamer monoids when the step size does not equal the distance between the generators. The ultimate goal is to prove that the Huneke-Wiegand conjecture holds for embedding dimension 2 numerical monoids for any  $s$  not in  $\Gamma$ . One approach is to attempt finding a closed form for  $x_0$ . In this paper, we found a formula to calculate the last step size before  $x_0 = x_f$  consecutively. In addition, we found a formula to find  $x_0$  and  $x_f$ , for the last time  $x_0 \neq x_f$  for that particular step size. As a result, we found a closed form for  $x_0$ , which involves Apéry sets and modular arithmetic.

**FRI-821****LEAMER MONOIDS GENERATED BY INTERVALS**

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The Huneke-Wiegand conjecture has earned much attention in commutative algebra. Once a theorem was developed connecting the Huneke-Wiegand conjecture to numerical monoids, the study of arithmetical sequences in numerical monoids was sparked. In our research, we restricted ourselves to characterizing numerical monoids with consecutive generators, otherwise known as intervals. In particular, we focus on determining when a numerical monoid  $\Gamma$  has an irreducible sequence of the form  $\{x, x+s, x+2s\}$  for some natural number  $s$  that is not in  $\Gamma$ . This can be phrased more simply through the use of Leamer monoids, additive algebraic objects in  $\mathbb{N}^2$ . These monoids helped develop conjectured forms of the first arithmetical sequence, characterizing the first column  $x_0$  in a Leamer monoid generated by  $\Gamma$ . This lays the groundwork for finding conditions for when  $\Gamma$  contains  $\{x_0, x_0+s, x_0+2s\}$ , thus satisfying the Huneke-Wiegand conjecture.

**SAT-819****A MEASURE OF CLOSENESS USING THE DISTANCE BETWEEN FINITE GROUPS**

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In his undergraduate research project at Virginia Tech, Mark Lewers defines the distance between 2 finite cyclic groups and mentions some interesting conjectures about this distance. In this project, we generalize Lewers' definition of distance for general finite groups, and the main goal of this project is to use this distance to measure how close 2 finite groups are from being isomorphic to each other. The concept of the distance relies heavily on what we call matching pairs as they give us a measure of structural similarity between the 2 finite groups. Our most important objective is to find a precise formula for the distance and to understand its properties. To address this, we explored different properties of the distance and the validity of Lewers' conjectures. Overall, we were able to prove Lewers' hypothesized upper bound for the distance between finite cyclic groups, find many different properties of the distance, and give explicit formulas for computing the distance between finite cyclic groups of small order. Our results suggest that the distance has almost all the properties of a metric, and we can find both an upper bound as well as a lower bound for the distance between all finite cyclic groups. This motivates us to look for even stronger upper and lower bounds for the distance in order to better approximate the true value of the distance and discover which finite groups have greater structural similarity.

## SAT-822

### P-ADIC VALUATION OF GENERALIZED FIBONACCI NUMBERS

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Fibonacci and Lucas numbers are well-known sequences given by a second-order recurrence that share many identities. Only the initial conditions differ. The Fibonacci numbers start with  $(0, 1)$  and the Lucas numbers with  $(2, 1)$ . These two form a basis for  $\mathbb{Z}^2$  linear combinations of these 2 sequences generating new ones, called *generalized Fibonacci sequences*, denoted by  $S_n$ . These satisfy  $S_n = S_{n-1} + S_{n-2}$  with the initial conditions  $(S_0, S_1) = \alpha(0, 1) + \beta(2, 1)$ . The  $p$ -adic valuation of an integer  $n$ , denoted by  $v_p(n)$ , is the highest power of  $p$  that divides  $n$ . Formulas for the  $p$ -adic valuations of the Fibonacci numbers and Lucas numbers are well-known. This project investigates the  $p$ -adic valuation of generalized Fibonacci numbers. This project is concerned with the following questions: Is there a generalized formula for  $v_p(S_n)$ ? Is this general formula related to the formulas for  $v_p(F_n)$  and  $v_p(L_n)$ ? Are there special values for  $\alpha$  and  $\beta$  for which  $v_p(S_n)$  shows any special properties? In particular, we are focusing on  $\alpha = 1$  and  $\beta = 2$ . For these conditions, we have determined the  $p$ -adic valuations for certain primes.

## FRI-826

### ARITHMETIC PROPERTIES OF INFINITE PRODUCTS

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The work discussed here develops methods to evaluate certain infinite products in closed form. These are finite products of values of the gamma function. Presented here are infinite products of rational functions  $R(n)$  raised to a power  $a(n)$ . These sequences satisfy certain regularity conditions, being either  $k$ -periodic or  $k$ -automatic. Of particular interest is the regular paperfolding sequence considered by J. P. Allouche. Also included are some results on the  $p$ -adic valuation of partial products of these types, which also contain predictable patterns. Connections to the alternating sign matrix sequence have appeared.

## FRI-817

### THE TOPPLING POLYNOMIAL FOR ABELIAN SANDPILES

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In the 1980's, Bak, Tang, and Wiesenfeld coined the term "self-organized criticality", which refers to naturally occurring dynamical systems that drive themselves to unstable states such as avalanches and earthquakes. Through algebraic graph theory, mathematicians are able to model these systems and gain more insight into what occurs when the system is unstable. In

this paper, we introduce the toppling polynomial on a graph that describes the exact sequence of topples induced on an Abelian sandpile by adding one grain of sand to a vertex in the graph. We generalize the structure of these polynomials for trees, complete graphs, cycles, wheels, and wired trees. Unlike the more general avalanche polynomial, the toppling polynomial provides more detail about which vertices topple due to an avalanche and further explores the structure of the avalanche. In fact, a toppling polynomial for a tree is detailed enough to describe one distinct tree. Through this polynomial, we are able to gain insight into various toppling patterns in families of graphs.

#### **SAT-824**

##### **CYCLIC JACOBIANS OF NEARLY COMPLETE GRAPHS**

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In this paper we examine nearly complete graphs with compliments composed of 2- and 3-paths, almost-paths, and giraffe graphs and observe the structure of the Jacobian group associated with such graphs. Particular focus is given to cyclic groups and how to determine their cardinality based on tree counting methods for graphs. Results include specific formulas for cardinality of 2-/3-path removal and the removal of certain classes of almost-paths. Furthermore, the cyclicity of Jacobians is characterized for graphs with three-paths and almost-paths removed.

#### **SAT-817**

##### **PURPOSE AND HUMANISM IN MATHEMATICS EDUCATION RESEARCH**

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One of the most influential journals in mathematics education research opened with an editorial titled “Why to teach mathematics so as to be useful.” Thus began an extended discussion on the purpose(s) of mathematics education that continued across many years and volumes, though mainly appearing as one undercurrent or hidden assumption among many. In our daily lives as mathematics students and researchers, we often directly confront this same question: Why should I learn mathematics? Though this version frequently comes coated in subtle hostility toward the subject and may sometimes be cast aside as such, the underlying question is still worthy of our scrutiny and understanding: Why teach mathematics? This research presentation will focus on this question and attempt to document how attitudes toward purpose evolved among mathematics education researchers. In particular, we will note in our research the emergence and development of the humanist and social constructivist paradigms on the one hand, and the interlocked themes of discovery, inquiry, and active learning in the classroom on the other and analyze how their proponents engaged with the question of purpose. Analyzing the different purposes of why math should be taught can give us a better understanding of why math is being taught the way it is.

**SAT-816****ON THE USE OF INTEGRAL TRANSFORMS TO EVALUATE SUMS ANALYTICALLY**

John Vastola, Costas Efthimiou.

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Evaluating sums analytically is a problem that is easy to pose and to give approximate solutions for, but is difficult to solve exactly in general. Many known results are byproducts of Fourier analysis, which require guessing that a given series corresponds to a particular function; for obvious reasons, this is undesirable. A method of evaluating sums using integral transforms is proposed that can reproduce many results obtained using other techniques. In particular, representing polynomials as Laplace transforms gives some nontrivial, exact results. Some applications of the method are demonstrated, and extensions of the method using integral representations of frequently appearing functions are suggested. One useful representation of the gamma function is supplied and used to provide both well-known and more obscure results. Interestingly, the application of this integral representation to evaluating sums suggests the introduction of a novel integral transform, which itself can be used to evaluate sums. Some of the transform's properties are given, and its usefulness in other areas, such as solving differential equations, is touched on. Some physical problems involving the partition functions of statistical mechanics and some infinite sums appearing in quantum mechanics are considered.

**FRI-825****RANKS OF GRAPHS IN  $\mathbf{Z}_2$** 

Oscar Leong, Cheryl Grood, Thomas Hunter.

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Determining the minimum rank of a set of matrices that are described by a particular graph is known as the *minimum rank problem*. The classic minimum rank problem examines real, symmetric matrices whose diagonal is allowed to be free, and it has been studied extensively along with its generalizations to other fields. In 2012, the minimum rank problem was investigated for real, symmetric matrices where the diagonal entries are restricted to zero. To date, very little is known about how the 0-diagonal results generalize to other fields. We consider the minimum 0-diagonal rank problem over the field  $\mathbf{Z}_2$ . A *graph*  $G$  is a set of *vertices*  $V(G)$  and a set of *edges*  $E(G)$  such that  $V(G)$  is finite and nonempty and every edge in  $E(G)$  consists of 2 distinct elements of  $V(G)$ . The *adjacency matrix* of  $G$  is the matrix  $A = (a_{ij})$ , where  $a_{ij} = 1$  if  $v_i$  is adjacent to  $v_j$  and  $a_{ij} = 0$  otherwise. We say that the *rank of a graph* is the rank of its adjacency matrix. Solving the minimum 0-diagonal rank problem over  $\mathbf{Z}_2$  for a graph  $G$  is equivalent to determining the  $\mathbf{Z}_2$ -rank of  $G$ . We show that the  $\mathbf{Z}_2$ -rank of  $G$  is full if and only if the graph  $G$  has an odd number of perfect matchings. We then compute the rank of  $G$  over  $\mathbf{Z}_2$  for a number of different graph families including paths, cycles, wheels, complete graphs, complete bipartite graphs, and ladder graphs.



**FRI-822****FACTORIZATION LENGTHS AND ELASTICITY IN NUMERICAL MONOIDS**

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Let  $\Gamma$  be a minimally generated numerical monoid. We explore methods of finding the maximum and minimum factorization lengths for elements in any monoid generated by an arithmetic sequence, as well as characterizing the elasticity of elements in monoids with only 2 generators. In particular, we provide conjectures on a closed form for the length of these factorizations. Also, we begin to examine elements in the more general case of monoids with 2 generators in the context of their elasticities, by providing a characterization of elasticities for all elements  $n$  in  $\Gamma$ . These conclusions and closed forms of the variables are of major significance to this developing field as many research projects are currently under way.

**SAT-815****ESTIMATING THE PERRON-FROBENIUS EIGENVECTOR OF POSITIVE MATRICES**

Joann Coronado, Pablo Tarazaga.

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Computing the eigenvectors of matrices is a useful tool in many areas of mathematics, including problems involving dynamic systems. More effective methods for finding eigenvectors can be discovered by analyzing the relationship between the eigenvector and its matrix. This study focuses on determining whether 2 relationships exist: 1) between the position of the Perron-Frobenius eigenvector and the angles between the columns of positive matrices, and 2) between the position of the Perron-Frobenius eigenvector and the lengths of the columns of positive matrices. We have already gathered evidence that the length of the columns affects the position of the eigenvector. Our experiments so far have dealt mainly with positive matrices of size 2. We are now experimenting with matrices whose columns are unit vectors in order to study the dependency of the eigenvector with respect to the position of the columns. By creating codes in MATLAB that modeled several combinations of unit vectors, we were able to obtain numerical evidence of this relationship. We are currently trying to fit a model to generated data to describe the relation between the location of one column and the location of the eigenvector in simple cases. The objective is to quantify this relation. Through this research, it may be possible to estimate the location of the Perron-Frobenius eigenvector of a positive matrix in at least some simple cases.

**FRI-816****P-ADIC VALUATIONS OF POLYNOMIALS**

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In the field of number theory, p-adic valuations are useful tools in the study of the divisibility of an integer by powers of a given prime. This project centers on p-adic valuations of polynomials. In turn, this will give a better understanding of roots of polynomials modulo the powers of a

prime. Polynomials that spark the most interest are ones that yield non-p-regular sequences in the p-adic metric. For instance, the 2-adic valuation of  $n^2 + 7$  produces an infinite, non-regular sequence of valuations. The sequences of interest are represented in a novel infinite tree form, and patterns in these trees are statistically analyzed to classify sequences generated by the p-adic valuations of polynomials.

### **FRI-823**

#### **PROPERTIES OF CATALAN NUMBERS MODULO $2^\alpha$**

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Catalan numbers have been studied since the eighteenth century due to their frequent appearance in fields such as set theory, graph theory, and combinatorics. However, there are still few results about their properties modulo prime powers. In particular, this project examines the number of residues obtained by viewing Catalan numbers modulo powers of 2. For example, it is known that no Catalan number is equivalent to 3 modulo 4. Similarly, it can be shown that  $C(n)$  is not congruent to 1 modulo 8 for  $n$  greater than or equal to 2. Can other residues that do not occur for higher powers of 2 be characterized? As these higher powers of 2 are analyzed, experiments show that more and more residues are not attained. Data has been produced to conjecture that as  $\alpha$  gets large, the proportion of residues modulo  $2^\alpha$  attained by some Catalan number goes to zero.

### **FRI-820**

#### **ASSOCIATING FINITE GROUPS USING DESSINS D'ENFANTS**

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Each finite, connected planar graph has an automorphism group; such permutations can be extended to automorphisms of the Riemann sphere. In 1984, Alexander Grothendieck, inspired by a result of Gennadii Belyi from 1979, constructed a finite, connected planar graph via certain rational functions by looking at the inverse image of the interval from 0 to 1. The automorphisms of such a graph can be identified with the automorphism group of this rational function. In this project, we investigate how restrictive Grothendieck's concept of a Dessin d'Enfant is in generating all automorphisms of planar graphs. We discuss the rigid rotations of the Platonic solids (tetrahedron, cube, octahedron, icosahedron, and dodecahedron), the Archimedean solids, the Catalan solids, and the Johnson solids via explicit Belyi maps.

**FRI-824****GENERATING AN ALGORITHM TO CONSTRUCT  $\mathbb{N}$ -SHAPED SEQUENCES FROM PRIMITIVE SHAPES**

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Consider a permutation of  $\{1, 2, \dots, n\}$  which we call a finite sequence built from  $\{1, \dots, n\}$ . Subsequences of length  $k$  of this sequence might have different shapes according to the number of times they change from increasing to decreasing, and vice versa. We wanted to take previous student research one step further and predict the probability of getting a subsequence of a certain shape and length of  $k$ . We began our research by learning ways numbers can be organized. This helped us develop an algorithm to find a longest increasing subsequence in a sequence of numbers. We also modified the patience sorting algorithm to give us all possible longest increasing sub-sequences (LIS). We studied previous student research that showed how they computed all possible LISs whose elements were sorted in ascending order, and the longest lambda subsequences (subsequences shaped like the Greek upper case letter lambda:  $\Lambda$ ). Our research went one step further to find all possible  $\mathbb{N}$ -shaped subsequences of length  $k$  given  $n$  elements. An example of a  $\mathbb{N}$ -shape is: 3,1,5,2. It is a sequence whose value is decreasing, increasing, and decreasing, and thus giving you a  $\mathbb{N}$ -shape. We also created an algorithm to reconstruct sequences from given subsequence information. Our work was done by hand, using LaTeX, and presented in a closing ceremony for Project ACCESO conducted at the University of California Channel Islands.

**OPERATIONS RESEARCH****SAT-826****A HEURISTIC METHOD FOR SCHEDULING BAND CONCERT TOURS**

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Scheduling band concert tours is an important and challenging task faced by many band management companies and producers. A band has to perform in various cities over a period of time, and the specific route they follow is subject to numerous constraints such as venue availability, travel limits, and required rest periods. A good tour must consider several objectives regarding the desirability of certain days of the week, as well as travel cost. We developed and implemented a heuristic algorithm in Java. Starting from an improved nearest neighborhood algorithm to create an initial solution, we then improved it based on simulated annealing with a relaxed cost function. As a result, our program automatically generates good schedules that both satisfy the above constraints and improve objectives significantly when compared to the manual schedule created by the client. Moreover, our program also enables the clients to easily change the relative importance of objectives and constraints, so they may see and explore trade-offs among objectives while choosing the best schedules that meet the requirements of their business. Although our algorithm is designated specifically for the concert

tour, the heuristic method developed here may be reused to solve other scheduling problems with many objectives and many constraints.

## OTHER MATHEMATICS

### SAT-827

#### **WORKING OUT: A SURVEY OF THE DESIGN OF WORKPLACE INCENTIVES TARGETING EXERCISE**

Jorge Dominguez, Heather Royer.

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In recent years, there has been a growing concern in America for the general health and well-being of its citizens. Both government and business officials, in an effort to reduce health insurance costs and increase worker productivity through healthier employees, have demonstrated this concern. However, American lifestyles are still characterized by poor diet and lack of physical activity. These unhealthy behaviors impact others through higher group-rated insurance costs, lower worker productivity, and higher government spending on Medicare and Medicaid programs. Previous literature indicates that the use of workplace financial incentives targeting exercise have strong positive effects for problematic health behaviors. For example, previous research in a large-scale workplace field experiment found that workers responded favorably to incentives targeting the use of the company gym. This paper uses data from the experiment to study the effects of incentives across subsamples of participants who might be particularly affected by the treatment. In particular, the focus here is to compare the effects of these incentives across participants who reported experiencing problems with self-control prior to the beginning of the program, and those who reported not having difficulties with self-control. Regression analysis will be performed using Stata to test whether or not these incentives matter for the increase in gym attendance across these subgroups. The results of this study will provide valuable insight for the future design and implementation of workplace incentive programs targeting exercise.

### FRI-828

#### **FINDING AND APPLYING THE VALUE OF SIMPLIFIED TWO-PLAYER PARCHEESI**

Nicholas Salvers, Aden Ahmed.

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Parcheesi, also referred to as Pachisi or Ludo, is an American adaptation of an Indian board game that dates back over 1,000 years ago. It is a game of perfect information, which means all players involved are aware of every move made. Additionally, it is an infinite game, so it allows the game to continue forever, making it difficult to apply game theory. A simplified version of the game found in “Playing for Real: A Text on Game Theory” by Ken Binmore illustrates the concept of the two-player game on a  $3 \times 2$  matrix, with the value of the game to be  $17/24$ . This means that, initially, the player who moves first will have a  $17/24$  probability of winning. The first objective of this research project is to calculate the value of the simplified game when various modifications are placed on the game. The second objective of this research project is to apply the values and concepts of these games to a field outside of mathematics.

## STATISTICS

### FRI-829

#### MATHEMATICAL EXPLORATIONS OF NATIVE HAWAIIAN PLANT GROWTH RATE

Andrew Chang, Dennis Perusse.

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'Uhaloa, also known as *Waltheria indica*, is an endemic shrub that is used as a traditional medicine (la'au lapa'au) plant in Hawai'i. As a medicinal plant, 'uhaloa is found to have healing properties that help relieve the symptoms of sore throat, cough, congestion, oral thrush, and wrinkles. Due to the medicinal versatility of 'uhaloa, it is important to study its growth rates using traditional methods (soil) versus nontraditional methods (hydroponics). We used 2 mathematical models to compare plant growth in soil vs. hydroponic media to determine which growing method produces a taller plant. A raised soil bed was used to grow the plants with a more traditional watering method. A hydroponic system was set up with 4 buckets in one reservoir. For the hydroponic method, plants were measured for a 4-week period and for the soil method, plants were measured for a 12-week period. Mathematica was used to plot height data and find a fitted polynomial function for the graph of each growth method. After determining the fitted growth functions, the growth rates were calculated from the first derivative of each function with respect to time ( $t$ ). When comparing the growth rates, a linear regression statistical model was also used as a comparison, and a t-test of the difference between the slopes of the 2 regression lines was performed.

### SAT-830

#### ANALYZING SIDS USING PIECEWISE LINEAR MODELS

Kevin Pelaez, BA, Theresa Chadwick, Jane Friedman.

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Sudden infant death syndrome (SIDS) is a phenomenon in which an infant under the age of one dies from causes which are undetermined, even after a thorough autopsy. It is the largest cause of infant deaths in the United States and other developed countries. Consequently, it is of great concern for countries around the world. The Back-To-Sleep campaign has attempted to lower SIDS death rates by encouraging parents to place their children on their backs when sleeping rather than on their stomachs to allow for smoother air flow and decreased body temperature. Our project aims to investigate the effect of the Back-To-Sleep campaign by providing a mathematical approach to model and analyze data using piecewise linear models. We use regression analysis and resampling methods to determine the number of linear functions used to model the data. This method is grounded in the need to balance between the complexity of the model with the goodness of fit of the model, which are both increased by adding more linear models.

**FRI-830****ELUCIDATING MECHANISMS OF RAPID AGING IN PEROXIREDOXIN MUTANTS**

Kyle Nakatsuka, Olena Odnokoz.

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Aging, the accumulation of cellular changes that occur over an organism's lifetime, is a driver behind many disease states. A *Drosophila melanogaster* model of rapid aging in which 2 peroxidoredoxin genes are knocked down may provide deeper insight into the aging process. This research investigated the mechanisms behind rapid aging in this mutant model in attempts to better understand the role of oxidative stress in aging. Genome-wide expression levels measured by RNAseq, were compared among double-mutant, wild-type, and single-mutant controls to identify genes that were differentially expressed uniquely in double mutants. Functional clustering of differentially expressed genes identified groups of genes with functional significance, including ribosomal proteins, nucleotide binding, and protein folding. Web tools, as well as a novel statistical method currently in development, are being used to determine the link between these downstream genes and the peroxidoredoxin knockout. Promising candidate genes will be functionally assayed by qPCR, and live organism tests of lifespan, weight, intestinal function, and other known biomarkers of aging will also be conducted to confirm rapid aging effects. This research can have potential to identify new targets for anti-aging therapeutics.

**SAT-829****DETERMINING CRITICAL COURSES THROUGH STUDENT PERFORMANCE**

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Every institution of higher learning has at least one funding model (formula) imposed on it by the state and federal government. The most common funding model is the enrollment model, in which institutions of higher learning receive funding based on how many full-time students are enrolled each academic year. In recent years an increasing number of states have adopted a new funding model called the performance-based model, in which funding is based on criteria such as the number of degrees awarded, time to degree completion, etc. In this research, we analyze patterns in student registration data to identify what we call critical courses: courses in which poor performance is predictive of delayed graduation. We analyze anonymized course data with statistical analysis and data mining methods, using both original grades and grades adjusted according to a regression approach that estimates course difficulty. Our procedure allows us to identify a relatively small set of courses in a given major which are highly correlated with delayed graduation. This information could be used to provide extra student support and/or better placement in these classes as a first step toward higher on-time graduation rates.

## PHYSICAL SCIENCES

### ASTRONOMY/ASTROPHYSICS

#### FRI-516

##### ULTRAVIOLET EXCESS EMISSION FROM HIGHLY-EVOLVED SUN-LIKE STARS

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Most of the components necessary for life (e.g., carbon, nitrogen, oxygen) are produced in stars, with the largest production occurring during a late stage of stellar evolution called the asymptotic giant branch (AGB) phase. Enriched material is liberated by the star during periods of heavy mass loss in the AGB phase. The heavy mass loss mechanism is uncertain, as AGB stars are difficult to observe because they are heavily enshrouded by circumstellar shells. We used archival ultraviolet observations performed by the Galaxy Evolution Explorer (GALEX) satellite to pierce these circumstellar shells. In our study, we have discovered numerous new sources of ultraviolet emission from AGB stars and expanded the number of known ultraviolet-emitting AGB stars by up to an order of magnitude. We studied the origin of this ultraviolet emission by comparing its characteristics to other properties of the AGB stars and to other ultraviolet-emitting stars. We find that it is difficult to reconcile the ultraviolet emission with currently understood spectral energy distributions of AGB stars. Alternative origins include binary companions, chromospheric emission, accretion, shocks in the circumstellar shells, and/or heretofore unknown physical processes. Ultimately, our results provide new avenues of exploration and potential constraints on the mass loss mechanism during the AGB phase in the evolution of a star like our sun.

#### SAT-503

##### CHARACTERIZATION OF THE M DWARF BINARY SYSTEM GJ 660 1.AB SEPARATED BY OVER 120 AU

Adam Burgasser<sup>1</sup>, Christian Aganze<sup>2</sup>.

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Brown dwarfs, since their discovery, have been a subject of debate in the astrophysics community. We present a characterization of the binary system GJ 660 1.AB, a pair of M dwarfs for which we have resolved near-infrared spectra from the SpeX Prism Library (SPL). We used these data to classify the companion and compare its spectrum to theoretical models. Previous work indicates the binary system appears to belong to the spectral type M9 and the GJ 660 1 is separated to GJ 660.1B by a distance of approximately 120 AU. In addition, GJ 660.1B is approximately 4 mag fainter than the host star in the J-band. The characterization of GJ 660 1.AB will contribute to the understanding of binary systems of cool stars/dwarfs.

## **SAT-502**

### **MASS TRANSFER AND ACCRETION DISK FORMATION IN WASP 12 SYSTEM**

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WASP-12b is a hot-Jupiter planet that orbits dangerously close to its parent star WASP-12 at a proximity of about 1/44th the distance the Earth stands from the Sun, or roughly 16 times closer than Mercury. Due to tidal forces from the gravitational influence of WASP-12 and their incredibly close proximity, WASP-12b gets distorted into an egg-like shape causing it to expand beyond its Roche lobe. This allows mass to be transferred onto its host star through the first Lagrangian point, the point between two binary objects where the net force is zero, at a rate of 6 billion metric tons per second. This mass transfer forms an accretion disk that transits the parent star. This aids measurements by sensitive instruments such as the Kepler spacecraft, whose role is to examine the periodic dimming of main sequence stars in order to detect ones with orbiting planets. By implementing the hydrodynamical code, FLASH, we model the behavior of mass transfer under the influence of the system's Roche potential and subsequent disk formation to compare to collected light curve data from the Hubble space telescope's Cosmic Origins Spectrograph (COS).

## **FRI-502**

### **UNDERSTANDING THE STREAM-DISK INTERACTION IN MASS-TRANSFERRING BINARY STAR SYSTEMS**

Aaron Lopez, Enrico Ramirez-Ruiz.

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Observations of a wide range of interacting binaries show that accretion disks in these systems display pronounced deviations from axisymmetry, for which the most obvious agent is the impact of the gas stream from the companion star onto the disk. The complexity of the stream-disk interaction mandates the use of hydrodynamic simulations to fully explore its consequences. Here, we use multi-dimensional, high-resolution simulations to provide quantitative estimates of the effects of the impact of the accretion stream on disks in interacting binaries. We will discuss our results.

## **FRI-501**

### **STATISTICAL ANALYSIS OF TRANSITING PLANET YIELDS USING LSST**

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The Large Synoptic Survey Telescope (LSST) is an 8.4 meter ground-based telescope that is being built on Cerro Pachón in Chile. Designed to survey over half of the sky in 6 different color filters, LSST will provide a uniquely comprehensive view of the universe once it becomes operational in 2020. LSST will generate light curves for an unprecedented one billion stars across the night sky. The telescope has 2 primary cadences: regular, which will amount to



approximately 1,000 observations for each target star over the course of LSST's ten-year life span, and deep drilling, which will take approximately 10,000 observations in selected fields. One of the many uses of this data is for exoplanetary transit detection, which examines a decrease in flux from a host star when a planet passes across the line of sight between Earth and the star. Each target star will be sparsely sampled, making transit detection unlikely for a given target star. However, the sheer number of light curves that LSST will produce could offset this result in a non-trivial number of transiting exoplanet detections. Our goal was to test the efficiency of a standard boxed-least-squares (BLS) algorithm as a function of period at detecting the period of an exoplanet using simulated LSST data.

## **ATMOSPHERIC SCIENCES/METEOROLOGY**

### **FRI-503**

#### **NORTH ATLANTIC ATMOSPHERIC BLOCKING AND ATLANTIC MULTIDECADAL OSCILLATION: ANALYSIS THROUGH CLIMATE MODELS, REANALYSIS, AND DATASETS**

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Atmospheric blocking is an unusual weather phenomenon that causes severe weather events such as heat waves and droughts. Improved understanding of the long-term variability of atmospheric blocking thus has important societal implication. Its mechanics are not well understood. Therefore, this project investigates the variability of atmospheric blocking in the North Atlantic and its relationship with multi-decadal oceanic variability represented by the Atlantic multidecadal oscillation (AMO) using observation data and the Community Earth System Model (CESM). The mean number of blocking days in the North Atlantic is examined in the 20<sup>th</sup> Century Reanalysis (20CR) and the 30 member CESM Large Ensemble (CESM1LE) simulations. The AMO index is examined in the Hadley Centre Sea Ice and Sea Surface Temperature dataset Version 1.0 (HADISST) and the CESM1LE. Preliminary results show that a high correlation exists between the number of observed blocking days and the observed AMO index on decadal time-scales. The CESM1LE has fewer blocking days overall with a good AMO index that has similar amplitude to the observed ones. Spatial pattern and spread of the number of blocking days will be examined from all 30 ensemble members of the CESM1LE, with focus on the relationship with the simulated AMO. This research will reveal how the extreme weather variability associated with atmospheric blocking interacts with the multi-decadal oceanic variability associated with the AMO. Implications for potential causal relationships that may exist between atmospheric blocking and the AMO will also be discussed.

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**FRI-504****SENSITIVITY OF A SIMULATED SQUALL LINE TO THE MICROPHYSICAL REPRESENTATION OF GRAUPEL**

Steven Naegele<sup>1</sup>, Sarah Tessendorf<sup>2</sup>, Greg Thompson<sup>2</sup>, Trude Eidhammer<sup>2</sup>.

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In order to accurately simulate storms and their precipitation within atmospheric models, we need to ensure that atmospheric processes are well parameterized. In the case of the Thompson microphysics parameterization, the vapor, rain, snow, cloud ice, and graupel/hail hydrometeor categories have their particle densities set to a constant value. This is a good assumption for particles where the density does not vary much, like rain or ice, but it is not very realistic for the graupel/hail category since the density of graupel and hail has been observed to vary greatly between and within storms. This study assessed the sensitivity of an idealized simulated squall line to the prescription of graupel density using the Weather Research and Forecasting model. The range of graupel density was varied from  $200 \text{ kg m}^{-3}$  to  $800 \text{ kg m}^{-3}$ , representing particles more characteristic of graupel to those of hail, respectively. As the

density of graupel particles was increased from graupel-like to hail-like, simulations showed a slower squall line with weaker maximum reflectivities aloft and stronger updrafts. There was also a decreased graupel melting rate, which created more graupel and less rain. Less rain meant less evaporation and therefore a less intense cold pool, causing a decreased propagation speed. The sensitivity of this simulated storm to the prescription of graupel density is motivation for microphysics parameterizations to have the density of graupel as a predicted variable to more accurately model storm formation characteristics such as precipitation, cold pool formation, and subsequent evolution.

#### **SAT-505**

##### **THREE-DIMENSIONAL VARIATION OF ATMOSPHERIC CO<sub>2</sub>: A COMPARISON OF AIRCRAFT MEASUREMENTS WITH INVERSE MODEL SIMULATIONS**

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<sup>1</sup>Haskell Indian Nations University, Lawrence, KS, <sup>2</sup>Institute for Mathematics Applied to Geoscience, University Corporation for Atmospheric Research, Boulder, CO.

In this paper, we compare vertical profiles of carbon dioxide concentrations from aircraft measurements to simulated CO<sub>2</sub> concentrations from an atmospheric inverse model simulation. The inverse model simulations are based on assimilation of atmospheric CO<sub>2</sub> observations from the Greenhouse Gases Observing Satellite (GOSAT) instrument, the NOAA/ESRL surface flask network, and the Total Carbon Column Observing Network. Since the inverse model simulations generate CO<sub>2</sub> fluxes at approximately 1 degree, these are fed into an atmospheric transport model to simulate the atmospheric CO<sub>2</sub> concentrations. The independent set of aircraft measurements are obtained from a suite of NOAA/ESRL and the HIAPER pole-to-pole flight campaigns (HIPPO-3 and HIPPO-5 field phases). Both qualitative and quantitative analyses are used to evaluate the quality of the simulated CO<sub>2</sub> concentrations from the inverse modeling approach. Results show a greater difference between the aircraft and the inverse modeling simulated CO<sub>2</sub> concentrations near the surface (1,000 - 800 hPa) relative to higher levels in the atmosphere (< 800 hPa) and over land regions relative to over ocean basins. Both of these differences can be attributed to the greater variability and heterogeneity in the CO<sub>2</sub> signal near the land surface, which does not get simulated well by the inverse modeling approach. Future work will examine possible ways to improve the inverse model simulations in order to obtain better agreement with the aircraft data.

#### **FRI-505**

##### **DETERMINING THE EFFECTIVENESS OF THE WRF MODEL'S WIND DIRECTION FORECASTS FOR AN IOWA WIND FARM**

Meghan Applegate, Renee Walton, Eugene Takle.

*Iowa State University, Ames, Ames, IA.*

Wind energy has become one of the leading alternative energy sources for reducing dependence on fossil fuels that contribute to climate change. Changes in wind direction can contribute to changes in power output of a wind farm due to wake-turbine interactions. Forecasting wind direction changes can help forecast changes in wind-farm power output. The

weather research and forecasting (WRF) model is widely used within the meteorology community for forecasting. Wind direction observations from 2 meteorological towers at an Iowa wind farm were compared to WRF model output to determine the WRF model's skill in forecasting wind direction for this wind farm. Cases were selected based on when the 2 towers agreed and when the farm was producing substantial power: wind speeds were above  $6 \text{ m s}^{-1}$  and under  $20 \text{ m s}^{-1}$ . The WRF model was run for two 48-hour cases and compared forecasted wind direction with observations from the towers. Model skill was assessed through calculations of mean absolute error, and biases were calculated to assess the systematic behavior of the model. These results will inform future research to determine which turbines may experience power reduction due to wakes within the wind farm. These results may also be useful for determining more efficient wind farm design and layout and for taking wind direction into account in wind farm power forecasts.

## **CHEMISTRY (EXCEPT BIOCHEMISTRY)**

### **SAT-423**

#### **ANALYSIS OF HEAVY METALS IN SEDIMENT AND SEAWATER IN THE NATURAL RESERVE, LA PARGUERA, PUERTO RICO**

Nicole Lopez-Pena, Rolando Tremont.

*University of Puerto Rico at Humacao, Humacao, PR.*

The natural reserve La Parguera, located on the island of Puerto Rico, has always been a major touristic attraction due to the fact this region is home to 1 of the of the 7 bio-luminescent bays in the world. The Department of Natural and Environmental Resources of Puerto Rico (DRNA), which is tasked with protecting and maintaining a balanced ecosystem, supervises this reserve. In the present study, we analyzed the concentration of Pb, Cd, Cu, and Zn heavy metals in seawater and sediments from 3 different places in the reserve. In order to verify seawater and sediment quality, 3 samples were collected in the most populated area and tested for these heavy metals. We collected 1 sample at the center and 2 more at the borders. Furthermore, an additional 3 samples were collected from the bio-luminescent bay. The samples were prepared by warming digestion with an  $\text{HNO}_3$  50% solution for 30 min. The resulting samples were filtered and adjusted to a 100 mL volume. Finally, all the samples were analyzed by flame atomic absorption spectroscopy. Preliminary results showed a high content of heavy metals in all the samples. Ultimately, we aim to study heavy metal content in marine life. This is the first step toward maintaining a balanced ecosystem and preserving our natural reserve.

**FRI-414****A THEORETICAL STUDY OF BIODEGRADABLE DISULFIDE MANGANESE (II) COMPLEXES AS POTENTIAL MRI CONTRAST AGENTS**

Lisa Martinez, Maria Benavides.

*University of Houston-Downtown, Houston, TX.*

Magnetic resonance imaging has become essential in clinical diagnostic imaging due to its ability to provide high contrast images of soft tissues. Currently, gadolinium (III)-based contrast agents are predominantly being used in the market. However, in high doses, these contrast agents can be toxic to body tissues if leaked in the system. Non-gadolinium-based contrast agents such as disulfide manganese (II) copolymer complexes are being developed since they could potentially be a safer alternative. Two biodegradable macromolecular complexes, Mn(II)-EDTA and Mn(II)-DTPA cystamine copolymers were recently synthesized, and their contrast imaging enhancement was investigated on mice. The chemical nature of these compounds play an important role in their application as contrast agents; therefore, our computational study focuses on the determination of the structures, molecular properties, vibrational frequencies, and IR spectra of these two manganese (II) complexes. Our approach involves the use of density functional theory (DFT) in combination with B3YLP functional and basis sets 3-21G and 6-31G. The highest occupied molecular orbital (HOMO) to lowest unoccupied molecular orbital (LUMO) energy gap were determined with values exceeding 2 eV, suggesting these complexes are chemically stable. The dipole moment values range between 6 to 8 Debye, which indicate these complexes are polar. Our computed vibrational frequencies were compared to experimental values and were found in excellent agreement, which indicates our proposed structures are good representations of the 2 manganese (II) complexes.

**SAT-425****NEW APPLICATION OF PRUSSIAN BLUE IN SENSORY CHEMISTRY**

Charles Punmathara, Sheeda Vo, Faisal Khan, Mian Jiang.

*University of Houston-Downtown, Houston, TX.*

Prussian blue (PB) was the first man-made compound ever used in recent industrial civilization. This classic molecule has found many applications in dye, medicine, and nuclear chemistry. In this work, we report a novel deposition of PB onto cost-effective substrates for sensing applications. The PB film formations were found to be successfully fabricated by either chemical, spontaneous deposition, or electrochemical *in situ* reduction preparation. The latter displays a controllable nature. Conventional stationary pencil leads were used to host the PB compound, and we found the resultant film promising in sensing applications. The optimal operation condition for PB is potassium-containing supporting electrolyte. Biochemical intermediates and environmental waste residues were tested for the sensing screening. Acetaminophen and thiocyanate were found electro-catalytically oxidized onto the newly made PB detectors. Our study adds a new analytical aspect of PB to its traditional application arena. [This work was supported by NASA-TSGC-NIP, DoED-MSEIP, NRC, NOAA, and Welch Grant (BJ-0027 )]

**FRI-418****LI AND MG ION BEHAVIOR IN ORGANIC SOLVENTS**

Ana Arteaga, Luke Reed, Erik Menke.

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Understanding the behavior of ions in electrolytes is essential in many areas of science and engineering. For instance, better electrolytes are likely to contribute to the development of longer-lasting batteries with higher energy densities. In this poster, we will present our recent experimental work on model electrolytes for lithium and magnesium batteries. In particular, we have measured the activity, molar conductivity, and diffusion constants for lithium perchlorate, lithium bis(trifluoromethane)sulfonamide (TFSI), and magnesium trifluoromethanesulfonate in propylene carbonate and diethylene glycol dimethyl ether (diglyme) to better understand what role lithium and magnesium salt concentration, supporting electrolyte (here, sodium borohydride), and solvent play in the behavior of lithium and magnesium battery electrolytes. We find that the chelating ability of the diglyme drastically affects the diffusing ability of the lithium and magnesium cations, which in turn impacts the electrolytes' conductivity. However, this chelating ability also creates more active ion species than in the propylene carbonate, resulting in an overall gain in electrolyte performance.

**SAT-414****SYNTHESIS AND CHARACTERIZATION OF NEW FE AND CU NANOPARTICLE HYDROGELS**

Miguel Algara, Juan Noveron.

*University of Texas at El Paso, El Paso, TX.*

Research in transition-metal nanoparticles has gathered momentum lately due to numerous applications in a variety of fields like biomedical sciences where they can serve as catalysts, sensors, drug-delivery systems, environmental remediation, and separation science. Because of the newly established health risks that nanoparticles pose, there is a need to develop new systems that make use of the extraordinary functions of nanoparticles yet anchor them within porous materials that encapsulate them and prevent their leakage into the environment. In this project, we developed hydrogels that contain Fe nanoparticles and Cu nanoparticles trapped within their interstitial environments. The gels were produced by combining the corresponding transition metal (II) nitrate with acrylic acid, polyethyleneglycol diacrylate, and a free-radical initiator and allowed to thermopolymerize in methanol. Afterwards, sodium borohydride reduction of the soluble product resulted in a colored hydrogel. The characterization of the transition metal hydrogels with transition electron microscopy, scanning electron microscopy, and electron paramagnetic spectroscopy will be presented.

**FRI-425****SYNTHESIS OF G-QUADRUPLEX MACROCYCLES: A POTENTIAL MODEL FOR ANTICANCER DRUG DISCOVERY**

Khalyd Clay, Jeremy McCallum.

*Loyola Marymount University, Los Angeles, CA.*

With the recent interest in the anticancer potential of G-quadruplexes, the need exists for understanding the self assembly of G-quadruplexes. As such, recent studies have focused on the formation of these structures from guanine derivatives. We report preliminary evidence indicating the successful synthesis of several guanine quadruplexes from N9-(3,5-bis(pent-4-enyloxy)benzyl)-guanine, N9-(3,5-bis(hex-5-enyloxy)benzyl)-guanine, N9-(3,5-bis(hept-6-enyloxy)benzyl)-guanine, and N9-(3,5-bis(oct-7-enyloxy)benzyl)-guanine. Formation of these G-quadruplex macrocycles was carried out through cation-templated, ring-closing metathesis. The synthesized macrocycles are currently being characterized using nuclear magnetic resonance (NMR), and high performance liquid chromatography mass spectroscopy (HPLC-MS).

**FRI-407****HEXAMETHYLENETETRAMINE AS A PREBIOTIC TRANSAMINASE**

Rebeca Vindas, Christopher Butch, Charles Liotta.

*Georgia Institute of Technology, Atlanta, GA.*

Hexamethylenetetramine (HMTA) is a refractory chemical formed readily from the reaction of formaldehyde and ammonia. Both ammonia and formaldehyde have been investigated extensively for their potential as prebiotic precursors to modern biochemicals. Consequently, the high stability of HMTA and its tendency to react similarly to both ammonia and formaldehyde indicates HMTA may be a prebiotic means of concentrating both of these molecules. To test the viability of HMTA as a source of ammonia, we investigated its reaction with  $\alpha$ -keto acids. In nature, these  $\alpha$ -keto acids react with primary amines to form a secondary ketimine species. This ketimine is then reduced to a secondary amine, and fragments to yield the corresponding peptide. When combined under acidic conditions, HMTA and  $\alpha$ -keto acids react to form an analogous ketimine adduct, which undergoes a similar reduction and fragmentation. Our poster will present the conversion of the  $\alpha$ -keto acids of the citric acid cycle to their corresponding peptide by reaction with HMTA. Data will also be presented indicating a higher degree of oligomer formation than expected based on literature precedent, implying the possible role of HMTA both in peptide formation and polymerization on early Earth.

**SAT-408****DESIGNING BISCAVITAND MACROCYCLES FOR SELF-ASSEMBLING OLIGOMERS AND MOLECULAR RECOGNITION VIA HYDROGEN BONDING**

Maria Escamilla, Linda Gutierrez-Tunstad.

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Cavitands are molecules that have a bowl-like conformation that enables them to bind or entrap smaller compounds. The framework for our molecules is the resorcin[4]arene

macrocycle, which is very attractive due to its easily modifiable structure. The goal of our project is to synthesize biscavitands with different functional groups that can self-assemble via hydrogen bonding. We will be exploring how different functional groups such as hydroxyl and carboxylic acids will affect the formation of oligomers or capsules, as well as shape, size, and guest complexation. Poly-hydroxy and –carboxylic acid compounds are of great interest, because of their ability to mimic biological interactions. Similar macrocycles have been used in protein surface recognition, drug discovery, and biotechnology. A synthetic route encompassing organometallic chemistry has been used to develop a series of biscavitands that are polyfunctionalized with hydroxyl and/or carboxylic acids. Characterization of all compounds will be made by nuclear magnetic resonance spectroscopy, high-resolution mass spectrometry, and infrared spectroscopy. Progress in physical studies will be reported, and we expect the hydrogen bonding network will influence the type of structures and functions observed for the biscavitands.

#### **SAT-409**

##### **DESIGN AND SYNTHESIS OF SELECTIVE GTPASE PROBES**

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*New Mexico State University, Las Cruces, NM.*

The Rab7 GTPase is a regulator of late endocytic membrane transport and, as such, presides over an integrated growth factor trafficking and signaling nexus, which is pivotal for proper balance of neuronal differentiation and growth. Abnormal regulation of the Rab7 GTPase has been implicated in a wide range of diseases including cancer, immune disorders, and neurological diseases such as Charcot-Marie-tooth disease (CMT). The central importance of the Rab7 GTPase in health and disease motivated us to develop fluorescent analogs of a selective small-molecule activator of the Rab7 GTPase to probe the binding mechanisms through *in vitro* assays and investigate cellular responses through imaging. We hypothesize that synthetic GTPase probes containing the fluorescent HPY dyes developed in the Arterburn laboratory will have favorable solubility, cellular uptake, and binding properties analogous to the parent activator. We have synthesized a series of derivatives of novel Rab7 GTPase-targeted activators and are developing methods for fluorescent labeling. The compounds will be evaluated for structure and activity using bead-based flow cytometry assays to directly measure their effect on GTP binding. These compounds will function as scaffolds for probe development and may lead to targeted therapies for diseases such as CMT, whose treatment may benefit from the modulation of specific GTPase activities.

#### **SAT-415**

##### **PRELIMINARY CONSIDERATIONS AND EXPLORATORY REACTIONS FOR THE DESIGN AND SYNTHESIS OF PLATINUM(IV) THERANOSTIC PRODRUGS WITH NOVEL MODES OF DELIVERY**

Jonathan Gordon, Wei Wang.

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Platinum anticancer drugs such as cisplatin, carboplatin, and oxaliplatin are among the most effective and widely prescribed chemotherapeutic compounds in clinical use today, with cure



rates for some cancers as high as 90%. However, these drugs are notoriously unselective and their administration is accompanied by a host of debilitating side effects. In addition, their highly reactive nature leads to minimal cellular accumulation. Attempts to circumvent these disadvantages led to the synthesis of Pt(IV) complexes exhibiting a cisplatin-like pharmacore, which act as prodrugs and undergo intracellular reduction to release their axial ligands. With this in mind, we set out to design and synthesize Pt(IV) prodrugs based on the cisplatin pharmacore with both cancer-targeting moieties and fluorescent ligands to monitor the distribution of the system *in vitro*. Fluorescent quenching of organic fluorophores by heavy metal atoms, like platinum, is the basis of the off-on fluorescent switch we applied to monitor active drug distribution. Preliminary tests of this imaging mechanism were conducted using spectrophotometry, and our molecular structures were verified using nuclear magnetic resonance spectroscopy. We are currently exploring cancer-specific vectoring ligands, fluorescent micellar delivery vehicles, and the synthetic means to construct these promising anticancer molecules. Once in hand, these theranostic prodrugs have the potential to elucidate small-molecule biological transport mechanisms and to improve the selectivity of effective chemotherapeutic drugs.

#### **FRI-420**

#### **SCANNING-PROBE ANALYSIS OF THE INHIBITION OF ELECTRODE CORROSION USING MONOLAYER MATERIALS**

Nancy Estrada, Shane Ardo, William Gaieck.  
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The corrosion of electrodes is a leading cause of failure in electrochemical systems. Strategies currently used to inhibit corrosion of these materials tend to be costly and bulky. Monolayer materials (MLMs) like graphene or hexagonal boron nitride (h-BN) present a class of materials with desirable thermo-mechanical and anti-corrosion properties that are relatively inexpensive, atomically thin, and amenable to scale-up. Using a variety of scanning probe techniques such as atomic force microscopy (AFM), optical microscopy, and Raman spectroscopy, we plan to investigate the corrosion resistance of MLMs in diverse electrochemical environments and propose failure mechanisms for each material. We hypothesize that the basal planes of MLMs will be able to protect underlying electroactive substrates from corrosion or passivation even in the presence of oxidants as strong as chlorine, but the edge sites will be weak points where corrosion or passivation will occur. To date, we have successfully exfoliated layers of graphene and h-BN and transferred them via the scotch tape method and drop casting to electroactive substrates such as copper and silicon. We have confirmed their transfer using the aforementioned microscopy and spectroscopic techniques. Moreover, these techniques suggest we have bilayer materials, and ongoing efforts are focused on transferring MLMs. Once we have MLMs, we will investigate their ability to withstand corrosion in electrochemically complex liquid environments. We suspect that select monolayer materials may be used as corrosion barriers that retain substrate electroactivity, provided edge sites are reduced.

**FRI-410****HYDROGEN DOPING OF ORIENTED TITANIUM DIOXIDE THIN FILMS FOR VISIBLE LIGHT ABSORPTION**

Marissa Martinez, Andrew Ichimura.

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The anatase phase of  $\text{TiO}_2$  is a versatile material for photocatalysis and photoelectrochemical applications due to its large band gap, chemical stability, and low toxicity. However, water splitting and other heterogeneous catalytic applications would be more practical if electron-hole pairs formed under visible-light excitation. One way to decrease the band gap to allow the  $\text{TiO}_2$  to absorb visible light is by doping with metals or nonmetals such as N, S, C, and B. Studies show that anatase could be hydrogenated, resulting in a strongly visible light-absorbing powder. In order to simplify the introduction of H into anatase, a 3.0 keV proton ion-beam was used to implant  $\text{H}^+$  into the anatase surface. In this study, anatase  $\text{TiO}_2$  films were synthesized using  $\text{TiF}_4$  as the titanium source and fluoride as a crystallographic controlling agent. The films were dosed with a flux of  $4 \times 10^8 \text{ cm}^{-2}\text{s}^{-1}$  for 15, 20, 30, 45, and 60 minutes, resulting in a maximum implantation of approximately  $10^{17} \text{ H}^+$ . Anatase films were characterized by grazing angle X-ray diffraction (gXRD), SEM, UV-vis spectroscopy, and FTIR. The films are polycrystalline with strong [001] texture and dominant {001} facets at the surface. UV-vis spectroscopy shows that increasing the implantation time increases the absorbance in the visible region of the spectrum. The films were tested for their ability to generate hydrogen and hydroxyl radicals under UV and visible-light irradiation. This report will focus on the film characterization, the effects of  $\text{H}^+$  implantation, and results of the photo-reduction/oxidation experiments.

**FRI-405****SYNTHESIS AND CHARACTERIZATION OF {[BIS(3,5-DIMETHYLPHENYL)PHOSPHINO]METHYL}DIPHENYL PHOSPHINE**

Tia Butler, Quinetta Shelby.

*DePaul University, Chicago, IL.*

Palladium complexes containing bis(diphenylphosphino)methane (dppm) or bis(diphenylphosphino)methanide (dppm-H) ligands demonstrate catalytic activity for organic transformations. Surprisingly, its unsymmetric derivatives remain relatively unexplored. Our research focuses on the synthesis of palladium complexes containing unsymmetrical diphosphine ligands and the steric and electronic effects of the phosphorus substituents on the reactivity at the methylene carbon. Previous results suggest sterically bulky phosphorus substituents favor the formation of binuclear Pd complexes in which the ligands bridge between the metal centers, and the methylene proton is more acidic when the phosphine substituents are aromatic. This study describes the synthesis of an unsymmetric  $\text{Ph}_2\text{PCH}_2\text{PR}_2$  ligand, where  $\text{R} = 3,5\text{-dimethylphenyl}$ . The compound was characterized by  $^{31}\text{P}\{^1\text{H}\}$  NMR spectroscopy to verify the successful isolation of the desired ligand. Currently, we are working on testing the air sensitivity of the chlorobis(3,5-dimethylphenyl)phosphine compounds to better isolate the diphosphine product before coordinating it to Pd.

**FRI-419****COMPUTATIONAL EXPLORATION OF STRUCTURE PROPERTY RELATIONSHIPS FOR MRI CONTRAST AGENTS**

Rafael de la Flor<sup>1</sup>, Christopher Collins<sup>2</sup>, Maria Benavides<sup>1</sup>, David Yaron<sup>2</sup>.

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Magnetic resonance imaging uses chemical compounds called contrast agents *in vivo* to enhance images of the human body. An especially successful class of contrast agents, known as GCBAs, include the toxic lanthanide metal ion gadolinium(III) and currently make up all of the 9 FDA approved contrast agents in common use. A variety of alternative metals have the potential to be used as contrast agents. Use of such metals requires development of ligands that can bind to all but one binding site of the metal ion, leaving the remaining site to reversibly bind water molecules. The goal of this project is to use quantum chemical computations to explore the structure-property relationships for such MRI contrast agents based on Mn(II) and Cr(II) in combination with DTPA and EDTA. The initial focus is on the stability of the metal-ligand complexes, since the metals are toxic if they become unbound from the ligand. Computationally efficient semi-empirical quantum chemical methods are used to allow studies to be carried out across a wide range of complexes. Comparison with higher-level density functional theory methods (DFT) on MnDTPA/MnEDTA using BYL3P functional and basis sets 6-31G and 6-31G + is used to estimate the reliability of the semi-empirical approaches.

**FRI-421****DESIGN AND SYNTHESIS OF FATTY ACID SYNTHASE PROBES**

Aarushi Gupta, Kara Finzel, Lorillee Tallorin, Joris Beld, Michael Burkart.

University of California, San Diego, La Jolla, CA.

*Plasmodium falciparum* is a powerful parasite that causes malaria, a disease most prominent in third world countries. *P. falciparum* has a different fatty acid synthetic pathway than humans and that has been shown to present a viable target for drug design. Fatty acid biosynthesis revolves around acyl carrier protein (ACP) and its interactions with various enzymes that serve to modify and elongate the fatty acid chain in a repetitive fashion. Enoyl reductase (ER) catalyzes the rate-limiting step in this iterative pathway and uses NADPH to reduce the growing chain to the fully saturated fatty acid. Powerful antimicrobials like triclosan, isoniazid, and diazaborine inhibit binding of NADPH to ER to inactivate the enzyme, halting fatty acid production and killing off the parasite. However, overexposure to these compounds has led to multidrug resistance. The goal of this project was to design and synthesize a crosslinking probe that could covalently link ER and ACP to trap the fleeting interaction. A phenylglyoxal warhead moiety was used to covalently attach to an arginine residue in the ER active site and a pantetheine moiety was loaded onto ACP. The protein complex can then be studied using protein NMR and X-ray crystallography for more specific drug development.

**FRI-427****ANALYSIS OF RHODIUM-CATALYZED REACTIONS BETWEEN ACCEPTOR/ACCEPTOR CARBENOID AND ALLYL ALCOHOLS**

Hernando Marin, Jon Rainier.

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When a diacceptor vinyl diazoester is treated with an allyl alcohol, the oxonium ylide intermediate follows either an O-H insertion mechanism or a [2,3]-sigmatropic rearrangement. The efficiency of the reaction and the nature of its product depend not only on the substrate, but also on the rhodium(II) complex that catalyzes the reaction. Primary, secondary, and tertiary allyl alcohols are used as substrates in the presence of different rhodium(II) complexes to explore the behavior of the oxonium ylide intermediate and the efficiency of each reaction in terms of the ratio of the products obtained. Isolated products are characterized by means of mass spectrometry and NMR, IR, and UV-VIS spectroscopy.

**SAT-404****QUANTIFYING POLYCYCLIC AROMATIC HYDROCARBONS IN PARTICULATE MATTER SAMPLES**

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Polycyclic aromatic hydrocarbons are comprised of 3 or more fused benzene rings and are ubiquitous in the atmosphere. These compounds are formed as a result of incomplete combustion processes including, but not limited to, incense burning, fireworks, and exhaust emissions. Along with the production of particulate matter (PM) these compounds are also highly carcinogenic, mutagenic, and teratogenic. Particulate matter samples were collected in the Los Angeles Basin using quartz filters in 2 different sampling instruments. One consists of a low-volume air sampling system while the other consists of a static particulate matter (SPAM) sampling system. The samples were analyzed using high performance liquid chromatography (HPLC) with tandem fluorescence detection. Static and low-volume sampling techniques showed that volatile compounds, such as naphthalene, are better preserved using the low-volume sampling technique. The use of 2 sampling instruments provides an opportunity to compare, and, importantly, facilitates further development of the SPAM sampling system. Preliminary results suggest that the SPAM technique is useful for educational purposes because it shows that PAHs are present in PM samples and is a less-expensive sampling technique. This project will continue to compare and contrast PAH sampling by SPAM and low-volume air sampling techniques, and optimize analytical techniques to acquire reproducible, quantitative data appropriate for both educational and research purposes.

**SAT-406****SYNTHESIS AND PHOTOCHEMICAL REACTIVITY OF 8-OXO-7,8-DIHYDROGUANOSINE IN RNA USING MONOMERS AND DINUCLEOTIDES AS MODELS**

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Extensive studies have shown the presence of high levels of oxidized RNA in neurons of patients with neurodegenerative diseases, such as Alzheimer's and Parkinson's. Formation of oxidative lesions along with subsequent reactions may be of importance in disease development and progression. We are interested in investigating the photochemical reactivity of monomers, dinucleotides, and oligonucleotides of RNA containing the most common and arguably most relevant oxidative modification, 8-oxo-7,8-dihydroguanosine (8-oxo-G). Our approach consists on the independent synthesis of 8-oxo-G and its incorporation into oligomers of RNA followed by studies of their photochemical reactivity. We synthetically produced 8-oxo-G by halogenation and acetylation at the C8-position followed by deprotection in the presence of ammonia in approximate 86% yield. Characterization of each intermediate was achieved via NMR, IR, UV-vis, and MS. The photochemistry of monomers and dinucleotides was carried out by irradiating ( $\lambda_{\text{max}} = 350 \text{ nm}$ ) buffered solutions (pH 7.2) of 8-oxo-G under aerobic and anaerobic conditions. Product analysis and characterization was accomplished using HPLC, UV-vis, and MS. Preliminary results show that exposure to UV light leads to depletion of 8-oxo-G under both aerobic and anaerobic conditions while its canonical analogue remains unreactive. We are currently in the process of determining the exact mechanism that leads to the depletion of 8-oxo-G on exposure to UV light.

**SAT-401****PROGRESS IN THE SYNTHESIS OF INTERDIGITATED QUINOXALINE-SPANNED HETEROCAPSULES FOR GUEST COMPLEXATION**

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Supramolecular chemistry includes molecules that can participate in host-guest interactions wherein one molecule encapsulates a guest molecule. Molecular capsules have potential applications in the field of sensors and chemical remediation. The synthetic scaffold used in this project is the resorcin[4]arene macrocycle, a versatile framework that can be modified to incorporate functional groups at various positions to promote guest complexation. Quinoxaline spanned resorcin[4]arene capsules can undergo a reversible conformational switching mechanism by varying temperature, pH, and solvent conditions. Previous studies indicated that excessive flexibility of the capsule prevented complexation. We propose that replacing quinoxaline moieties with 1-carbon bridges will rigidify the capsule, thus potentially allowing complexation of guest molecules. Well-established synthetic methodologies were used to construct 3 key components of the interdigitated heterocapsule: a tetraazaanthracene linker, a monoquinoxaline dimethylene bridged cavitand, and a diquinoxaline monomethylene bridged cavitand. Progress toward completing the target heterocapsule requires a carefully developed plan involving templating agents. All cavitand intermediates will be verified through nuclear

magnetic resonance spectroscopy and high-resolution mass spectrometry. After obtaining the heterocapsule, we expect to observe binding of guest molecules. Complexation studies of this capsule will lead to a greater understanding of host-guest interactions for further development of intricate recorcin[4]arene based cavitands for determination of binding specificity.

#### **SAT-422**

##### **BIOGUIDED-SCREENING OF MARINE BACTERIA NATURAL PRODUCTS TO IDENTIFY NEW POTENTIAL DRUG LEADS**

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Natural products from plants and bacteria including marine microorganisms are important sources of valuable secondary metabolites. Recent studies have shown that marine microorganisms can orchestrate the synthesis of novel therapeutic agents. For instance, natural products belonging to the structural classes of anthracyclines, isoprenoids, and enedynes produced by marine actinomycetes exert antitumor activity. Our main objective is to identify novel natural products as potential sources of anticancer agents, particularly for the treatment of drug resistant acute lymphoblastic leukemia (ALL). ALL is the most common type of childhood cancer. ALL affects white blood cells and causes excessive immature lymphoblasts to uncontrollably spread in the human body. Although the current pediatric ALL cure rate is high (> 94%), a small population does not respond to the treatments, and a significantly higher population relapses (~30%). Relapse is usually accompanied by resistance. Therefore, new medicines to treat resistant ALL are needed. This project performs a pilot study to evaluate and identify compounds from marine actinomycetes to be used for antimicrobial and anticancer screens. Various marine bacteria strains were cultured in either marine or Mueller Hinton broth. The secondary metabolites were extracted, fractionated, and evaluated for their biological properties against drug sensitive and resistant ALL cells. Structure elucidation was carried out by column chromatography, HPLC-MS, and NMR techniques. We were able to isolate promising compounds. Final structural determination is underway.

#### **SAT-416**

##### **SYNTHESIS OF 4-CARBOXYPHENYLBORONIC ACID N-HYDROXYSUCCINIMIDE ESTER VIA CARBODIIMIDE/NHS COUPLING FOR GLUCOSE DETECTION**

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The rising numbers of cases of diabetes in the United States and worldwide has increased the need for blood glucose monitoring devices. This has led researchers to develop non-enzymatic glucose sensors which are more robust, low-cost, and simple compared to enzymatic glucose sensors in the market today. One method for the development of such a sensor involves the attachment of boronic acids, a known saccharide receptor, onto a quartz nanopore. In order to investigate the feasibility of such a device, the boronic acid can be modified and studied in solution then transferred to its solid state counterpart. Using established methods, the synthesis of 4-carboxyphenylboronic acid N-hydroxysuccinimide ester (4-NHS-CPBA) was

carried out using 4-carboxyphenylboronic acid (4-CPBA), N-hydroxysuccinimide (NHS), and by varying carbodiimide crosslinkers: N-(3-dimethylaminopropyl)-N'-ethylcarbodiimide (EDC) or N,N'-dicyclohexylcarbodiimide (DCC). The progress of each reaction was monitored using thin layer chromatography (TLC). Next, a pseudo amine analog was reacted with the 4-NHS-CPBA to mirror the attachment of the boronic acid onto an amine functionalized glass nanopore. Lastly, a sugar displacement assay was performed and analyzed via UV-Vis spectrometry to determine the binding affinity of several monosaccharides to the amine bound boronic acid receptor. Ultimately, the results of this study will act as a bridge between solution based and solid state chemistry for our boronic acid saccharide sensor. This would lead to further improvements in the field of non-enzymatic saccharide sensors for blood glucose monitoring.

#### **FRI-429**

##### **EFFECT ON FLUORESCENCE INTENSITY WITH PVP COATING WITH DIFFERENT MOLECULAR WEIGHT ON GLUTATHIONE-CAPPED CADMIUM SELENIDE QUANTUM DOTS**

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Quantum dots (QDs) have a key role in bio-imaging due to their optical properties, which allows them to be fluorescent probes for biological sensing. It has been reported that QDs have better sensitivity, stability, biocompatibility, and minimum invasiveness compared to other nanomaterials with detection purposes. They can be coated with ligands or polymers to prevent degradation or precipitation. The main objective of this research was to stabilize CdSe-GSH QDs with PVP and analyze differences in absorbance and fluorescence intensity after coating. Synthesis of CdSe-GSH QDs was performed in water in an oxygen free environment, with  $[Cd^{2+}]/[Se]$  and  $[GSH]/[Cd^{2+}]$  ratios of 0.2 and 11, respectively. For the polymerization process, aliquots of QDs were exposed to different concentrations of polyvinylpyrrolidone (PVP) (8,000 and 40,000 MW) and were left at room temperature from 5 to 7 days covered with aluminum foil. Results demonstrated that GSH-CdSe QDs have a maximum absorption peak at 350 nm with a red-orange color, and fluorescence peak at 450 nm. However, PVP-coated QDs showed a 50 to 100 nm shift compared to GSH ones. Fluorescence intensity diminished when excited at the original absorption. Stability and coating are dependent on polymer molecular weight. FTIR results showed that the thiol group (S-H,  $2,513\text{ cm}^{-1}$ ) disappeared indicating that GSH had capped the surface of the QDs. However, when covered with PVP the GSH peaks disappeared and decreased broader nitrogen bonds ( $1,491$  to  $1,414\text{ cm}^{-1}$ ) appeared. This work represents a step ahead for the fabrication of biological markers. Our current efforts with these nanomaterials include cytotoxicity tests on eukaryotic cells.

**SAT-411****MOLECULAR SIMULATIONS OF INTERMOLECULAR HYDROGEN BOND ARRANGEMENTS IN  $[\text{Au}_{25}(\text{AIB})_{18}]^{-1}$  CLUSTERS**

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In this project, we develop a molecular mechanics (MM) force field to determine the amount of intermolecular hydrogen bond interactions found between the 18 oligopeptides ligands (L) protecting a 25-atom gold cluster. The oligopeptides consist of chains of 2-aminoisobutyric acid (Aib) units. Although, the  $[\text{Au}_{25}(\text{L})_{18}]^{-1}$  structure has not yet been experimentally solved, <sup>1</sup>H NMR data gives clues as to how these ligands are structured around the Au cluster. This project used molecular simulations to carry out the following simulations: geometric optimization of a 1,393 atom structure of  $[\text{Au}_{25}(\text{L})_{18}]^{-1}$ , detection of the 18 intermolecular hydrogen bonds formed by the Aib ligands as suggested by the <sup>1</sup>H NMR data, and determination of the integrity of the Aib's 3-10 helical structure.

**FRI-404****IDENTIFICATION OF PYRENE AS A SENSITIZER OF SINGLET OXYGEN IN THE LOWER ATMOSPHERE**

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The goal of this experiment was to test the capability of pyrene to serve as a sensitizer of singlet oxygen (<sup>1</sup>O<sub>2</sub>), a reactive oxygen species (ROS), which may impact the oxidation capacity of the lower atmosphere. A Nd:YAG laser was employed to irradiate the sample at 355 nm, and an oscilloscope recorded the luminescence decay of <sup>1</sup>O<sub>2</sub>. To minimize error due to the <sup>1</sup>O<sub>2</sub> production by the solvent, the <sup>1</sup>O<sub>2</sub> production by pyrene was measured relative to a standard. The singlet oxygen luminescence decay curves for pyrene and the standard were used to measure the rate constants of <sup>1</sup>O<sub>2</sub> with respect to each compound. The ratio of these rate constants was analyzed to assess the quantum yield of <sup>1</sup>O<sub>2</sub> by pyrene. Buckminsterfullerene (C60) served as the standard, with a known <sup>1</sup>O<sub>2</sub> quantum yield near unity. The experimental quantum yield by pyrene in deuterated chloroform was  $0.366 \pm 0.040$ . The ubiquitous presence of pyrene in the lower atmosphere suggests pyrene may be a significant source of <sup>1</sup>O<sub>2</sub>, even at these moderate <sup>1</sup>O<sub>2</sub> quantum yield values. Future experiments will be carried out to test the consistency of the <sup>1</sup>O<sub>2</sub> quantum yield across different solvents.

**SAT-430****SYNTHESIS OF AMBIPHILIC NICKEL-SILYL COMPLEXES FOR COOPERATIVE SMALL MOLECULE ACTIVATION**

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Multiple bonds between silicon and late transition metals (metal silylenes) are promising platforms for cooperative small molecule activation due to the combination of strong  $\sigma$ - and



weak  $\pi$ -bonding leading to highly reactive adjacent Lewis-acidic and -basic sites. We have prepared several nickel silyl species stabilized by tridentate pincer ligands as possible precursors to reactive silylenes and useful precatalysts for a variety of transformations. Our recent results regarding the formation and reactivity of these complexes, including the role of base in promoting hydrosilyl versus halosilyl formation, will be presented. We will also present preliminary results toward abstracting the halide from nickel as well as abstracting the hydride from silicon in order to reach the nickel silylenes.

#### **SAT-426**

##### **INVESTIGATION OF THE INFLUENCE OF ENVIRONMENTAL FACTORS ON BROMELIAD INSECT BIODIVERSITY**

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Bromeliaceae is a family of Neotropical plants that retain water between leaves of a rosette arrangement. Each water-retaining tank is referred to as a phytotelma. This particular system is important to consider in the understanding of biodiversity because it creates an ecosystem of its own, providing a habitat for many insects and larvae. In this study, the relationship between environmental factors such as water quality and the biodiversity of insects in epiphytic bromeliads is examined in 2 different settings. Sample sizes of 10 bromeliads are taken from the primary and secondary forests of the Las Cruces Biological Station in Coto Brus County, Costa Rica, and compared. Prior to extraction from the trees, temperatures of the water in the inner phytotelmata of the bromeliads are recorded. Parameters including pH, nitrate, and phosphate levels in each bromeliad are then measured using approximately 15 mL of bromeliad water, the TetraTest Laborett water kit, and the Hanna Instruments nitrate and phosphate kits. The pH levels of the bromeliad waters in the primary forest are expected to be higher than those of the secondary forest, and a higher pH is expected to correlate to greater biodiversity. Excess nitrate and phosphate levels are expected to have a negative effect on the amount of biodiversity. Generally, studies of water quality are crucial to a greater understanding of biodiversity within bromeliads because the existence of living organisms can be correlated with environmental conditions.

#### **FRI-430**

##### **PURSUIT OF SELECTIVITY AND SENSITIVITY FOR SACCHARIDE RECOGNITION BY A TWO-COMPONENT BORONIC-ACID-BASED FLUORESCENT SYSTEM**

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The application of boronic acids as synthetic receptors for sugar recognition has been previously demonstrated to be a successful method. Boronic acid groups are effective synthetic receptors due to their ability to reversibly bind 1,2- and 1,3- cis-diols. Based on the properties of boronic acids, a two-component saccharide sensing system was previously developed, composed of a bipyridyl (viologen) unit substituted with boronic acid groups that act dually as a quencher and receptor, and a fluorescent pyranine dye (HPTS) as the reporter unit. The

fluorescence sensing mechanism is dependent on the formation of a ground-state charge-transfer complex between the HPTS dye and the viologen quencher. This 2-component system allows identification of mono, di-saccharides, and sugar alcohols in aqueous solution at physiological conditions. Three quenchers, mono or bis-boronic appended viologens (o-monoalkyl, o-MBV, and o-BBV) were synthesized to test the selectivity and sensitivity for achieving a fluorescence signal. The quenched fluorescence for the 3 quenchers was measured at a concentration of 400  $\mu$ M to 4  $\mu$ M HPTS, yielding 43.9%, 87.9%, and 94.4% fluorescence decrease, respectively. Stern-Volmer (S-V) plots were generated to examine the quenching properties of mono or bis-boronic substituted viologens. Results demonstrate that the bis-substituted viologen receptor has a greater fluorescence recovery than the mono-substituted viologen.

#### **FRI-402**

##### **GATE TUNABLE EFFECTS OF SURFACE PLASMON RESONANCE IN METALLIC NANOPARTICLES**

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Surface plasmon resonance is a phenomenon observed in nanostructured materials in which the conduction electrons oscillate with the oscillating electric field of light. When appropriately engineered, the highly energetic surface plasmons can decay into hot electrons that can be used for various applications such as photovoltaics and photocatalysis. In gold nanoparticles, surface plasmon resonance occurs by illumination with the solar spectrum, providing the opportunity to generate charge carriers using sunlight as a free and renewable source. This research aims to gain insight into the charge transfer process that would allow us to further understand the fundamental science behind surface plasmons for the benefit of many applications such as solar water-splitting devices and sunlight-driven catalysis. By assembling tin (IV) oxide nanowires decorated with gold nanoparticles into a field effect transistor, we are able to observe the current resulting from the surface plasmon decay into hot electrons with respect to the visible light spectrum. Also, by applying an appropriate potential via the gate, we are then able to tune the surface and bulk electronic properties of both the nanowire and gold nanoparticle. This would then allow us to potentially control catalytic reactions occurring on the surface, solely based on electronic manipulation of the structure.

#### **SAT-421**

##### **STEREOSCHEMICAL ALLYLATION OF ALDEHYDES**

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One of the fundamental goals in organic chemistry is to synthesize natural compounds and their derivatives. There is much interest in natural products because several have been shown to have medicinal value. Many active drugs contain several stereocenters which possess specific 3-dimensional spatial arrangement of 4 different atoms on a center atom. The stereochemistry in a compound can significantly affect its biological activity. One stereochemical form of a compound may be an effective drug in the body while another can be

toxic one. We are interested in the reaction of allylsilanes with aldehydes. The homoallylic alcohol product of the reaction is a useful intermediate in the synthesis of natural products and their derivatives. In this reaction, the aldehyde, which has a 2-dimensional central atom, is converted into a 3-dimensional homoallylic alcohol compound containing a new stereo center. Our goal is to develop catalysts that act to specify the face on which the aldehyde reacts, thereby controlling the stereochemistry of its product. We focus on improving the product yield and stereocontrol of this reaction. Our research focuses on testing whether palladium (P~P) mixes are effective catalysts for the reaction between allylsilanes and aldehydes and modify the steric and electronic characteristics of the (P~P) effects on the stereochemistry of the reaction products. We think that the steric and electronic behaviors of atoms within the (P~P) groups can guide the aldehyde to approach the palladium center in a specific position during the reaction, thereby acting to control the stereochemistry of the reaction.

#### **SAT-429**

#### **REACTIVE ANALYSIS OF THE CATALYTIC INFLUENCE OF M-TERPHENYL ISOCYANO MODEL COMPLEXES IN RELATION TO CLASSICAL CARBONYL COMPLEXES**

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Transition metal catalysts dramatically decrease the energy required and the time needed for chemical reactions. Since precise transformations are not always known, optimizing and applying such catalytic behaviors are often difficult. In an effort to intimately understand the catalytic influence of cobalt carbonyls in hydroformylation and Pausen-Khand [2+2+1] cycloaddition, the synthesis of novel isocyano model complexes were discovered and characterized in reactivity. Such model complexes encourage reactivity through vacant coordination while promoting stability. These complexes are paramount in navigating through catalytic cycles and are centered in our goals to isolate intermediates between catalytic transformations. A sterically-encumbering m-terphenyl isocyanide ligand-  $\text{CNAr}^{\text{Mes}_2}$  (Mes = 2,4,6-trimethylphenyl) was applied to promote such a model. Introduction of bulky isocyanides into the traditional dicobalt octacarbonyl complex results in the substitution of the two  $\mu$ -carbonyls in the dominating  $\text{C}_{2v}$  isomer, with concurrent loss of the 6 terminal carbonyls. The resulting analog -  $\text{Co}_2(\text{CNAr}^{\text{Mes}_2})_2$  was successful in showing kinetic stability in the solid phase, while also containing hemilabile  $\eta$ -6 arene interactions that promote open coordination in solution. Moreover, spectroscopic characterization of the  $\text{Co}_2(\text{CNAr}^{\text{Mes}_2})_2$  complex shows isolobal character in relation to the classical dicobalt octacarbonyl complex, allowing noteworthy comparison between the 2 in reactivity, driving the project to reach a remarkable milestone. Moving forward, intermediary  $\text{Co}_2(\text{CNAr}^{\text{Mes}_2})_2$  complexes are showcased with a range of coordinated reagents centered in hydroformylation, Pausen-Khand [2+2+1] cycloaddition, and hydrosilylation. Each reacted complex was examined through various spectroscopic instruments (nuclear magnetic resonance, FTIR, and X-ray crystallography), and all data is presented.

**FRI-416****COMPUTATIONAL ANALYSIS AND OPTIMIZATION OF THE CATALYTIC OXIDATION OF WATER FOR USE IN ARTIFICIAL PHOTOSYNTHESIS**

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Artificial photosynthesis is an increasingly promising avenue of research which seeks to generate complex hydrocarbons from atmospheric carbon dioxide and solar radiation by mimicking the processes used in plants. Further optimization of the various catalytic mechanisms used in photosynthesis is integral to developing commercially viable alternative fuel sources. It has been shown that the cationic cobalt porphyrin Co-5,10,15,20-tetrakis-(1,3-dimethylimidazolium-2-yl)porphyrin is a useful catalyst for water oxidation. A computational analysis of the transition species in the published mechanism using density functional theory (DFT) methods and a 6-21G basis set has been undertaken in order to propose more efficient catalysts. A study of the stability of the catalyst / reagent complex and the reactivity of the catalyst is underway to improve the current generation of photosynthetic systems by substituting novel electron-withdrawing substituents and the metals zinc and manganese into the established structure. The stability of the transition species involved in the rate determining step is measured by establishing steric strain at key points in the optimized structure, calculating the HOMO-LUMO gap, and calculating the ionization energies of the primary compound. The validity of the computer models has been established by comparing theoretical IR spectra of the porphyrins to experimental data, with characteristic peaks at  $1300\text{ cm}^{-1}$ ,  $1500\text{ cm}^{-1}$ , and  $1650\text{ cm}^{-1}$ . The HOMO-LUMO gap of the activated catalyst ranges from 0.70 to 0.80 eV and can be shown to decrease with increasing reactivity, while the dipole moment of the successive transition species increases from the 9.3 debye calculated for the activated catalyst.

**FRI-424****TiO<sub>2</sub> PHOTOCATALYSIS PARTICLE SIZE DEPENDENCY**

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TiO<sub>2</sub>-assisted photocatalytic degradation of rhodamine B (a wastewater contaminant) was investigated. The dependence of particle size on photocatalytic activity of TiO<sub>2</sub> was explored. For this purpose TiO<sub>2</sub> particles of various sizes were prepared by both hand grinding and ball milling processes. The experiments were conducted using a solar simulator, from which samples were taken at different times throughout the exposure. The absorbance of each solution was quantified employing a UV-Vis spectrophotometer, which enabled monitoring the degradation as a function of time. A comparison between the hand-ground samples with those obtained from ball milling revealed that the former exhibits higher photocatalytic activity. The ball-milling process resulted in an increased average particle size, which in turn caused less suspension and reduced surface area and photocatalytic activity of the particles. Furthermore, the role of other variables such as doping, temperature, and pH will be presented.

**FRI-408****DEVELOPMENT OF THERMOSENSITIVE SUPERPARAMAGNETIC IRON OXIDE NANOPARTICLES FOR HYPERTHERMIC CANCER TREATMENT**

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In oncology, the term magnetically induced hyperthermia refers to the type of cancer treatment in which heat is generated by the response of administered ferrofluid to an alternating magnetic field. Malignant tumors are more susceptible to the damaging effects of the heat within the range of 42 to 45 °C than healthy tissue. However, a major limitation associated with hyperthermic cancer treatment is the difficulty of temperature control due to the uneven distribution of magnetic nanoparticles and variations in tissue heat conductivity that results in localized overheating of healthy tissue. The focus of this project is the development of self-regulating thermosensitive magnetic nanoparticles that lose their magnetic moment when temperatures reach the upper limit of the biologically tolerable range. As demonstrated by Shimizu's group (Nagoya University, Japan), the reduction in Curie temperature can be accomplished by doping nanoparticles with various biocompatible oxides; nevertheless, due to the method of fabrication, the morphology and size distribution of the particles prepared by the group renders them inapplicable to biological systems. To overcome disadvantages noted previously, we develop (Mg, Ti)-ferrite system prepared by co-precipitation synthesis in aqueous solution of polymer matrix. Preliminary results indicate that synthesized particles are nanoscaled and possess superparamagnetic properties. However, the decrease in Curie temperature was not significant. The described approach would make hyperthermia-based treatment minimally invasive and reduce associated side effects.

**FRI-428****CHEMICAL LIFT-OFF LITHOGRAPHY FOR THE FABRICATION OF ULTRASENSITIVE NEUROTRANSMITTER BIOSENSORS**

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Neurochemical measurements in organisms have been critical in advancing our understanding of chemical reactions in the central nervous system. Chemical lift-off lithography (CLL) is a novel technique that can produce high resolution patterns on a large scale without the need for special equipment. This project uses CLL to develop highly sensitive biosensors that can detect trace amounts of neurotransmitters such as dopamine. Facile patterning of field-effect transistor electrodes on a large scale was achieved using CLL, and the same technique was used to fabricate a bio-sensing device using In<sub>2</sub>O<sub>3</sub> nanobelts as the semiconducting device material. Biosensors with less than a 100 nm feature size are being pursued, and we anticipate they will have ultra-high sensitivity for the detection of dopamine and neurotransmitters. To test the biosensors, biologically active entities such as aptamers will be covalently attached to the

sensing platform of the device, and the device will be exposed to various neurotransmitters to determine the sensitivity and selectivity of the biosensor.

#### **FRI-403**

##### **SOLVATION AND LIGAND EFFECTS ON THE CATALYTIC PRODUCTION OF ACETALDEHYDE FROM ALKYNES ON ORGANOTRANSITION METAL CATALYSTS**

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Ruthenium catalysts with pyridyl or imidazolyl ligands have been used to accelerate the formation of aldehydes from alkynes. We carry out electronic structure calculations in an effort to reproduce the observed effects of ligand selection, solvent selection, and temperature on the reaction while also including conditions that quench the reaction before completion and lead to observation of vinylidene or hydroxycarbene intermediates. The calculations employ B3LYP density functional theory and correlation-consistent basis sets to optimize intermediate and transition state geometries with 2 to 3 explicit water and solvent molecules, followed by temperature-dependent COSMO-RS continuum solvent corrections to estimate the free energy at each geometry. The intermediates and corresponding transition states at 3 points in the 10-step reaction are investigated for 4 distinct ligands and several solvents and solvent-to-water ratios.

#### **FRI-412**

##### **THERMALLY INITIATED METAL OXIDE REDUCTION USING A REDOX ACTIVE BIPYRIDINIUM-BASED COLLOIDAL GEL**

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An electroactive bipyridinium-based amphiphile has been synthesized and was found to undergo thermotropic liquid-to-gel-to-crystal phase transitions at concentrations above 1.6 M. At ambient temperature the gel phase completely crystallizes yielding single crystals suitable for X-ray analysis, which has provided us with a snapshot of the molecular ordering in the condensed, non-liquid state. While the photoreduction of bipyridinium-based molecules from the dicationic species to the radical cationic species is well known and documented, we have discovered that our novel bipyridinium-based amphiphile gels can also undergo a thermally activated reduction process in the presence of oxidized copper metal surfaces. We have further elaborated this process, developing a material and methods by which it is possible to reduce oxidized copper metal surfaces ( $\text{Cu}_2\text{O}$  and  $\text{CuO}$ ) to elemental Cu metal. X-ray photoelectron spectroscopy (XPS) reveals the disappearance of  $\text{CuO}$  and  $\text{Cu}_2\text{O}$  satellite peaks (binding energies of about 944 eV and 964 eV) following treatment with the bipyridinium-based gel. This discovery of oxidized metal surface reduction by bipyridinium gels is unprecedented in the literature and is a major step for material science as this chemistry can be done at the gel-metal interface without the need of an electroplating bath.

**FRI-409****MECHANISTIC STUDIES OF THE INTRAMOLECULAR CYCLIZATION REACTIONS OF IMINOXYL RADICALS AND RADICAL CATIONS WITH ALKYNE AND ALKENE DERIVATIVES**

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The synthesis of heterocycles is a popular field of study often associated with drug and natural product synthesis. In such applications, many studies have explored the possibility of using oximes and oxime ethers as building blocks for heterocycle synthesis, but very few have explored the radical or radical cation cyclization aspect. Previous studies have revealed that o-alkynyloxime derivatives can undergo efficient electrophilic cyclization, yielding isoquinoline or isoquinoline N-oxide derivatives. Interestingly, o-phenylbenzaldehyde and o-phenylacetophenone oximes do not show such reactivity. Instead, their oxime ethers were found to be reactive, suggesting that the aromatic ring acts as a nucleophile, attacking the nitrogen of the oxime ether moiety. However, not much attention has been focused on the oxime radical cation or iminoxyl radical cyclization processes of o-alkenyloxime derivatives. To study these cyclization processes, we prepared a series of o-alkenylbenzaldehyde and acetophenone oximes. The oximes were subjected to photooxidation in different solvents, and the product formation was followed by GC/MS and NMR. The o-alkenyloximes are expected to show reactivity similar to both the alkynyl and phenyl oximes or exhibit selectivity toward one pathway, depending on whether the alkene acts as a radical trap or nucleophile. To further investigate the mechanistic pathway of o-alkenyloximes, a transition metal catalyst screen will be conducted in order to compare and contrast the photochemical and transition metal catalyzed pathways.

**FRI-422****DEVELOPMENT OF A BORON-CONTAINING, UV-POLYMERIZABLE FILM FOR NEUTRON-SHIELDING**

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Boron-containing products have been used for various purposes in industry and the medical field. Therefore, new materials for use in these fields have been emerging. The purpose of this study is to develop a UV-polymerizable film using boron powder for application in the nuclear industry, such as in a nuclear reactor or in applications where there is a need for neutron-shielding. For these purposes, a stable formulation that contains a relatively large amount of boron and produces a strong, flexible film must be developed. In this study, a free radical polymerization process was used to polymerize an acrylate-functional, urethane-based formulation containing 10% by mass elemental boron. To ensure adequate "cure," different photoinitiator packages were investigated. On completion of the optimization of the formulation and the curing process, samples of boron-10 enriched material will be substituted into the formulations to enhance neutron absorption capabilities. Subsequently, these polymer films will be evaluated for their thermophysical properties and neutron absorbing characteristics.

**SAT-419****SIMPLE CONTROL OF VALENCY IN CARBORANEDITHIOL SELF-ASSEMBLED MONOLAYERS**

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Self-assembly, defined as the spontaneous organization of a disordered molecular system, has proven to be a viable route for bottom-up design approaches in nanotechnology. Recently, carboranethiols have been shown to assemble on Au{111} substrates and to form 2-dimensional plastic lattices, monolayers made rigid through intermolecular dipole-dipole interactions. Because of molecular symmetry and the resultant reduction in types of defects, these assemblies are significantly different and simpler than the prototypical and well-studied n-alkanethiols on Au{111} which have a multitude of distinguishable domains and defects. Within this new family of molecules, ortho carboranethiols display 2 different binding modes – doubly and singly bound – after adsorption. We demonstrated that we can switch between the singly bound and dual bound modes using simple acid-base chemistry. These surfaces have been studied and explored with scanning tunneling microscopy and infrared (IR) spectroscopy. Scanning tunneling micrographs reveal hexagonally close-packed arrangements, and IR experiments enable detection of the increase or decrease of the S-H stretch in different acidic or basic environments respectively. Plane-wave density functional theory is employed to elucidate the energetics of different binding sites on stoichiometric gold; binding energies of the local minima of both binding modalities are obtained. Experimental evidence supports majority control of the singly (dual) bound moieties shown on the local and ensemble scales, which is further supported by ground-state calculations.

**SAT-417****THE HIGHER MOLYBDENUM BORIDES: SYNTHESIS AND PHASE RELATIONS**

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Refractory metal borides have recently generated intense interest in materials chemistry. These compounds have been shown to possess many advantageous properties such as exceptionally high hardness, electrical conductivity, and even superconductivity. Previous research was directed at the tungsten tetraborides in conjunction with a current graduate student, but new research has been re-directed at molybdenum borides due to the iso-electronic relationship between molybdenum and tungsten. Higher molybdenum borides like MoB<sub>2</sub>, Mo<sub>0.91</sub>B<sub>3</sub>, and MoB<sub>3</sub> are currently under exploration as compounds of interest in this category of materials. However, the complex phase relationships in the molybdenum-boron system complicate the preparation of phase-pure samples. Here we expand on the phase relationships in arc melted MoB<sub>2</sub>, Mo<sub>0.91</sub>B<sub>3</sub>, and MoB<sub>3</sub>. Systematically varying the ratio of boron to molybdenum in sub- to super-stoichiometric amounts has yielded samples approaching phase purity. System compositions are examined by X-ray diffraction (XRD) and their grain structure analyzed by scanning electron microscopy (SEM). We also demonstrate preferential phase formation of the MoB<sub>2</sub> structure in both binary and ternary solid solutions despite wide stoichiometric variation,



as suspected from previous reports. This work enables further exploration of the properties of molybdenum borides by other methods like hardness measurements, thermogravimetric stability testing, and crystallographic phase design.

#### **FRI-413**

##### **METHODOLOGY FOR A CHIRAL PHOSPHORIC ACID CATALYZED ENANTIOSELECTIVE FRIEDEL-CRAFTS ALKYLATION REACTION OF INDOLES AT THE 2 POSITION**

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Indoles are of great interest to synthetic organic chemists due to the significant number of biologically active natural products that contain this scaffold. From the medicinal chemistry perspective, these privileged structures represent an important component in many approved pharmaceuticals used as therapeutic agents. Substituted indoles, especially those substituted at the 2 position, are latent intermediates for numerous alkaloids and pharmacologically important substances. Alkylation methods using the well-known Friedel-Crafts reaction have been of significant interest in recent years. Developing enantioselective methodologies that can perform these transformations using organocatalysts can expand the already important synthetic utility of indoles. The work presented here describes the development of a methodology for an enantioselective, Friedel-Crafts alkylation reaction of indoles at the 2 position by a BINOL-derived phosphoric acid.

#### **FRI-423**

##### **COMPUTATIONAL STUDIES OF GADOLINIUM (III)-BASED LIGANDS USED IN DIAGNOSTIC MEDICAL IMAGING**

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Magnetic resonance imaging (MRI) is a powerful clinical imaging technique that requires the use of contrast agents. Most MRI contrast agents consist of gadolinium (III) complexes. This is because gadolinium is a lanthanide with 7 unpaired electrons and long electronic relaxation times that produce high resolution imaging scans. However, gadolinium is a highly toxic metal that cannot be used in the free ionic form; instead it must be administered in a chemically stable chelated form. Different gadolinium complexes exhibit different chemical stability and imaging qualities which are directly related to the type of ligand used. Our study focuses on 5 gadolinium (III) ligands: DTPA, MS-264-L, BOPTA, COPTA, and MS-325-L. All calculations were performed using Gaussian 09. The methodology consists of geometry optimization calculations followed by frequency calculations using density functional theory (DFT) in combination with B3-LYP functional and 2 basis sets (3-21G and 6-31G). Our calculations yielded structures, molecular properties, vibrational frequencies, and IR spectra for all 5 ligands. The highest occupied molecular orbital (HOMO)–lowest unoccupied molecular orbital (LUMO) energy gaps were calculated for all ligands with values exceeding 4 eV, indicating the ligands are chemically stable. The dipole moments values range between 2 to 8 Debye which indicate the ligands are polar. The computed IR spectra were compared to experimental IR spectra and they were found in good agreement, suggesting the proposed models are good representations of the actual molecular structures of the 5 ligands.

**SAT-410****CREATING OXAZOLE COMPOUNDS USING SUZUKI COUPLING AND BORONIC ESTERS AND CREATING 1,3 CARBONYL COMPOUNDS FROM SULFOXIDES**

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The field of organic chemistry is driven by the need to explore new ways to construct carbon-carbon bonds in an economically and selective way for use in natural products total synthesis. For example, the Maio laboratory has recently developed a method to generate tri-substituted oxazole-containing alkenes via a carbolumination/suzuki cross coupling strategy. Oxazoles are features of numerous natural products and are known to be biologically active. Several examples have been generated, showing the functional group tolerance of this novel reaction sequence. A second area of exploration involves the union of methyl (phenylsulfinyl) acetate with nitriles for the construction of 1,3- carbonyl compounds. These moieties are common in natural products.

**FRI-426****ENERGY TRANSFER IN COMPACT AND EXTENDED DENDRIMERS**

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We investigated the reaction efficiency of diffusion-controlled processes on dendritic structures having chemical receptors at the center. Computational random-walk calculations using Markovian chains are used to predict the kinetics, diffusion, reaction rates, and overall dynamics of the given chemical systems. Extensive calculations were performed with mathematical programs such as Maple and Mathematica for determining numerically-exact values for the absorption time (or mean walklength) of a particle performing a nearest neighbor random walk from different sites on finite dendritic structures. We analyzed both compact and extended versions of the branched structures while manipulating the particle's probability of reaching the reaction center from a terminal starting point. The full dynamical behavior is further investigated for each case studied via the numerical solution of the stochastic master equation, and the results obtained were shown to be a direct consequence of the structural properties of the dendrimeric system such as valency, size, and growth. Conclusions garnered from computational evidence on dendritic systems both inform and are informed by experimental evidence and literature in the field of catalysis research. The possible relevance of the results obtained to catalytic processes and on-going research on dendrimeric supermolecules as affinity ligands, pharmaceutically active compounds, drug delivery systems, and light harvesting compounds is noted.

**SAT-428****THE EFFECT ON VARIOUS CAPPING LIGANDS ON RHODIUM-GOLD ALLOY NANOPARTICLES FOR THE USE IN ELECTROCHEMICAL REDUCTION**

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Many studies have shown that platinum (single metal) is the optimal catalyst for oxidation/reduction of proton exchange/polymer electrolyte membrane fuel cell (PEMFC). However, platinum is scarce, which limits its use in commercial settings. Therefore, other catalysts are being developed that decrease cost and show activity comparable to platinum for both oxidation and reduction reactions. Recent studies have shown that rhodium (Rh) nanoislands on gold (Au) increases the oxygen reduction reaction (ORR) when compared to pure Au. Hence, we synthesized Rh-Au alloy nanoparticles (NPs) using a modified Brust phase transfer method. Various ligands such as dodecyne, dodecanethiol, triphenylamine (TPA), and 4-ethylphenylacetylene (EPA) were used to cap the Rh-Au alloy NPs in order to examine the ligand effect on catalytic activity. Spectroscopic measurements including UV-vis, FTIR, transmission electronic microscope (TEM), and X-ray photoelectron microscopy (XPS) were utilized to characterize the Rh-Au nanoparticles. UV-Vis confirmed that nanosized Rh-Au alloy NPs were synthesized, and FTIR indicated all ligands are surface bound. Rh-Au catalysts were analyzed by cyclic voltammetry (CV) in nitrogen saturated 0.1 M NaOH. Results indicated both Rh and Au are active components of the metal core surface. Rotating ring disk electrode (RRDE) voltammetry in oxygen saturated 0.1 M NaOH was used to evaluate the electro catalytic oxygen reduction activity. This activity will be dependent on choice of capping ligands due to different interfacial connection between ligands and metal core that will ultimately alter electronic structure of the metal core and, consequently, ORR activity.

**SAT-427****ELECTROCHEMICAL ANALYSIS OF 1-METHYL-2-NITROIMIDAZOLE IN THE PRESENCE OF WEAK ACIDS**

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1-methyl-2-nitroimidazole (2-NI) and its derivatives are highly active biological compounds that can be used for therapeutic purposes. Benznidazole, a 2-NI derivative, is 1 of only 2 drugs used for the treatment of Chagas disease. In cancer treatment, 2-NI has also been studied as a radiosensitizer of hypoxic cells. In both cases, the reduced, radical intermediates are believed to be toxic to cells. The 2e<sup>-</sup> reduction product of the 2-NI forms 1-methyl-2-nitrosoimidazole (nitroso) which is the active form of the pro-drug. Aromatic nitrosos are known to be active compounds which react cysteine residues to inactivate enzymes and shift the redox balance of the cells. The fact that an initial reduction of the 2-NI is required makes electrochemical methods a powerful tool to study the 2-NI. Our aim is to gain a qualitative understanding of the specific redox pathways of 2-NI in the presence of weak acids. Cyclic voltammetry (CV) experiments of 2-NI have been conducted in aqueous and aprotic solvents. In an aqueous system, we use the L-cysteine•HCl (CysHCl) as the guest. In aprotic solution, we use 2-naphthol

(naphthol) and N-tertbutoxycarbonyl-L-cysteine-methyl-ester (Cys) as the guests. In an aqueous environment, the 2-NI is reduced to the hydroxylamine/nitroso rodox pairs, without any guests. In experiments with naphthol, the 2-NI also forms the hydroxylamine/nitroso rodox pairs. In aqueous and aprotic environments, CysHCl and Cys react with the nitroso to form an amino-thioether compound. This shows that nitroso is the more active form of the reduced 2-NI, which reacts with cysteine.

#### **SAT-405**

##### **CHARACTERIZATION AND SYNTHESIS OF SUPERPARAMAGNETIC IRON OXIDE NANOPARTICLES**

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Superparamagnetic iron oxide nanoparticles (SPIONs) coated with dextran possess high potential for biomedical applications. The purpose of this work is to coat the iron core of the particles with a dextran layer that can be modified for site-specific nanomedical applications and, at the same time, prevent the degradation of iron particles in physiological conditions. Some of the biomedical applications include computed tomography, magnetic resonance imaging, drug delivery, gene therapy, and thermal ablation of tumors. SPIONs were synthesized using chemical co-precipitation of ferrous iron ( $\text{Fe}^{2+}$ ) and ferric iron ( $\text{Fe}^{3+}$ ) in a dextran solution. Once prepared, the nanoparticles were then analyzed for average size, hydrodynamic radius, magnetic properties, and chemical composition. Due to the size-dependent properties such as surface to volume ratio, superparamagnetic characteristics, specific heat, and surface reactivity, the characterization of the particles is essential to the research in order to measure these assets. Now that we have successfully synthesized and characterized the SPIONs, the next step is to modify the surface with specific conjugates for desired biomedical application. This research will eventually be used to improve treatment of certain ailments which are difficult to treat with current medical technology by providing a less toxic alternative to current medical procedures, higher resolution for medical imaging, and site-specific drug delivery.

#### **SAT-407**

##### **SIMULATION OF ION MOVEMENT IN ACTIVATED CARBON BASED SUPERCAPACITOR**

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Electric double layer capacitors (EDLCs) are devices that store electric energy in the electric double layer that is formed at the interface between the electrode and the electrolyte. It has been observed experimentally that, as the voltage in an EDLC is increased for a certain threshold voltage, the capacitance increases abruptly. One possible explanation of this phenomenon is the liberation of charges around ions after their entrance through the pores of the electrode. A simple molecular dynamics (MD) model has been formulated to model this process that supports the hypothesis. Using the Nanoscale Molecular Dynamics (NAMD) program, we performed MD simulations of ion transport in activated carbon supercapacitors. We used graphene and single wall carbon nanotubes to model the pores in the activated carbon. In particular, a given pore is modeled using a conical structure whose diameter tapers

from 1.6 nm to 0.6 nm. We used sulphate and hydronium with charges of -2.0 and +1.0 e respectively to simulate the ions of the electrolyte. Our model predicts ion transport into the activated carbon pores which is the first step in the process of charge liberation around ions. To validate the model, we are comparing the capacitance predicted by the model with that obtained from laboratory experiments (currently in progress). Also we will measure the capacitance of the system and study its dependence on the porous size, weight percent of the sulfuric acid, as well as other types of electrolytes.

#### **FRI-406**

##### **MULTIVALENT TUMOR-TARGETING WITH 1,3,5,7-TETRAKIS(AMINOMETHYL)ADAMANTANE USING BIOTIN AS A TARGETING DOMAIN**

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We aim to test the notion that the biodistribution of MRI contrast agents can be influenced by the deliberate inclusion of modular targeting domains on these molecules. We have used the biotin-avidin ligand-receptor pair as a tumor-targeting domain in the development of these contrast agents, which also contain domains to complex the Gd(III) contrast agent and another to mediate the solubility of the complex in biological fluids. These domains have been attached to 1,3,5,7-tetrakis(aminomethyl)adamantane, a symmetrical tetrahedral polyamine. This has been achieved through selective acylation of the polyammonium conjugate acid, in effect using protons as protecting groups. We have designed a C<sub>3</sub>V-targeting motif based on the tetrahedral 1,3,5,7-tetrakis(aminomethyl)adamantane. Three of the equivalent amine groups are selectively acylated with biotin; the fourth remains for conjugation to the diagnostic agent. Here, we describe work on the synthesis of this targeting domain. Adamantane was brominated to 1,3,5,7-tetrabromoadamantane, which was converted to 1,3,5,7-tetracyanoadamantane by a photochemical free radical nucleophilic substitution. The tetranitrile was reduced to yield the core 1,3,5,7-tetrakis(aminomethyl)adamantane, which was isolated as the tetra(hydrochloride) salt. We have developed chemistry for the selective acylation of this core to produce the tri(biotin) targeting domain. Future work will include the incorporation into MRI components for tracking of these molecules *in vivo*.

#### **SAT-424**

##### **LC-MS AND NMR CHEMICAL PROFILING OF THE INDONESIAN SPONGE *ZYZZYA FULIGINOSA*: CHEMICAL DEREPLICATION AND OVARIAN CANCER CELL (OVC-5) ANTICANCER ACTIVITY**

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Natural products research is crucial to the discovery of potential treatments for cancer and other ailments. Nearly 50% of all cancer drugs are natural products or derived from natural products. The marine environment, in particular, has been shown to be a productive source of natural product lead compounds. In this study, the Indonesian sponge *Zyzzya fuliginosa* was shown to have activity against human ovarian cancer cells *in vitro*. This finding prompted the chemical investigation of this marine sponge to determine the chemical compounds responsible

for the observed activity. Crude methanol extracts of *Z. fuliginosa* obtained from the National Cancer Institute were subjected to liquid chromatography-mass spectrometry to determine known molecular weights that have previously been isolated from this genus of sponge. This dereplication process allowed identification of two known pyrroloiminoquinone compounds, tentatively assigned as makaluvamine C and makaluvamine L, based on mass spectral characteristics. Nuclear magnetic resonance was utilized to confirm the presence of these compounds based on diagnostic chemical shift patterns. Studies like these illustrate the potential of marine organisms to produce bioactive compounds.

#### **FRI-401**

##### **DEPENDENCE OF THE LI-ION CONDUCTIVITY AND ACTIVATION ENERGIES ON THE LOCAL CRYSTAL STRUCTURES AND IONIC RADII IN $\text{Li}_6\text{MLa}_2\text{Ta}_2\text{O}_{12}$**

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Lithium batteries with solid-state electrolytes have the potential to become important power sources due to their safety, energy density, and electrochemical stability. The limitation of current lithium-ion batteries and promising results of lithium conducting solid electrolytes inspired our group to study the influence of alkaline earth metal cations  $\text{M}^{2+}$  ionic radii, and crystal structure on the ionic transfer of  $\text{Li}_6\text{MLa}_2\text{Ta}_2\text{O}_{12}$ . The bulk material samples were prepared via ceramic synthetic methods, and X-ray diffraction was used to assess phase purity. Further physical and structural characterizations of the samples were done using neutron diffraction, synchrotron diffraction, scanning electron microscopy (SEM), and AC impedance measurements. Our work revealed that unit-cell size increases linearly as ionic radius increases from  $\text{Ca}^{2+}$  to  $\text{Ba}^{2+}$ , with a simultaneous increase in ionic conductivity. A larger unit-cell results in a less compact lattice, which affects the local structure and increases the rotational freedom of the octahedral  $\text{TaO}_6$ . Furthermore, we observed a decrease in the activation energy as the  $\text{M}^{2+}$  cation radius increased showing that higher ionic conductivities are connected to lower activation energies. The results suggest that changing the structural parameters of  $\text{Li}_6\text{MLa}_2\text{Ta}_2\text{O}_{12}$  directly influences the ionic conductivity, Li-ion diffusion, and activation energies of these types of materials, which implies that lattice parameters are important in the design of solid-state electrolytes.

#### **SAT-413**

##### **BIPYRIDINIUM-BASED POLYMER SPONGES FOR THE SELECTIVE SEQUESTRATION OF PI-ELECTRON RICH AROMATIC HYDROCARBONS FROM WATER**

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Emerging trends in materials chemistry, specifically, the incorporation of information rich structural motifs capable of imparting molecular recognition to reticular networks and polymeric scaffolds, has yielded excellent examples of functional soft matter that display materials processability suitable for efficient device fabrication. Motivated in part by the

pressing need to develop similar materials that are capable of sequestering pollutants from aqueous solution, a well-known, albeit nuisance reaction, namely the heat activated disulfide exchange polymerization of lipoic acid, was employed in efforts to obtain a novel pi-electron deficient bipyridinium-based polymer network. This polymer sponge material was found to be insoluble in water yet still retains its ability to sequester pi-electron rich aromatic hydrocarbons from solution. The material is partially hydrated at the surface where the partially solvated bipyridinium recognition groups remain active. On exposure to di(ethylene glycol)-disubstituted 1,5-dihydroxynaphthalene (DNP-DEG), the material exhibits a dramatic color change from yellow to red. This is characteristic of the donor-acceptor charge transfer absorption band that accompanies the binding of bipyridinium derivatives with DNP-DEG. This is an indication that DNP-DEG has been absorbed by the polymer sponge. These results bode well for the future development of polymeric materials for use in the environmental remediation of polluted waters.

#### **SAT-420**

##### **CHEMISTRY FOR CHIRAL SKELETONS: A PILOT STUDY ON BUILDING DIVERSE, CHIRAL FRAGMENTS FROM ENANTIOPURE 1,2-AMINOALCOHOLS**

Juan Serrano, Zarko Boskovic, Steven Ferrara, Laura Furst, Samuel Figueroa, DeMarcus Crews, Adrian Guerrero, Christina Brackeen, Shawn Nelson, Siva Dandapani, Andrew Phillips, Stuart Schreiber.

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Chemical biologists seek to explore human biology through the use of small molecule therapeutics and biological probes. One approach to this is fragment-based drug discovery (FBDD), where biologically active molecules are built from core-fragment scaffolds. Currently, most of the chemical libraries used in FBDD are dominated by  $sp^2$ -rich aromatic compounds. Building an expanded library containing  $sp^3$ -rich chiral fragments would allow the exploration of a larger chemical space which in turn would open avenues for unexplored biological space. In this project, we seek to exploit the power of modern organic chemistry to create a pilot library of 86  $sp^3$ -rich, highly soluble chiral fragments derived from 1,2-amino alcohols. These fragments will be synthesized using the principles of diversity-oriented synthesis (DOS) to generate a set of molecules diverse in chemical and structural properties. To begin building our  $sp^3$ -rich chiral fragment library, we focus on optimizing and devising reaction conditions for the synthesis of sulfamidite and sulfamidate fragments derived from 1,2-amino alcohols. Once synthesized, these chiral fragments will be characterized by  $^1H$  NMR, and their solubility and stability in phosphate-buffered saline (PBS) will be assessed. The results of this pilot study will serve as a blueprint in designing, evaluating, and building more focused libraries of chiral fragments. In turn, this will lead to building more structurally diverse fragment libraries which will expand the scope of fragment-based drug discovery.

**FRI-411****PROGRESS IN THE SYNTHESIS AND CHARACTERIZATION OF A RESORCIN[4]ARENE BASED HETERODIMER**

Ephraim Morado, Yanwei Cai, Linda Gutierrez-Tunstad.

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In supramolecular chemistry, the discovery of resorcin[4]arene frameworks and their potential applications in molecular recognition, catalysis, and toxin sequestering has piqued scientists' interest. Resorcin[4]arene molecules feature a bowl-shaped cavity that is used as a primary scaffold for developing molecular containers known as cavitands, which can form dimeric capsules via metal coordination, covalent, and hydrogen bonding. Previous capsule designs in our lab did not exhibit guest binding due to their flexibility. In this study, we predict that rigidifying covalently linked capsules will improve conformational switching induced by external impetuses such as pH, solvent, and temperature, thereby potentially improving binding with guest counterparts. To perform this work, a resorcin[4]arene scaffold is employed to generate a heterodimer capsule, consisting of a dimethylene bridged cavitand and a diquinoxaline cavitand tethered together by two tetraazaanthracene linkers. Well-established organic methodologies were used to synthesize the capsule intermediates in fair yields and were characterized by nuclear magnetic resonance and high-resolution mass spectrometry. Understanding the capsule's structure and behavior will permit control over these molecules and influence their guest selectivity. This will eventually lead to further development of more sophisticated covalently linked capsules.

**SAT-403****DESIGN AND SYNTHESIS OF A NEW CLASS OF SELECTIVE ESTROGEN RECEPTOR ANTAGONIST**

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Estrogen is involved in the development of many breast tumors. The expression of ER $\alpha$  is important for diagnosis, prognosis, and treatment, and is a target for development of improved therapeutics. Recent studies have revealed important functions for a new G protein coupled receptor (GPER or GPR30) in multiple cancers. Existing anti-estrogen therapeutics, such as tamoxifen, bind to both receptor classes but produce opposite responses. We have recently discovered a new small molecule that selectively binds to estrogen receptors (ER) and does not interact with GPER. Using structure-guided design, we have identified a series of synthetic analogs that are predicted to function as selective antagonists of ER $\alpha$ / $\beta$ . We have developed a 3-step synthesis process that involves Diels-Alder cycloaddition, followed by a lithium aluminum hydride reduction of the ester and/or cyano groups, and a Prins cyclization with a substituted benzaldehyde. The novel synthetic analogs will be evaluated for binding affinity and functional activity for agonism/antagonism of estrogenic responses in a panel of cancer cell lines. These compounds will serve as structural foundations for the development of a promising new class of chemotherapeutic and diagnostic imaging agents.



**SAT-412****CONFORMATION-DEPENDENT TRIPLET DYNAMICS IN POLY-3-HEXYLYTHIOPHENE**

Cody Aldaz, Alan Thomas, Jian Gao, Eric Martin, John Grey.

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Triplet excitons play a significant role in the photophysical processes of conjugated polymers such as singlet-triplet quenching, triplet-triplet annihilation, and triplet-charge annihilation. It is hypothesized that polymer conformations impact these processes. While a great deal is known about singlet excitons in conjugated polymers, less is known about triplet excitons because their decay pathways are non-radiative. Poly-3-hexylthiophene (P3HT) conjugated polymer nanofibers are an ideal system to study the effects of morphology on triplet dynamics because these nanofibers have been demonstrated to exist in 2 distinct conformations, H- and J-aggregates. This presentation will report efforts to understand the structure-function relationships of triplet excited states in P3HT using single molecule modulation spectroscopy. In this approach, the time-resolved fluorescence intensity of a single-conjugated polymer nanofiber will be recorded under variable-intensity sub-millisecond pulsed irradiation. The data can reveal differences in the kinetics of triplet formation and decay for different polymer morphologies. These correlations can give insight into the structure-dependent exciton dynamics in conjugated polymers and can be leveraged in the future design of solar cells and other optoelectronic devices.

**SAT-402****STRUCTURAL CHANGES INDUCED BY 8-OXO-7,8-DIHYDRO-ADENOSINE ON RNA**

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It has been suggested that oxidative damage to RNA is involved in neurodegeneration. As observed in DNA, oxidized lesions on RNA are known to form base-pair mismatches that can lead to significant structural changes. Reactions between reactive oxygen species and adenosine are known to produce 8-oxo-adenosine (8-oxo-A). We tested the effects of this lesion in oligomers of RNA to study structural alterations in the biopolymer. The modified monomer was synthesized via a 3-step reaction starting with bromination and acetylation of the C8-position followed by hydrolysis in the presence of ammonia to yield the desired lesion in an approximate 53% yield. The oxidized nucleotide was then protected at the N6- and C5'-positions by treatment with N,N-dimethylformamide dimethyl acetal followed by 4,4'-dimethoxytriphenylmethyl chloride, respectively. Silylation of the C2' position was achieved using standard conditions in the presence of tert-butyldimethylsilyl chloride. Phosphitylation of this material yielded the desired phosphoramidite of 8-oxo-A for its incorporation into oligonucleotides of RNA via solid phase synthesis. Each synthetic intermediate was characterized via NMR, IR, UV-Vis, and MS, while the identity of each oligonucleotide was confirmed via MALDI-TOF MS. Structural studies were carried out using CD (charge detection), MS, and gel electrophoresis. The design of each sequence was such that the effects of 8-oxo-A were probed on different secondary structural motifs. Preliminary data suggest that the effects

of 8-oxo-A on the overall structure is dependent on both the amount of damage and its position.

#### **SAT-418**

##### **MAKING THE NEGATIVE POSITIVE: $\alpha$ -OXYGENATIONS AND $\alpha$ -AMINATIONS OF $\beta$ -KETONITRILES VIA NITROSOCARBONYL INTERMEDIATES**

Benjamin Huffman, Javier Read de Alaniz.

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The demand for nitrogen and oxygen containing pharmaceutical drugs increases the need for inexpensive and environmentally responsible methods of adding nitrogen and oxygen functionality to organic molecules. The goal of this research project is to show that electrophilic aminations and electrophilic oxygenations, using nitrosocarbonyl intermediates, are a selective and efficient way to add nitrogen and oxygen functionality to organic molecules. The electrophilic source of oxygen and nitrogen explored in this research relies on nitrosocarbonyl intermediates, which are currently underdeveloped. Using an oxidation technique developed in our lab, the nitrosocarbonyl intermediate is generated *in situ* by oxidizing readily available hydroxamic acid derivatives using copper (I) salts and oxygen gas. Since copper (I) salts are relatively inexpensive and the only byproduct of the hydroxamic acid oxidation is water, it is hoped that these new electrophilic amination and oxygenation strategies will prove to be an economically reasonable and greener way of synthesizing carbon and nitrogen and carbon and oxygen bonds.

#### **EARTH SCIENCES/OTHER PHYSICAL SCIENCES**

#### **SAT-621**

##### **SUSTAINABLE APPROACH FOR DUST SUPPRESSION**

Presley Ramirez, Teamrat Ghezzehei.

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Dust emission is a major environmental problem that has negative implications on health and industrial applications. This problem is expanding for a number of reasons, including climate change-induced increase in drought frequency and magnitude and rapid growth of solar power plants in areas where the soil has been protected by fragile bio-crust. Current technologies for suppression of dust emission involve either slowing down wind using breakers (e.g., plants or mechanical structures) or (bio)chemical stabilization of the soil surface. Most stabilizers are toxic and expensive, which limits their application. The objective of this study is to test inexpensive and non-hazardous approaches to soil stabilization. Recent research in our group has revealed a process of soil stabilization by using small amounts of cementing agents. Wetting and drying cycles in the presence of dilute solutions of biologically derived long-chain polymers results in strong adhesion between soil particles. In this study, we tested whether dilute solutions of xanthan gum and PGA can be used as soil stabilizers. Both of these polymers are mimics of plant and bacteria derived polymers that are known to form stable soil aggregates. The commercially available compounds we used are widely used as additives in the food

industry and are non-toxic. We tested the effectiveness of this approach by subjecting the soil crusts to artificial wind energy. The results of this research can have important implications for dust suppression in areas where airborne diseases are prevalent and near solar-power facilities.

#### **FRI-620**

##### **GEOCHEMICAL ANALYSIS ON BAT GUANO FOR MATOS CAVE AT ARECIBO, PUERTO RICO**

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Matos Cave is located in the north-coast karst belt region of Puerto Rico. The cave is located in a subtropical, moist-forest biome and is the habitat of more than 50,000 bats. The cave is home for 3 types of bats: *Artibeus jamaicensis*, *Erophylla bombifrons*, and *Brachyphylla cavernarum*. The bat colonies are separated in the cave because of the temperature gradients created by the bat population, droppings, and exterior temperature. This study presents a geochemical analysis of the bat guano found at the surface of the cave. The analysis consisted in measuring the pH, nutritional composition (LOI and organic digestion), and the chemical and mineral composition by using FTIR spectroscopy. A total of 12 sampling sites were selected in the cave. From the results obtained, the pH varied from neutral (outside sample) to acidic as a function of the depth of the cave or bat species. The nutritional composition varied from 10 to 70% and did not have a particular pattern. The combination of nutritional composition and pH provides what the soil mesofauna needs to have a stable ecosystem. The mineralogy results included calcite, gypsum, and clay and were measured using FTIR for a complete characterization of the bat guano. In conclusion, this study presents a methodology for characterizing the bat guano of the cave, and these results can be used to understand the soil mesofauna, which varies depending on the species of bat producing the guano.

#### **SAT-620**

##### **CAN PLANT JUICE BE USED TO MINIMIZE WIND EROSION OR DUST EMISSION**

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Wind erosion and dust emission degrade air quality and can cause health concerns. In agricultural lands, keeping a vegetative cover has been the most efficient way to minimize wind erosion. With the increasing use of biomass for fuel conversion, there is a need to find a way to reduce wind erosion when the biomass is removed. Plant juice, a natural product from harvesting fiber from green biomass, may have a potential to reduce wind erosion. We tested the soil crust strength under a sand abrader with and without the plant juice extracted from field corn, sweet corn, and kudzu plants. The wind erosion resistance was measured by the amount of soil lost from different abrading times. The Amarillo soil from western Texas, where dust storms occur frequently, was used in the study. With 10 ml of 25% juice, a mix of 1:3 juice/water dilution, applied to the soil contained in a 3-inch diameter ring, the soil lost was reduced from 2.6 g for the control treatment with 10 ml of water applied, to 0.2 g under the juice treatment after 2.5 seconds of abrading. We found very similar levels of reduction from corn and kudzu juices as compared to the control. Results from this investigation may lead to

the commercial development of a natural product from green biomass that can be used to reduce wind erosion and dust emission. The beneficial use of a nuisance plant such as kudzu may also change how we manage invasive species in the ecosystem.

## **GEOLOGY**

### **FRI-621**

#### **INVESTIGATION OF OXYGEN VALUES AND POSSIBLE DIAGENETIC ALTERATION OF BONE CARBONATES AND BIOGENIC APATITES FROM MORRISON FORMATION**

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Recent oxygen isotope analyses from turtle scute phosphate of the Morrison Formation showed values lighter than expected, especially for samples from Fruita, Colorado [ $d^{18}\text{O} = 9.9\text{‰}$  vs Vienna standard mean ocean water (VSMOW)]. Using these values along with coeval palustrine carbonate  $d^{18}\text{O}$  from the Cleveland Lloyd Dinosaur Quarry, colder than expected temperatures were estimated for the Morrison Formation (as cold as  $3.7\text{ °C}$ ). These values are inconclusive without a fundamental evaluation diagenesis. The goal of this study is to test whether the phosphate values may have experienced late diagenetic alteration by analyzing the carbonate component of the turtle scutes. If no diagenesis has occurred, then a consistent offset is expected between the  $d^{18}\text{O}_{\text{carb}}$  and  $d^{18}\text{O}_{\text{phosphate}}$  of approximately 6 to 10‰. We will also evaluate calcite spars where present as they are expected to be a late diagenetic end member to compare. Samples will be drilled to produce approximately 200  $\mu\text{g}$ , enclosed in helium flushed Labco Exetainers®, and dosed with 100% phosphoric acid to produce  $\text{CO}_2$ . This will be sampled with the Gasbench II then transferred to a ThermoFinnigan Delta +XP IRMS. If the oxygen isotope offsets are what are expected for modern vertebrates, and if later calcite phases diverge from these compositions, we may conclude that the bioapatite values are true biogenic values. The colder than expected temperatures may be the result of later diagenesis of the palustrine carbonate values. Further analyses of these materials will be needed to confirm this.

### **SAT-622**

#### **$\text{SO}_2$ FLUX MONITORING AT POPOCATEPETL VOLCANO, MEXICO, USING THE OZONE MONITORING INSTRUMENT**

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Volcanic eruptions emit large amounts of gases to the atmosphere, especially water vapor, carbon dioxide, and sulfur dioxide. The monitoring of these volcanic emissions is very important because they can be used to understand and forecast an eruptive process. Approximately 44 satellite images (2012 and 2013) from the Ozone Monitoring Instrument (OMI) were downloaded and processed to measure the  $\text{SO}_2$  mass in the plume and then to calculate the  $\text{SO}_2$  fluxes from one of the most active volcanoes in the world: Popocatepetl, Mexico. Two different techniques were used to determine the  $\text{SO}_2$  fluxes on Popocatepetl: the single pixel

emission rate estimation technique and emission rate estimation based on SO<sub>2</sub> plume transect technique. Based on the analysis, the most active period between 2012 and 2013 was during April to May 2012, with an average SO<sub>2</sub> flux of 6,710 t/d. This corresponded to the period right before and at the beginning of the eruptive crises in 2012. On the other hand, the period with less activity was between August and October 2012, with an average flux of 1,930 t/d. A trend of increasing SO<sub>2</sub> flux was found for the period January to May 2013. Finally, the results were compared with previous works, demonstrating a general correlation in the data, even though the differences were high for certain dates, probably because of errors in the wind-speed data.

## OCEANOGRAPHY

### FRI-623

#### REVISITING ANTARCTIC CIRCUMPOLAR CURRENT TRANSPORT ESTIMATES

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The Antarctic circumpolar current (ACC) is the world's strongest current and acts as a conduit that transports water between the Atlantic, Pacific, and Indian Oceans. ACC transport is a key metric used to evaluate the accuracy of ocean and climate models. The canonical ACC transport through Drake Passage of 134 Sv derives from a year-long experiment conducted in 1979 (DRAKE79). Drake Passage is the ACC's narrowest choke point. Recent studies suggest that the DRAKE79 ACC transport estimate may be biased low by as much as 20%. This study will use the Southern Ocean state estimate as a test bed to evaluate DRAKE79 methods. Transport estimates from DRAKE79 resulted from a complicated synthesis of historical data and *in situ* measurements. The DRAKE79 approach relied heavily on the outcome of referencing 3 hydrographic sections with directly measured currents. This study focuses on evaluating DRAKE79's geostrophic referencing technique. We hypothesize that the horizontal spacing and temporal averaging of current meters led to a bias in the historical estimate. First, the nominal horizontal spacing of 45 km may not have resolved the narrow jets of the ACC, and 2 critical moorings were lost in a particularly energetic region. Second, DRAKE79 chose averaging periods for the reference currents that minimized the adjustment from geostrophic shear referenced to 0 at 2500 m, yet contemporary measurements indicate that the eastward ACC flow extends to the sea floor. Ultimately, we seek to determine whether DRAKE79 and contemporary ACC transports differ due to methodological uncertainties or inter-annual/decadal variability.

### FRI-622

#### RECONSTRUCTION OF MASTER IMAGES USING DINEOF AND 3D INPAINT

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One of the fundamental limitations associated with airborne or satellite remote sensing is the presence of unusable data in the form of cloudy pixels. The presence of whitecaps in ocean

color imagery also represents unusable data at high spatial resolution, and error for imagery does not spatially resolve the whitecaps. This study compares the efficiency of 2 data reconstruction methods, the Data Interpolating Empirical Orthogonal Functions (DINEOF) and 3D Inpaint programs, applied to clouds/whitecaps in MASTER images. The DINEOF program was initially developed to use time series images to develop patterns that it uses to fill in the gaps in satellite data under clouds. This project evaluated whether the mathematical techniques of DINEOF could be used to fill in otherwise unusable data using discrete bands from a MASTER image. The 3D Inpaint program, which is MATLAB code that replaces the missing data by interpolating the non-missing elements, was evaluated compared to DINEOF. For the purpose of this study, 3 MASTER images were selected from the DC-8 Airborne Science Laboratory flight during June 18, 2013, over the Santa Barbara Channel in California. With respect to data missing due to the presence of clouds, this study concludes that the mathematical technique employed in DINEOF makes a reasonable reconstruction of MASTER clouded images, reducing the size of the clouds. With respect to data which is unusable due to the presence of whitecaps, 3D Inpaint works better to reconstruct images that have a large number of whitecaps and a small percentage of clouds.

### **SAT-623**

#### **VARYING DIEL TRENDS IN NEARSHORE OCEAN ACIDIFICATION**

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<sup>1</sup>*California State University Monterey Bay, Seaside, CA,* <sup>2</sup>*Monterey Bay Aquarium Research Institute, Moss Landing, CA.*

The purpose of this study was to offer an explanation for varying nearshore, diel-pH trends. The following questions were addressed: what is the description of diel-pH signals along a cross-shore transect in Monterey Bay, CA, and are these signals concomitant with ocean mixing and/or photosynthetic variables? Based on 2 weeks of data from the summer of 2014, nearshore ocean acidification patterns in conjunction with current, tide, wind, upwelling, chlorophyll, nutrient, and solar intensity data are described. Small moorings with surface and bottom pH sensors were deployed from the intertidal to 20 m depth. The intertidal and relatively offshore (~0.5 km) surface pH signals associated more closely with photosynthetic (sunlight availability, nutrient, and chlorophyll) and ocean mixing (current, tide, wind, and upwelling) variables, respectively. We also observed that pH decreased with depth. How pH at depth changes with distance from shore is described. The results prompt further inquiry into nearshore pH variability and lead to a better understanding of nearshore ocean acidification, which endangers organisms' survivorship regionally and globally.

## OTHER GEOLOGICAL SCIENCES

### FRI-624

#### EL NIÑO-SOUTHERN OSCILLATION VARIABILITY IN THE EASTERN EQUATORIAL PACIFIC DURING THE HOLOCENE AND LAST GLACIAL MAXIMUM

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El Niño-Southern Oscillation (ENSO) is a basin-scale, interannual climate variation that originates in the tropical Pacific Ocean. There is disagreement over how ENSO dynamics will change with a changing climate. We seek to better understand the differences in ENSO variability over the last 20,000 years to improve predictions of future ENSO behavior. *Neogloboquadrina dutertrei*, a species of planktic foraminifera that lives within the thermocline, records ENSO-related changes in subsurface temperature via the Mg/Ca of its CaCO<sub>3</sub> shell. This study used individual *N. dutertrei* Mg/Ca to investigate ENSO variability during the LGM (~ 20,000 - 22,000 years before the present (BP)), the mid-Holocene (~4,000 - 6,000 BP), and the late Holocene (< 3,000 BP), 3 periods with different global climate forcings. Samples from core RC13-140, a sediment core from the eastern equatorial Pacific, were analyzed using an ICP-MS for Mg, Ca, and contaminant elements Fe and Al. Samples from the LGM showed the greatest range of temperatures (17.0° C, n = 60), followed by the Late Holocene (12.3° C, n = 60) and the mid-Holocene (10.3° C, n = 62). The standard deviations in temperature followed the same pattern, with the LGM showing a statistically significant difference from the other periods (LGM = 3.7, LH = 2.5, and MH = 2.2). ENSO variability appears to have been higher during the LGM than during the Holocene, suggesting that global climate impacts ENSO dynamics. El Niño variability could change drastically with climate, therefore challenging predictions and requiring more information about ENSO's past response to external forcings.

### SAT-625

#### FEASIBILITY OF USING HYDROGEN AND OXYGEN ISOTOPES IN CLAY MINERALS TO UNDERSTAND MARTIAN WATER INVENTORY

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Clays are hydrous phyllosilicate minerals that form by chemical weathering of silicate rocks in the presence of water. The rovers Opportunity and Curiosity and NASA's Mars Reconnaissance Orbiter have identified clay minerals on the surface of Mars. Accurate analysis of hydrogen and oxygen isotope ratios within clay minerals preserved in ancient rocks on Earth and Mars can provide important information about the aqueous history of the depositional environment, including information that assists in evaluating the existence of past potentially habitable environments. In order to better understand data being acquired on the surface of Mars, we use clay minerals from Earth as analogs for Martian clays to develop new analytical techniques and laboratory instrumentation for precise and accurate determination of hydrogen and oxygen isotopic composition. Clay minerals have a high surface area and readily adsorb water

on external and interlayer surfaces. When measuring hydrogen and oxygen isotopes, specific precautions are necessary in order to exclude contributions from adsorbed water. We employ methods similar to those of Bauer and Vennemann to do this. This involves placing samples under vacuum and then heating them to moderate temperatures to drive off weakly-bound (adsorbed) water before delivering them to a high-temperature conversion element analyzer (TC/EA) coupled to an isotope ratio mass spectrometer (irMS) for measurement of hydrogen and oxygen isotopes. The findings of this study support the applicability of using hydrogen and oxygen isotopic ratios in clay minerals to understand the evolving water inventory in ancient surface environments on Earth and Mars.

#### **SAT-624**

##### **QUANTITATIVE DEMONSTRATION OF CAPILLARY MOVEMENT THROUGH POROUS MEDIA**

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The movement of water within soils greatly impacts the sustainability of life on Earth. For instance, the upward movement of moisture driven by capillary forces provides water to plant and tree roots, a process that is essential to plant life. The fact that soil moisture can migrate upwards against gravity is often illustrated using popular qualitative demonstrations, such as a paper towel capillary siphon. Our goal is to construct a quantitative demonstration of capillary action to serve as an engaging educational tool for courses in hydrology and groundwater. In addition, we plan on utilizing our sensor instrumentation to study the efficiency of water conserving planter boxes from a Boulder-based company and optimize their design. In our study, we investigated the physical phenomena of capillary rise and the capillary siphon in order to illustrate that the behavior is consistent with the expected physics of soil water flow. In order to study capillary rise, we utilized a flow cell embedded with 5 pairs of tensiometer and soil moisture sensors that measure the water suction of the medium and volumetric water content respectively. An industrial silica sand medium is packed into the flow cell and submerged in water and held at a constant head in order to achieve hydrostatic conditions. The sensors will also be used to quantify the enhanced capillary rise provided by wicks embedded in the planter boxes and evaluate alternative wick configurations. Preliminary results coincide with the expected physics of capillary rise.



## PHYSICS (EXCEPT BIOPHYSICS)

### SAT-517

#### LIMITS ON NEUTRINO-OSCILLATION PARAMETERS USING IMPROVED REACTOR ANTINEUTRINO SPECTRA

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Neutrino oscillations are the only experimentally observed phenomenon that does not fit within the standard model of the electro-weak interaction. Due to the characteristics of neutrinos, experiments are sensitive only to the squared mass difference ( $\Delta m^2$ ) of the neutrino states and to the mixing angles ( $\theta$ ). Using improved predictions of reactor antineutrino spectra, the experimental limits on neutrino oscillation parameters are recalculated for an old experiment where the data was taken from 2 nuclear reactors located at Krasnoyarsk. These corrections provide us more information regarding the behavior of neutrinos and the allowed regions where a fourth non-standard neutrino could exist. A computational analysis is made, and the results are represented as exclusion plots for the oscillation parameters.

### FRI-515

#### PLASMA GLOBE FILAMENTARY STRUCTURE AND PROPAGATION TRENDS BY VOLTAGE WAVEFORM CHANGE

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Filamentary structures are seen in many types of plasma discharges. However, principal aspects of their physics are unclear. In order to study plasma filaments, we have used popular commercial plasma globes, which typically have a neon-based mixture near atmospheric pressure. Previous work has provided initial estimates of the speed of plasma globe filaments. Our work analyzes the effects of voltage amplitude and frequency on filament speed and structure using a programmable high voltage supply with phase-triggered high-speed photography. Observed trends are discussed in detail along with their possible relation to discharge structures found in nature (e.g., lightning leaders) and various industrial applications.

**FRI-508****SUPPRESSION OF OPTICAL DAMAGE IN HOLMIUM DOPED LITHIUM NIOBATE AT 532 NM**

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Lithium niobate (LN) is an important optical material used in a multitude of applications including waveguides and acousto-optic and electro-optic devices. It is especially valued for its nonlinear properties, e.g., second harmonic generation. However, when LN is irradiated by light above a certain intensity level, defects inside the crystal act as electron traps creating internal photovoltaic fields. These photovoltaic fields modulate the local refractive index through the linear electro-optic effect and severely distort the transmitted beam. This undesirable effect is known as photorefractive damage and is one of the main contributors of optical damage in LN. We have examined the effect of Ho<sup>3+</sup> doping on the 532 nm optical damage in a series of congruent LN crystals with Ho<sup>3+</sup> concentrations ranging from 0.01 to 2 wt. %. A continuous wave 532 nm Gaussian beam, polarized parallel to the z-axis of the crystals, was focused on the front face of each sample and, after 5 minutes of continuous illumination, an image of the transmitted beam was captured with a CCD camera. Transient optical damage measurements were also recorded using the pseudo Z scan configuration. Notably, the optical damage was almost entirely suppressed in the 2 wt. % doped crystal for the entire range of experimental intensities (up to 15 kW/cm<sup>2</sup>). This suppression is thought to originate from the reduction of the bulk photovoltaic effect caused by the modification of the defect structure of congruent LN by the incorporation of the Ho<sup>3+</sup> cations or from higher order pyroelectric effects.

**SAT-513****SUBSTANTIATING THE FOURTH NEUTRINO HYPOTHESIS USING ELECTRON ANTINEUTRINO ENERGY SPECTRA**

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Recent evidence from nuclear reactor experiments indicate unique, non-zero neutrino masses per flavor state; furthermore, data also suggests the existence of neutrino oscillations as a result of the superposition of their mass and flavor eigenstates. Despite this extension beyond the standard model of particle physics, not all of the world's data may be ultimately corroborated in terms of the three-neutrino model. As a result, a fourth model, light “sterile” neutrino uncoupled from the Z boson, has been posited, limited by a lower mass-squared difference of  $\Delta m^2_{\text{sterile}} > 1 \text{ eV}^2$ , following from experiment. Here, a Fortran 95 program simulation was created in order to obtain the data reported from an electron antineutrino vanishing experiment conducted in Gösigen, Switzerland, using a 2800 MW thermal nuclear reactor at varying distances from a proton-rich liquid scintillator detector, and a two-neutrino mixing model. The output was formatted specifically for easy importing of the data into

Gnuplot. We will analyze the data with a three-neutrino model, and then finally a four-neutrino model, having generated 2 x 2 contour plots with  $\chi^2$  magnitudes for the mixing parameters  $\Delta m^2$  and  $\sin^2 2\theta$ . Based on similar analyses of other experimental data, we expect that the four-neutrino hypothesis will be a more cogent explanation of the reactor data recorded worldwide.

#### **SAT-514**

##### **A REVIEW OF QUANTUM FIELD THEORY (QFT) AND GRAVITY**

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The standard model (SM) and the theory of general relativity (GR) describe the 4 fundamental forces in the universe. However the 2 theories do not work together. SM physics is fundamentally a quantum mechanical theory. GR on the other hand describes the geometry of spacetime. Attempts to quantize gravity yield non renormalizable theories. Part of this problem is that the coupling constant for gravity is dimensionful. In this work we review the lattice formulation of quantum gravity (QG) with non-trivial ultraviolet fixed points with the aim to apply numerical lattice calculations with the Python programming language.

#### **FRI-510**

##### **NIR UPCONVERSION IN KYB<sub>2</sub>F<sub>7</sub>:TM<sub>3</sub>+ NANOPARTICLES IN BIOLOGICAL SYSTEMS**

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Contrast agents used in magnetic resonance imaging have limited value in deep tissue imaging. Due to the high transparency of biological tissue, near infrared (NIR) light has become increasingly useful. This property has been exploited for the application of biomedical imaging by the synthesis of biocompatible, fluorescent nanoparticles (NPs) that emit tunable NIR light. To facilitate this, potassium ytterbium fluoride doped with trivalent thulium ions (KYb<sub>2</sub>F<sub>7</sub>:Tm<sup>3+</sup>) is synthesized using a ligand-mediated hydrothermal synthesis. Tm<sup>3+</sup> was chosen as the dopant for the unique properties at NIR and visible wavelengths. Using an NIR light, we excite the Yb resulting in an upconverted emission from Tm<sup>3+</sup>. These NPs are characterized using scanning electron microscopy, X-ray diffraction, and absorption/transmission spectroscopy. At concentration levels under 100  $\mu$ mol, the particle's low cytotoxicity makes for an ideal candidate for magnetic resonance imaging. Normally the NPs are hydrophobic, discouraging any transfer across the lipid bilayer membrane of a cell. To facilitate the cellular uptake, the NPs are coated with a variety of hydrophilic polymers including PEG, PVP, and PMAO. Analysis of concentration levels will be studied for hydrophilic properties of each polymer. In the case of high cellular uptake, these particles present a useful means of drug delivery and provide new applications for deep tissue imaging.

**SAT-507****SINGLE CHARGED PARTICLE TRAJECTORY SIMULATION IN VARIOUS MAGNETIC FIELD CONFIGURATIONS AND MICROWAVES THROUGH THE LEAP-FROG ALGORITHM**

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Electron cyclotron resonance (ECR) plasma is created by electron-impact ionization in a vacuum chamber containing a low pressure gas. Electrons orbiting the magnetic field are accelerated by resonant interaction with a microwave field with a frequency matching the cyclotron frequency. This project's objective is the theoretical calculation of the electron orbits in the combined magnetic and microwave field. The simulation is based on a leap frog algorithm based in the Lorentz force law and Newton's law. The magnetic field in the ECR chamber is calculated numerically using Maxwell's equations. Fields are located in a 3D grid representing the physical space in the plasma device. As a result of this research, knowledge will be gained in plasma orbit theory related to the trajectories of charged particles in resonant fields. The possibility of particle trapping by the ECR fields will also be studied.

**FRI-509****TEMPORAL CHANGES IN THE FREQUENCIES AND WIDTHS OF THE SOLAR P-MODE OSCILLATIONS DURING THE RISING PHASE OF SOLAR CYCLE 24**

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We investigated the temporal changes in the frequencies and widths of the solar p-mode oscillations during the rising phase of solar cycle 24 by analyzing a time series of full-disk dopplergrams obtained by the Michelson Doppler imager (MDI) and helioseismic and magnetic imager (HMI) between late-2007 and mid-2012. The MDI dynamics runs obtained between 2007 and 2012 were divided into 83, 3-day time series. The first 792 days of HMI observations were divided into an additional 264, 3-day time intervals. We computed a set of un-averaged power spectra from all 347 time series. We collapsed the 347 sets of un-averaged power spectra into sets of m-averaged power spectra and subsequently fit more than 12,000 peaks in each of these 347 sets of m-averaged power spectra using a power spectral fitting code. We then performed linear regression analyses of the differences in the fitted p-mode frequencies and widths as functions of the differences in as many as 10 different solar activity indices. From these linear regression analyses we extended our previous discovery of unique signatures of the frequency and width shifts of the p-modes into the rising phase of the current solar cycle. One key aspect of these signatures is that the frequencies and the widths are both positively correlated with the changes in solar activity at low frequencies before switching to being anti-correlated with those activity differences at higher frequencies. We found that these fiducial frequencies were substantially higher than they were during the period from 2008 to 2009 extended minimum of solar activity.

**SAT-509****GROWTH OF ORIENTED  $\text{Li}_{0.9}\text{Mo}_6\text{O}_{17}$  THIN FILMS BY PULSED LASER DEPOSITION**

Alexandra Cote, Joshua Cohn.

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Transverse thermoelectric devices facilitate the transformation of waste heat into electricity by producing a voltage where there is a temperature difference across a material. Transverse thermoelectric devices currently available commonly make use of multilayer structures that remain both difficult and expensive to manufacture. Preference for these structures has developed out of the scarcity of single compound materials with large thermoelectric power at room temperature. Materials used in transverse thermoelectric devices are generally exploited for the high off-diagonal Seebeck effect exhibited, which occurs in anisotropic materials with an oriented, layered structure. Here, voltage generated is proportional to the material's thermopower anisotropy ( $S_{ab} - S_c$ ), the ratio of length to thickness of the sample ( $l/t$ ), the tilt angle of the c-axis, and the temperature gradient present. Recently, a transport anisotropy roughly an order of magnitude higher than materials currently widely used in transverse thermoelectric devices was observed in  $\text{Li}_{0.9}\text{Mo}_6\text{O}_{17}$  or lithium purple bronze (LiPB). Previous work on bulk LiPB has demonstrated a large transverse Peltier effect; however, thin films of this material have not yet been created. Voltage dependence on  $l/t$  suggests that a thin film could generate a much greater voltage signal for a given temperature gradient. This study will report the attempt to grow thin films of LiPB using pulsed laser deposition on  $\text{SrTiO}_3$ ,  $\text{SrLaAlO}_4$ , and  $\text{MgO}$  substrates. Films grown will be characterized using X-ray diffraction. Success in developing thin films of LiPB would serve as an improved foundation for engineering single compound materials for ultimate use in transverse thermoelectric devices.

**FRI-507****A COMPARISON OF OPTICAL SCATTER FROM COATED AND UNCOATED OPTICS FOR QUANTUM NOISE FILTER CAVITIES**

Daniel Vander-Hyde, Joshua Smith.

*California State University Fullerton, Fullerton, CA.*

We report on scattered light measurements from super-polished fused silica surfaces before and after applying ion-beam sputtered highly-reflective coatings. Using a calibrated imaging scatterometer that illuminates the sample with a linearly polarized 1,064 nm wavelength laser beam at a fixed 4 degree angle of incidence, we use a charge coupled device camera to image back scatter from 12 degrees to 76 degrees from normal in the plane of the laser beam (azimuthal angles). Angle-resolved bidirectional distance distribution function (BRDF) values were extracted from the images and total integrated scatter for large angle scattering is estimated. We find that the highly reflective coating roughly doubles the BRDF and total integrated scatter when compared to the uncoated fused silica. In addition to this increased scatter, the BRDF function of the coated optics takes on a periodic structure versus scattering angle, with a period of between 8 and 10 degrees. These results contribute to studies of optical loss in quantum noise filter cavities for interferometric gravitational-wave detectors.

**FRI-513****DYNAMICS OF HYDRAULIC FRACTURE IN TOUGH HYDROGELS**

Aria Hamann<sup>1</sup>, Will Steinhardt<sup>2</sup>, Shmuel Rubinstein<sup>2</sup>.

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Hydraulic fracturing is an extremely important technique for the extraction of oil and natural gas previously considered inaccessible. A greater understanding of what happens during an underground fracking operation is of extreme environmental, economic, and political importance and is the aim of rigorous scientific investigation. Since these fractures cannot be directly observed, our lab has developed a novel approach for studying their dynamics and morphology. We use heavily cross-linked hydrogels as a model brittle material in which we induce and investigate hydraulic fractures. The advantages of this method are the gels' transparency and slower fracture speed, which enable us to directly visualize the dynamics of hydraulic fractures at unprecedented temporal resolution. Our work focuses on how fractures interact with boundaries. We have developed a system of polymerizing multiple gels of differing strengths within the same mold. These gels have well defined, discernable interfaces that allow us to study how inhomogeneities in the material affect the fractures' path and morphology. This may help address containment issues in fracking operations, where the target shale formations are often capped by, or intertwined with, rocks of differing strengths. This remains an active area of research.

**FRI-512****MULTIFIELD DYNAMICS AND NON-MINIMAL COUPLINGS OF INFLATION**

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Inflation represents the idea that the universe underwent a period of exponential expansion immediately after the big bang. This period of rapid expansion could have been driven by one or several scalar fields. Realistic models of high-energy physics typically involve more than one scalar field, and each field may be expected to include a non-minimal coupling to the spacetime Ricci curvature scalar, since such couplings are required for renormalization. Hence, multifield models with non-minimal couplings offer one promising way to characterize the period of early-universe inflation. Moreover, predictions from such models for observable features of the cosmic microwave background radiation are in excellent agreement with recent observations from the Planck satellite. Unlike single-field models, multifield models produce different types of quantum fluctuations, which can interact with each other and yield interesting effects, both during inflation and during the post-inflationary reheating period. Analyzing such phenomena requires understanding conformal transformations, which can be used to relate different representations of such models, as well as understanding parametric resonance, which dominates the early stages of reheating where the energy that had driven inflation dissipates into other forms of matter.

**FRI-511****DESICCATION CRACK FORMATION IN SEDIMENTS**

Mauricio Gomez, Eric Hetherington.

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Crack formations appear on soil surfaces during desiccation, weakening the structure of the soil. There are many variables which control the geometry and rates of mud crack formation. Our purpose is to identify variables that affect crack characteristics. We will examine and document the mud crack characteristics of various soil sediments. We will use 1 cubic meter boxes to test soil sediments from the eastern foot-hill side of the San Joaquin Valley in California. Using time-lapse photographic footage, we will examine the rate of crack formations and the geometry of the cracks. From prior research, we expect crack formation to rapidly increase then abruptly slow down once much of the crack tension is released. Identifying how these variables affect crack formation will give us a better insight into geological features and topographic surface soil formations.

**SAT-508****CALCULATE THE MAGNETIC FIELD PRODUCED BY HELMHOLTZ COILS USING THE BIOT-SAVART LAW**

Felix Diaz Medero, Ernesto Ulloa.

*Polytechnic University of Puerto Rico, San Juan, PR.*

The electron cyclotron resonance (ECR) plasma device at the Polytechnic University of Puerto Rico consists of an aluminum chamber at high vacuum pressure, the Helmholtz coils used to create a mirror or cusp magnetic field, and a high power microwave source. The electrons are accelerated by the resonant wave-particle interaction. This project consists of the creation of a MatLab code for modeling of the magnetic field created by the Helmholtz coils in the ECR device. This program can be modified to add different Helmholtz coils at any point or angle of the ECR device. The program generates a grid in space and calculates the magnetic field vectors at each point in the grid. The program creates a 3D quiver plot to map the magnetic field vector in the chamber, allowing it to calculate the surface of resonance where the electron cyclotron frequency matches the microwave frequency. The data generated in the program will be used in the leap frog algorithm to calculate the electron cyclotron resonance-particle trajectories. The program will also be used to analyze experimental data for the magnetic field measurements in the presence of the electron cyclotron resonance plasma.

**SAT-516****DRAG-ASSISTED SIMULATED ANNEALING METHOD FOR GEOMETRY OPTIMIZATION OF MOLECULAR SYSTEMS**

Bilguun Woods<sup>1</sup>, Paulo Acioli<sup>2</sup>, David Capota<sup>2</sup>.

*Northeastern Illinois University, Chicago, IL.*

One of the methods to find the global minimum of a potential energy surface of a molecular system is simulated annealing. In molecular dynamics the system is initially at a high

temperature and then slowly cooled off so there is a chance to explore the different degrees of freedom and ultimately find the global minimum. One of the most traditional methods was first implemented by Woodcock in 1971. In this method, the velocities are scaled down after a given number of molecular dynamics steps. In this work we propose to use a viscous friction term, similar to the one use in Langevin dynamics, to slowly bring down the temperature of the system in a natural way. The linear drag term, which is proportional to the velocity, will become 0 when the system reaches a minimum. We tested the method in Lennard-Jones clusters of up to 21 atoms. We started the system in different initial conditions and used different values for the temperature and the drag coefficient and found the global minima of each cluster. This method is conceptually very simple, but very robust in finding the global minima.

#### **SAT-506**

##### **DETERMINATION OF THE MAGNETIC FIELD IN MIRROR AND CUSP CONFIGURATIONS FOR ELECTRON CYCLOTRON RESONANCE PLASMA**

Naomi Delgado Cruz, Ernesto Ulloa.

*Polytechnic University of Puerto Rico, San Juan, PR.*

In the search for tomorrow's energy supply, plasma technology has emerged as a possible candidate to provide clean and safe energy resources. The Polytechnic University of Puerto Rico's mirror/cusp electron cyclotron resonance (ECR) plasma reactor creates plasma by the process of electron impact ionization. A static magnetic field is created by Helmholtz coils in a spherical aluminum chamber at  $1 \times 10^{-3}$  Torrs, where the high energy microwave signal is launched into the chamber through a rectangular wave guide in TE<sub>10</sub> mode. The confinement of particles created by the magnetic field allows the acceleration of orbiting electrons by resonant particle-wave interactions, ionizing the noble gases present. In this experiment a shielded Hall effect probe was used to measure the axial magnetic field inside the ECR plasma as a function of microwave power, coil current, and magnetic field configurations (mirror or cusp). The axial magnetic field measured in the presence of plasma was subtracted from the axial magnetic field measured in the absence of plasma. The effect of the shielding in the hall probes was taken into consideration for the analysis of the magnetic field in an interval of time. The outcome of this research will serve to study populations of hot electrons using the magnetic field structure of the plasma.

#### **SAT-515**

##### **MECHANICAL EXFOLIATION OF GRAPHITE**

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Single layer graphene has attracted attention because of its excellent thermal and electrical properties. Graphene is readily produced using 2 methods, a chemical synthesis and a mechanical exfoliation of graphite. The aim of this research is to use mechanical exfoliation of highly oriented pyrolytic graphite to produce a single layer of graphene on a silicon substrate so it may be studied using an atomic force microscope (AFM). A small piece of graphite is removed with tweezers and placed on a piece of scotch tape on the adhesive side. The scotch tape is



folded on itself so the adhesive sides touch. The separation of the sides pulls the graphite apart. This step is repeated until an increasingly faint layer is produced. The tape is then pressed on a clean silicon substrate. The silicon with the graphene layer can now be imaged with the AFM. The images are on the order of microns in the lateral dimensions and nanometers in the z dimension. Many images must be taken at various spots to identify single layers of graphene. A single layer of graphene is expected to be about 0.80 nm to 1.3 nm in thickness. Several structures on that scale were observed. Using mechanical exfoliation of graphite does produce a single layer, but it is difficult to locate due to size and irregular deposition of graphene.

#### **SAT-510**

##### **OPTIMIZATION OF THE WIND FARM LAYOUT PROBLEM THROUGH A MODIFIED GENETIC ALGORITHM**

Grant Williams<sup>1</sup>, April Taylor<sup>2</sup>.

<sup>1</sup>*University of Oklahoma, Norman, OK,* <sup>2</sup>*South Central Climate Science Center, Norman, OK.*

Wind energy is a rapidly growing source of energy for the United States, but there are still technical problems to resolve before it can become the major source of energy production. One of the biggest problems with land-based wind farms is minimizing wake-turbine interactions within a constrained space and thus maximizing power. When wind blows through a turbine's blades, a choppy, turbulent wake is created that interferes with the ability of nearby turbines to produce power. Research has already been done on finding ways to model wind farms and place the turbines in a way that minimizes wake-turbine interactions, but current methods are either computationally intensive or require proprietary software. We present a modified genetic algorithm that is able to produce reasonably optimized results in a relatively short amount of computation time. The algorithm presented is able to make use of the computation power of graphical processing units and multiple processors and, by doing so, produces results more quickly than an algorithm run sequentially on a single processor.

#### **SAT-512**

##### **THE REACTION OF SMALL SILVER CLUSTERS WITH CARBON MONOXIDE USING MOLECULAR DYNAMICS SIMULATION**

Cesar Bustos, David Capota, Bilguun Serod, John Gonzales, Paulo Acioli.

*Northeastern Illinois University, Chicago, IL.*

Burning of fossil fuels contributes to carbon monoxide levels in our atmosphere. The catalysis of carbon monoxide into the less toxic carbon dioxide is an important chemical reaction. In this work, we study the catalytic properties of small silver clusters and their reaction with carbon monoxide using molecular dynamics simulations. We use the velocity Verlet algorithm together with a realistic potential that includes 2- and 3-body terms for the study. For the Ag-Ag interaction, we tested the Sutton-Chen potential and Tersoff potentials. The interaction between the carbon, oxygen, and silver atoms is described by a Lennard-Jones potential that is parameterized to describe the ground-state configuration of the AgCO molecule as obtained from density functional theory calculations. We present the cross section of the reaction  $\text{Ag} +$

CO  $\rightarrow$  AgCO. Future work includes extension of the work to determine the cross section of the reactions  $\text{Ag}_N + \text{CO} \rightarrow \text{Ag}_N\text{CO}$ .

#### **FRI-506**

#### **DESIGN OF AN OPTICAL CAVITY AS AN ALTERNATIVE METHOD FOR MEASURING THE SPEED OF LIGHT**

Daniel Inafuku, Eric Szarmes.

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The speed of light ( $c$ ) is one of the most recognizable physical quantities in science, and its measurement often occupies an important place in advanced, undergraduate laboratory classes in the modern physics curriculum. Common experiments for measuring  $c$  in such classroom settings often replicate the original procedures used by early scientists by measuring the time it takes for light to travel a certain distance. Other experiments employ more sophisticated techniques such as interferometry. The equipment used in these classroom experiments, however, is often limited by its spatial or temporal resolution, yielding significantly large fractional errors compared to the precision of  $c$ . In this study, we demonstrate a novel method for the measurement of the speed of light, based on resonator optics and modulation techniques, that yields errors significantly smaller in magnitude than those found in contemporary undergraduate experiments. We describe this new technique and present preliminary measurements of the speed of light.

#### **FRI-514**

#### **A NOVEL, COMPACT CRYOCOOLER-BASED MEASUREMENT SYSTEM FOR SUPERCONDUCTING ELECTRONICS**

Vito Iaia<sup>1</sup>, Travis Wong<sup>2</sup>, Ethan Cho<sup>2</sup>, Shane Cybart<sup>2</sup>, Robert Dynes<sup>2</sup>.

<sup>1</sup>*University of California, Los Angeles, Los Angeles, CA*, <sup>2</sup>*University of California, San Diego, La Jolla, CA.*

In this work, a novel, compact portable superconducting electronics system is presented for low-noise, magneto-transport measurements of Josephson devices. Portable superconducting Josephson devices using materials such as  $\text{YBa}_2\text{Cu}_3\text{O}_{7-\delta}$  would advance medical, defense, and space systems requiring sensitive magnetometers. The current state-of-the-art, superconducting electronics, constructed from niobium- $\text{Al}_2\text{O}_x$  materials, require large, heavy cryocoolers operating near 4 K, which use many kilowatts of power. In contrast, the 100 W cryocooler used in this work is compact, rack-mountable, and battery powered. The primary components of the electronics include filtered preamplifiers, EMI filters, integrated sinusoidal oscillators, and closed loop magnetic feedback circuitry. RF shielding of the electronics was incorporated to reduce the environmental noise coupling between components to allow for very low noise measurements. Types of supplementary circuits that could benefit from these low noise measurements include RF amplifiers, bolometers, and broadband RF sensors. Thus, the compact measurement system engineered here is an ideal tool for a wide range of advanced industrial applications.

## PROFESSIONAL CAREERS

## COMMUNICATIONS

### SAT-106

#### **DIFFUSION-TENSOR, BRAIN-CONNECTIVITY IMAGING, AND GENDER DIFFERENCES IN PERCEPTUAL-MOTOR COORDINATION**

Makenzi Wagner, Blas Espinoza-Varas.

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Diffusion tensor imaging (DTI) reveals structural and functional differences across genders. In males, DTI brain networks show increased front-to-back intra-hemisphere connectivity and greater cross-hemisphere cerebellar connectivity. Females show increased left-to-right connectivity across hemispheres. Predominant intra-hemisphere connectivity facilitates the coordination between perception and action, but predominant inter-hemisphere connectivity facilitates information integration across the right and left hemisphere (e.g., analytical reasoning, spatial processing). We hypothesized that for tasks requiring skilled perceptuo-motor coordination of auditory inputs to hand responses, males would outperform females in accuracy and speed. Seventeen males and 18 females, 16 - 22 years old, in good health, underwent testing on each of 3 executive-function tasks that required skilled coordination of hand responses to auditory inputs. On the left or right ear, participants listened to spoken commands and identified their voice tone (lenient or stern) with a left- or right-hand response. In a no-conflict task, the match between the ear side and the correct-response side was always congruent, but it could be incongruent or incompatible in conflicting information tasks, requiring skilled perceptual-motor coordination. Compared to males, females exhibited larger mean percent errors and longer mean response times in most conditions. Gender differences in accuracy or speed reached significance in 2 conditions ( $p \leq 0.05$ ), and marginal significance in another 2 ( $0.05 \leq p \leq 0.11$ ). In the remaining conditions, the differences did not reach significance, but pointed in the same direction. The agreement between the DTI and the behavioral evidence lends support to the hypothesis as males outperformed females in accuracy and speed.

## PSYCHOLOGY & SOCIAL SCIENCES

## ANTHROPOLOGY/ARCHEOLOGY

### FRI-107

#### **SUBSISTENCE PIER FISHING AND FOOD INSECURITY IN LOS ANGELES COUNTY**

Rita Kirkpatrick, Ana Pitchon.

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Subsistence living is a term associated with indigenous Tribes as an integral part of both cultural and physical survival. In urban Los Angeles County, there are examples of subsistence living through practices like the consumption of pier-caught fish, guerilla gardening, and community

gardens despite possible knowledge of and exposure to toxins found in the water and soil. There is extensive literature regarding the types of toxins, like dichlorodiphenyltrichloroethane (DDT) and polychlorinated biphenyl (PCB), that are found in Los Angeles County's water and soil, associated health risks from exposure to these toxins, and community efforts on a city and statewide level to educate the public regarding the risks of consumption. This research investigates the issue of continual consumption of toxic food despite knowledge of the possible health risks associated from toxin exposure and its link to food security. The study will focus specifically on pier fishers and data will be collected from Belmont Shore Pier in Long Beach, California, and Redondo Pier in Redondo Beach, California. Using extensive literature review and specific information from California's and Los Angeles County's policies and demographics on food assistance and the questionnaire from the EPA's Survey on Recreational and Subsistence Fishing in Southern California Coastal Waters, a questionnaire and interview will be developed to create an assessment of food security among the pier fishers at the 2 specified piers. The results will add to the limited research regarding food security and pier fishing in Los Angeles County and provide a base for future research with a wider sample area.

## **CLINICAL PSYCHOLOGY**

### **FRI-109**

#### **RISK TAKING AND ITS INFLUENCE ON ATTRACTIVENESS**

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<sup>3</sup>*University of California, San Diego, La Jolla, CA*.

Previous research has established that risk taking can influence how attractive individuals are perceived to be. Because the types of risks that have been examined are varied, it is hard to understand the precise nature of these effects. In the present study, we address this issue by focusing on the effect of physical risk taking such as willingness to run on a frozen pond. Participants were provided with a survey and asked to read a series of scenarios. We examined the effect of physical risk taking on perceived attractiveness for both men and women at high, moderate, and low levels of risk. We also examined how risk taking influences desirability of short-term and long-term romantic partners. We hypothesize that individuals taking higher risks will be perceived as more attractive and be more suitable for short-term relationships. In addition, we also hypothesize that participants will be more willing to engage in a long-term relationship with a moderate physical risk taker.

### **SAT-107**

#### **A QUALITATIVE ANALYSIS OF SELF-CONCEPT CLARITY IN 3 THERAPEUTIC MODALITIES**

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Self-concept clarity (SCC) is the extent to which self-beliefs are clearly and confidently defined, internally consistent, and stable. Low SCC is associated with low self-esteem, suicidal ideation, self-injurious behaviors, and symptoms of depression and anxiety. Consequently, psychological

interventions often seek to increase SCC. While most therapeutic modalities address SCC in their theoretical models, little empirical evidence is available regarding the impact of these treatments on SCC. In the current pilot study, we use consensual qualitative research methodology to evaluate SCC within a popular series of training tapes with three leading psychotherapy theorists: Carl Rogers (Person Centered Therapy), Fritz Perls (Gestalt Therapy), and Albert Ellis (Rational Emotive Behavior Therapy), each working with a real patient named Gloria. Therapy sessions were transcribed and a team of 4 different raters met to develop domains, construct core ideas, and complete cross analyses. Identified domains included explicitly high and low SCC statements as well as general self-concept statements regarding self-perceptions and desires of self and others. Results compared SCC across each therapeutic modality. Rogers allowed Gloria to explore areas of low SCC in depth, focusing on her desires for acceptance for herself and her children. Ellis provided moderate opportunities to explore low SCC and focused on her difficulties acting like herself with men. Perls provided few opportunities to explore SCC and what did occur was focused on present moment interactions. Results may provide therapy researchers with tools for understanding the processes of therapy and maximizing effectiveness.

#### **SAT-108**

#### **THE EFFECT OF A PEER EDUCATOR INTERVENTION ON THE REDUCTION OF PERCEIVED PUBLIC AND INTERNALIZED STIGMA IN DEPRESSED OLDER ADULTS**

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The prevalence of late-life depression has become a rising concern. The stigma associated with having late-life depression can be a significant barrier to seeking mental health treatment. Peer educators (PEs) are individuals who have previously recovered from depression and are trained to provide support and education to acutely depressed individuals with whom they are similar to socioeconomically and demographically within their community. These PEs may help to reduce the stigma associated with depression and of seeking treatment in this population. The purpose of the present study is to examine the effect of a PE intervention on stigma in a sample of depressed older adults ( $n = 21$ ), aged 60 years or older. Participants completed a demographic questionnaire and public stigma (PDD) and internalized stigma (ISMI) measures pre- and post- PE intervention. Paired-sample T tests will be used to evaluate changes in participants' perceived level of public stigma and internalized stigma before and after the PE intervention. We hypothesize results will indicate the use of PEs will significantly reduce both public and internalized stigma among depressed older adults. We also hypothesize that African Americans and women will report experiencing more stigma than Caucasian and men participants in this sample. Lastly, it is anticipated that the younger older adults will experience more of a significant reduction in stigma than the oldest older adults. Identifying strategies like peer education that can reduce stigma may help to alleviate stigma as a barrier to treatment and enhance treatment acceptability and use among older adults with depression.

**FRI-108****THE IMPACT OF SUBTLE AND BLATANT STEREOTYPE THREAT ON HEART RATE VARIABILITY**

Nicholas Joseph<sup>1</sup>, Julian Thayer<sup>2</sup>.

<sup>1</sup>*University of Central Florida, Orlando, FL,* <sup>2</sup>*The Ohio State University, Columbus, OH.*

Stereotype threat (ST) is defined as the threat of confirming a negative stereotype about one's group, and occurs when negative stereotypes associated with a particular group are made salient by environmental cues. Previous research suggests that ST has a detrimental impact on health in ethnic minorities. Nevertheless, few studies have directly investigated this claim. The present study attempts to rectify this by exploring the effects of ST on heart rate variability (HRV), a marker of overall health. Low HRV has been associated with decreased endocrine, immune, cardiovascular, and inflammatory function. Continuous HRV was recorded on 93 participants during a 5-minute baseline-resting period. The participants were randomly assigned to one of 3 experimental priming conditions in which they received implied but not directly mentioned stereotype (implicit), bluntly mentioned stereotype (explicit), or no manipulation (control condition). Afterwards, the participants completed the Simon effect task. Research shows that attentional resources are needed to inhibit the distractor item and correctly respond to the target. Following the Simon effect task, participants underwent a 5-minute recovery (resting) period. Based on prior research, we hypothesize that those in the implicit ST, but not the explicit ST or control conditions, will exhibit lower HRV. Additionally, minorities should exhibit lower HRV than non-minorities in the implicit ST condition only. Also task performance, particularly in the incongruent trials, should be worst among those minority individuals who received the implicit ST manipulation. Overall, the current study will explore HRV as a possible psychophysiological mechanism linking ST and health within ethnic minorities.

**COUNSELING PSYCHOLOGY****SAT-109****THE RELATIONSHIP BETWEEN CULTURAL DIFFERENCES AND WILLINGNESS TO SEEK MENTAL HEALTH SERVICES**

Robert Altamirano, Kimberly D'Anna-Hernandez.

*California State University San Marcos, San Marcos, CA.*

Stigma, cultural issues, and lack of communication may block individuals in some ethnic groups from seeking mental health services. It was hypothesized that Latinos would be less likely than 2 other ethnicities, Caucasians and Asian/Pacific Islanders, to seek mental health services. Undergraduate students from California State University San Marcos (90 females and 79 males) were surveyed using haphazard sampling for willingness to seek mental health services. Latinos were the most likely to self-report desire to seek mental health services [ $F(2,166) = 4.12, p = 0.02$ ]. Additional analysis was done on willingness to seek mental health services for suicide ideation and we found that Latinos were the most inclined to seek mental health services for suicide ideation [ $F(2,166) = 3.79, p = 0.03$ ]. The results of the study suggest that further

research is needed to understand Latinos high willingness to seek but low usage of mental health services,. Finding the link could foster more culturally competent care.

#### **FRI-110**

##### **EFFECTS OF BOARDING SCHOOLS ON AMERICAN INDIAN/ALASKA NATIVE POPULATIONS**

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Intergenerational trauma can be viewed as transmission of historical oppression and related negative behavior consequences across generations. Emerging research suggests trauma of this type experienced by victims can be passed through multiple generations. Additional research studies indicate the impact of intergenerational trauma may impact one's health and the social disparities facing Aboriginal peoples in Canada and other countries. American Indians and Alaska Natives (AI/AN) attending Indian boarding schools as children experienced historical trauma due to the separation of children from their families. This forced AI/AN individuals into an unfamiliar environment lacking a nurturing, loving caregiver to care for them properly. Research suggests Indian boarding schools created a cycle of intergenerational trauma, where pseudo parenting skills taught in the schools were passed down from generation to generation in families. This loss of family attachment along with the absence of positive parenting in Indian boarding schools resulted in adults lacking positive parenting skills. Specifically, this study looks at AI/AN families with a history of attending boarding school, and AI/AN families without a history of attending boarding school. Neglectful parenting styles and parental bonding will be assessed to determine differences. The study will use the Parental Bonding Instrument survey (PBI) and the Multidimensional Neglect Scale-Parent Reports survey to assess parenting skills. We hypothesize that families with a history of attending boarding schools will report more neglectful parenting and less parental bonding than families with no history of boarding schools.

#### **ECONOMICS**

#### **SAT-110**

##### **VOLATILITY IN CALIFORNIA SCHOOL DISTRICT REVENUE 1995-2011**

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The revenue provided to California school districts varies significantly from year to year. School districts may wish to smooth out this variation in revenue in order to smooth expenditures and therefore maintain constant student resources over time. Since education is a long-term and steady process, maintaining constant resources for students over years is vital for the quality of education. As a result of this need to maintain consistency, this paper assesses the ability of K-12 school districts to smooth out variations in their revenue by saving and borrowing. We first analyze how changes in revenues affect school district expenditures. If districts are saving and borrowing, then the variation in revenue from year to year should not affect expenditures.

Rather, the expectation of future revenues should play a role in how much districts spend. Therefore, we also examine the role of expectations of future revenue. Do districts spend more when their expectation of future revenue is high? How does a change in those expectations affect current expenditures? To measure expectations, we use revenue projections produced each year by California's Legislative Analyst's Office. We use real per-pupil growth rates to measure the change in each variable. Methods consist of linear regression and trend analysis. Our results imply that districts' behavior lies in a midrange between perfectly maintaining expenditures constant overtime and completely failing to save and borrow.

## **EDUCATIONAL PSYCHOLOGY**

### **FRI-111**

#### **TEST-ENHANCED LEARNING FROM ONLINE QUIZZES: RELATIONSHIPS AMONG TEST-TAKING BEHAVIORS AND EXAM SCORES**

Victoria Vento, Ivan Avila, Matthew Johnson.

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Studies show repeated testing as a means of learning increases long-term retention compared to repeated studying. This is demonstrated using a variety of stimuli to imply repeated student testing can be used to increase long-term course concept retention. Currently, numerous course management systems are available for delivery of online quizzes, making it easy for instructors to set up online quizzes for the purpose of assessing and increasing learning. Few studies have examined the correlations between quiz-taking behavior and course grades. The current study gave students an unlimited amount of time to take quizzes and an unlimited number of quiz attempts. Unit exams included short-answer (recall) items and computational problems. The average quiz score, the average number of quiz attempts, the average length of time taking quizzes, the median number of days prior to the quiz deadline when a quiz was taken, and unit exam scores were used as dependent measures. Pearson correlations among the dependent measures revealed quiz scores were positively correlated with exam scores ( $r = .73$ ,  $p < .001$ ), which replicates the findings of Anthis and Adams. Unlike, Anthis and Adams, both exam and quiz scores were negatively correlated with the number of quiz attempts students made ( $r = -.43$ ,  $p < .001$ ;  $r = -.38$ ,  $p = .002$ , respectively), suggesting that repeated testing per se does not increase retention, but performance on them does.

### **SAT-111**

#### **EVALUATING THE TELEVISION SHOW DANIEL TIGER'S NEIGHBORHOOD AS A VIDEO-BASED MODEL TO TEACH SOCIAL SKILLS TO CHILDREN WITH AUTISM**

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Deficits in social communication result in abnormal social exchanges and social relationships in children with autism spectrum disorder (ASD). Children with ASD do not follow typical patterns when developing social skills and are unable to predict or understand other people's actions, which results in failure to develop positive relationships. The purpose of this study is to



evaluate whether watching episodes of Daniel Tiger's Neighborhood can help children with ASD learn social skills taught in the show. Targeted social skills include sharing, waiting patiently, calming down, time to stop playing, and trying new foods. Skills are taught through direct instruction provided by the preferred cartoon characters, along with a facilitator such as a teacher or parent. The percent of each skill performed correctly will be measured using a multiple baseline across skills design replicated across participants. The study includes 3 phases: baseline, intervention, and maintenance. We have already begun baseline data collection to evaluate deficits in the targeted skills for 2 participants.

## **EXPERIMENTAL PSYCHOLOGY**

### **FRI-113**

#### **EFFECTS OF CHRONIC ALCOHOL CONSUMPTION ON COLON CANCER RISK**

Patricia Cintora, Jerrold Penprase, Octavio Medrano, Danielle Erwin, Emily Driver, Jessica Godfrey, Susan Brasser, Mee Young Hong.  
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Previous studies have associated chronic alcohol consumption with colorectal cancer (CRC) development, yet the mechanism(s) mediating the relationship between alcohol consumption and CRC remain largely unclear. Experimental studies in humans and using animal models have demonstrated that alcohol and its metabolites interfere with control mechanisms that prevent (i.e., tumor suppressor genes, DNA repair enzymes) or induce (proto-oncogenes) cancer development. Predominantly, acetaldehyde, a toxic metabolite of alcohol (ethanol), has been identified as a principal factor mediating carcinogenic effects. The present study sought to identify potential causal mechanisms by which ethanol consumption may contribute to the development of CRC using a rodent model. Outbred Wistar rats ( $n = 24$ ) were individually housed in home cages and exposed to a 2-bottle-choice voluntary drinking paradigm. The ethanol group ( $n = 12$ ) was exposed for 13 weeks to a 20% ethanol intermittent-access drinking paradigm and the non-ethanol-exposed control group ( $n = 12$ ) was given access only to water. Ethanol intake (g/kg) and preference data will be analyzed to determine levels and patterns of alcohol consumption across time. In addition, expression of genes related to colon cancer risk will be analyzed using quantitative real time PCR. In sum, alcohol consumption has been associated with increased risk for CRC. Identifying the specific mechanism(s) that contribute to CRC is important to develop effective treatments and care for patients affected by this disease or for those at risk for developing it.

### **SAT-114**

#### **EFFECTS OF ACCULTURATIVE-STRESS AND EARLY SEX BEHAVIOR ON MATERNAL ANXIETY, DEPRESSION, AND CORTISOL**

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During pregnancy, women are vulnerable to the onset of mental health symptoms, particularly anxiety and depression. Early exposure to risky behaviors, such as sex behavior, as well as

biological changes caused by the stress-related hormone cortisol can contribute to anxiety and depression. Mexican American women may be more at risk for these adverse outcomes as they often engage in sex behavior earlier in adolescence than the general population and experience unique cultural stressors. One stressor is acculturative-stress, a stressor associated with acculturation, the process of adapting from one culture to another. While research has begun to link acculturation with early sex behavior, few studies have looked at the effects of acculturative stress and early sex behavior together on subjective (anxiety and depression report) and objective (cortisol) mental health symptoms during pregnancy. This study examines whether increased acculturative stress and early sex behavior are associated with increased anxiety, depression, and cortisol levels during pregnancy in Mexican-American women. In an ongoing study, pregnant women of Mexican descent were recruited during their first trimester. Participants self reported on acculturative stress, anxiety, depression, and their age at first sexual intercourse. Three centimeters of hair were also collected to assess first-trimester cortisol levels. Preliminary results suggest pregnant women with increased acculturative stress and early sex behavior had elevated depressive symptoms during the last trimester and more overall anxiety symptoms throughout the pregnancy. Cortisol analysis is ongoing. This work suggests the importance of evaluating early sex behavior and acculturative stress in identifying Mexican-American women at risk for mental health symptoms during pregnancy.

#### **FRI-112**

##### **THE EFFECTS OF COMPETITIVENESS ON VISUAL SEARCH**

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While many studies have examined the factors that influence visual search performance, the way competitiveness may affect a visual search task has not been investigated. The goal of this study was to seek the potential relationship between interpersonal competitiveness (IC) and improvement in reaction time in a visual search task. Competitiveness of the participants was measured using the IC subscale of the competitiveness questionnaire. IC is a desire to win or do better than others. The stimulus consisted of multiple red or green circles or squares that were presented on a computer screen. Each shape contained a white line segment in its center. The spatial configuration of the shapes was either circular (aligned on an imaginary circle) or random. The participant's task was to judge the orientation of the line segment (vertical or horizontal) as soon as possible in a target shape that was unique. Reaction time and response accuracy were recorded. Participants ran a first session of both spatial configurations followed by the completion of the CQ. They were informed that their reaction time and response accuracy would be rank ordered and compared with all the participants. Finally, the participants ran a second session of both configurations. They were categorized into 2 groups based on their IC score: the competitive group and the noncompetitive group. The results indicated that the improvement in reaction time from the first to the second session tended to be larger for the competitive group for both configurations of the stimuli.

**SAT-112****THE POTENTIAL EFFECT OF EXERCISE ON ATTENUATING THE DEPRESSION-INDUCED DEREGLATION OF CYTOKINES INTERLEUKIN-6 AND INTERLEUKIN-10**

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Depression is associated with an increase in the production of pro-inflammatory cytokines (immune signaling proteins), particularly interleukin-6 (IL-6). In a healthy immune system, the production of pro- and anti-inflammatory cytokines, such as IL-6 and interleukin-10, respectively, is balanced. In both human and animal models, exercise promotes the production of anti-inflammatory cytokines, particularly IL-10. To explore the preventive benefits of exercise in combating the loss of regulation between IL-6/IL-10 found in depression, Sprague-Dawley rats (N = 40), will be subjected to the chronic, mild stress (CMS) model of depression after a period of 30 days of voluntary exercise. A sucrose test will be used to measure the level of depressive behavior as shown by the symptoms of depression and anhedonia, which is characterized by a loss of ability to experience pleasure. Access to a 1% sucrose solution is given pre- and post-CMS treatment to evaluate the development of anhedonic behaviors, which are described as a significant reduction in the amount of sucrose consumed post treatment. We hypothesize that, for animals experiencing the CMS treatment, exercise would show significantly more balanced production of IL-6 and IL-10 compared to the no exercise CMS group, respectively. We also expect that the exercise-CMS condition animals will exhibit lower levels of anhedonic-behaviors indicated by a non-significant change in sucrose consumption. Data collection for this project is just underway; expected results are the only results available at this date. Preliminary results will become available during the month of September 2014.

**FRI-114****CHARACTERIZING CUE-RELATED NEURAL CONSEQUENCES OF INDIVIDUAL DIFFERENCES IN THE VENTRAL PALLIDUM OF RODENTS**

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<sup>1</sup>*University of Texas at El Paso, El Paso, TX,* <sup>2</sup>*University of Michigan, Ann Arbor, MI.*

Our overall goal is to characterize neural consequences of individual differences involved in addiction. In a Pavlovian conditioned approach (PCA) task, some animals approach the incentive cue (sign trackers) while others are more likely to approach the reward-goal location (goal trackers). Experimentally, an illuminated, retractable lever, the conditioned stimulus, predicts the delivery of a banana pellet, the reward. After multiple presentations, approach differences become apparent and animals are characterized as sign trackers (STs), goal trackers (GTs), or intermediates (INs). The goal of the present study is to determine the efficacy of visual relative to auditory components of the cue. When presented with a complex sound/light cue, both STs and GTs display an increase in neural firing at the onset of the cue. Removing one component, in this case, the sound, will allow for us to identify its effect in neural responses. For this analysis, we will record neural activity in a group of GTs. The lever will remain in the chamber at all times. It is never retracted and thus makes no sound. Bilateral, single-unit, ventral pallidum recordings will be obtained and analyzed in relation to previous GTs exposed

to a sound/light cue as oppose to a light-only cue. If the sound is critical, we expect to see a decrease in neural response at the onset of the cue for those rodents presented with a light-only cue. Future work will also compare STs, where cue differences might be more exaggerated

## **OTHER PSYCHOLOGY**

### **FRI-119**

#### **EFFECTS OF FOOD INTAKE AND EXERCISE FREQUENCY ON RESPIRATORY SINUS ARRHYTHMIA (RSA) IN THE TOWER OF LONDON TASK**

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The current study investigates how diet and exercise effects heart rate and respiration synchronization during a planning task. Participants will be healthy 18 to 35 year olds. The sample will consist of half collegiate athletes and half non-athletes. Participants will fill out a thorough nutrition questionnaire and an exercise frequency survey. Participants will covertly solve Tower of London spatial puzzle-like planning task continuously for a 6-minute epoch. During this epoch, respiration and heart rate will be recorded. Frequency analysis will reveal the extent of breathing and heart rate synchronization. We expect the non-athletes to have less heart rate and respiration synchronization during the covert epoch because of their more labile heart rates. The athletes are expected to have more heart rate and respiration synchronization due to their more stable heart rates. This study will inform us about the effects of nutrition and exercise on the mind and body connection during a challenging cognitive task.

### **SAT-119**

#### **BREAKTHROUGHS OF ANALOGICAL LEARNING: HOW LANGUAGE INFLUENCES AN INFANT'S ABILITY TO RECOGNIZE RELATIONS**

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We aim to uncover the role of language and its impact on analogical learning in infants. Learning by analogy is essential in order to obtain higher learning abilities. Recent studies have revealed that 7- and 9-month-old infants possess the ability to detect the most basic relation among a pair of same and different objects. This initial study showed 2 components of analogical learning: multiple exemplars enhance infants' ability to learn relations, while individual object focus disrupts their ability to detect the relations. The current study investigated a third attribute of analogical learning: the influence of language. The participant sample involves 36 full-term infants between 7- and 9-months old. Results suggest when the individual objects are labeled, it hinders detection of the relation. However, labeling the relation does not have a facilitative effect at 7 and 9 months. It is possible that infants require experience with language to comprehend the relational labels. Future studies will investigate whether the relational labels work at older ages.

**SAT-116****INFLUENCE OF ACCULTURATIVE STRESS AND SLEEP ON MATERNAL DEPRESSION AND BIRTH OUTCOMES**

Berta Luis Sanchez, Kimberly D'Anna-Hernandez.

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As the Mexican-American population increases steadily, interest in investigating mental health symptoms within this community grows. Pregnant Mexican-American women exhibit high rates of depressive symptoms associated with adverse perinatal outcomes, but the reason this occurs is not known. Mexican Americans experience unique cultural stressors including acculturative stress that may affect health behaviors such as sleep. The authors of this study hypothesized that acculturative stress will be related to adverse sleep outcomes and that effects of sleep will moderate the effects of acculturative stress during pregnancy on birth outcomes. Pregnant Mexican-American women ( $n = 25$ ) ages 18 to 45 years old were assessed for acculturative stress, depressive symptoms, and sleep outcomes averaged over 3 intervals: early pregnancy (15 - 17 weeks), mid pregnancy (25 - 27 weeks), and late pregnancy (33 - 35 weeks). A sleep diary was completed for 3 consecutive days at each interval, and postnatal outcomes were collected through self-reports at an in-home birth visit. A regression analysis showed that increased acculturative stress was associated with women's self-reports of feeling less refreshed on waking during pregnancy ( $R^2 = 0.211$ ,  $p = 0.04$ ). In addition, women that report more acculturative stress and adverse sleep outcomes (longer to fall asleep and shorter total time asleep) predicted increased depressive symptoms during pregnancy ( $R^2 = 0.73$ ,  $p < 0.05$ ). Socio-cultural factors along with altered sleeping patterns may present an opportunity for identification of those at risk for mental health symptoms during pregnancy in Mexican-American women.

**FRI-116****TO CATCH A CRIMINAL ONLINE: THE RELATIONSHIP BETWEEN NARCISSISM AND DELINQUENT ACT POSTS ON SOCIAL MEDIA**

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The popularity of social media (e.g., Facebook, Twitter) continues to grow. These social media platforms afford people the ability to publicly update their family, friends, and even coworkers about their life events. More surprisingly, social media has also become a place where people have shared their criminal activity or, to a lesser extent, people have shared activities that may border on being illegal. Often, an individual's decision to post illicit activities on social media, whether it was to brag or confess, has eventually led to their arrest. Previous research has found that individuals with high levels of narcissism not only engage in frequent Facebook use, but narcissism has also been found to correlate significantly with delinquent behaviors, primarily among adolescents. However, the literature behind this phenomenon of sharing illegal activity online is scant, and further investigation is needed to understand the mechanisms behind this over-sharing behavior. This study explores whether individuals who share narcissistic traits will or have posted online their criminal or illicit activities. Data will be

gathered from a wide range of young adults from Southern California through an online questionnaire, which will include measures of narcissism, social media and technology use, sensation seeking behaviors, and self-reported delinquency.

#### **SAT-117**

##### **CAUSAL CONCEPTIONS OF HYPERTENSION PERTAINING TO HEALTHY AGING**

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Hypertension (high blood pressure) affects more than half of older adults. Illness management is integral to self-care and unfortunately, many older adults do not successfully manage their hypertension. Having a better understanding of older adults' causal beliefs for their hypertension may be critical for developing improved educational strategies that promote self-care of chronic illness. The purpose of the present study is to examine the relationship between hypertension knowledge, illness duration, self-rated health, and older adults' causal beliefs of their hypertension. Two hundred and fifty-seven hypertensive or healthy adults were recruited from micro-urban areas in central Illinois. Participants completed the Brief Illness Perception Questionnaire (BIPQ) and provided general demographic information. An established coding scheme was then applied to the open-ended questions on the BIPQ which pertained to causal beliefs about hypertension. We expect the results to indicate that individuals with higher education levels, more knowledge about hypertension, and better self-rated health are more likely to attribute their hypertension to more biomedically accepted causes such as natural or physical causes. The assessment of causal beliefs using a coding scheme for the BIPQ provides a more comprehensive view of illness representations and may facilitate the development of tailored educational strategies that promote self-care behaviors among chronically ill older adults.

#### **FRI-121**

##### **THE ROLE OF DISCRIMINATION STRESS ON INFANT TEMPERAMENT IN MEXICAN-AMERICAN MOTHERS AND THEIR INFANTS**

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Pregnancy is a time of many changes for women, and feeling stressed is very common. However, chronic stress is associated with adverse pregnancy outcomes and behavior in children. Mexican-American women may be at greater risk for the effects of stress during pregnancy as they report higher rates of psychosocial stressors, discrimination, and mental health symptoms (depression) during pregnancy relative to Caucasian women. Cultural stressors may play a unique role at this time, but this is yet unknown. This study hypothesizes that discrimination stress above general stress during pregnancy is associated with adverse infant temperament in the postpartum period. To address this question, in an ongoing study, 15 women were recruited during pregnancy and followed until 3 months postpartum. Mothers self-reported on discrimination, perceived stress, and depressive symptoms at 3 timepoints: early (15 - 17 weeks), mid (25 - 27 weeks), and late pregnancy (33 - 35 weeks). In addition, mothers reported on infant temperament (3 subscales: negative affect, effortful control, and

surgency) on infants at 3 months of age. High levels of perceived stress, but not discrimination or depressive symptoms, in the second trimester of pregnancy was associated with less effortful control at 3 months ( $r = 0.54$ ,  $p = 0.03$ ). In addition, when mothers reported increased discrimination stress as well as depressive symptoms during pregnancy, they also reported increased negative effects on the newborn ( $R^2 = 0.35$ ,  $p = 0.07$ ). This work suggests that discrimination stress in Mexican-American mothers may exacerbate the negative effects of mental health disorders on infant outcomes and should be assessed for culturally competent care.

#### **SAT-118**

##### **PARENT-CHILD COMMUNICATION AND SEXUAL BEHAVIOR IN ADULTHOOD**

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Lack of parental communication about sex can have an influence on a child's sexual attitudes and behaviors. Sex may be considered a sensitive subject between the caregiver and child. Some parents find this conversation to be difficult to discuss, although it is necessary. The purpose of this study was to examine who spoke to the participant about sex when growing up and determine if that had an influence on their sexual attitudes and behaviors. College students attending a western university reported their attitudes about their sexual activities on an anonymous online survey. After reading each item on the online survey, participants gave their input. It was hypothesized that African Americans and Latino/a adults would be less likely to have been spoken to about sex while growing up by their mothers and/or fathers than Caucasians. Additionally, it was hypothesized that the lack of parental communication about sex when growing up would be associated with females' and males' likelihood to engage in risky sex behaviors. Furthermore, it was also hypothesized that women would be less likely to be spoken to about sex when growing up. Results of this study will provide important information for sexual health programs for adolescents and their parents.

#### **FRI-120**

##### **RECONFIGURING MASLOW'S: IDENTIFYING THE HIERARCHICAL NEEDS STRUCTURE IN ONLINE GAMES**

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With the diffusion of the internet and the increasing availability of new technology, millions of people across different races, genders, and socioeconomic backgrounds currently engage in immersive virtual environments known as massively multiplayer online games (MMOs). MMOs are socially focused online environments where people virtually represent themselves in a new world and interact with other users on a daily basis and in real time. Because of the high level of social interaction that takes place within these environments that is not associated with the objectives of the game itself, online games could potentially serve as platforms where different social constructs can be tested. This research uses a phenomenological approach and focuses on identifying the hierarchical structure of the virtual needs experienced by players to further

understand gamer motivation. The hierarchical representation of needs present in online games, similar to the one that Abraham Maslow identified for the physical world (e.g., physical needs are more important than self-esteem needs), could provide needed evidence suggesting that human behavior online is driven by how much we value a specific reward similar to the way human behavior is driven in the offline world. By studying the live experiences of gamers, the goal is that the identification of the online hierarchical needs structure will provide evidence supporting immersive virtual environments as platforms where the needs-motivation process is comparable to the offline world and to understand the motivations of online game play and virtual living.

#### **SAT-115**

##### **EFFECTS OF CODE SWITCHING ON LEXICAL ACCESS AND COMPREHENSION**

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Inhibition models of lexical access have been developed to explain how lexical items are accessed by bilinguals based on the language needed. Also, models of lexical access predict if and how lexical items from multiple languages may compete for selection. The purpose of this current study was to examine the effects of placing bilinguals in either a monolingual or bilingual language mode on lexical access and situational model creation (i.e., comprehension ability). One hundred balanced bilinguals were either presented with an all-Spanish, all-English, or code-switched story passage and were subsequently given a lexical decision task and a comprehension assessment. Results confirmed that bilinguals were slower at responding to the first initial switch trial when placed in a monolingual mode (i.e., only English or only Spanish) than when placed in a bilingual mode (i.e., code-switched), although no significant difference was found between the English and code-switched conditions. Based on the current results, the placement of bilinguals in either a monolingual or bilingual mode creates differences in terms of lexical accessing times.

#### **SAT-120**

##### **SOCIO-CULTURAL PREDICTORS OF DEPRESSIVE SYMPTOMS IN PREGNANT MEXICAN-AMERICAN WOMEN**

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As more pregnant Mexican-Americans integrate into United States culture, they are vulnerable to a unique stressor termed acculturation. Acculturation and the stresses associated with this process have detrimental effects on maternal health. Social support and Mexican cultural values can buffer against the effects of acculturation and may alleviate prenatal mental health symptoms. The current study explores the relationship between cultural stressors and protective support on maternal physiological and psychological outcomes (cortisol levels and depression) during pregnancy. In an ongoing study, 37 participants in their first trimester completed questionnaires on acculturative stress, cultural values, depressive symptoms, and social support. Salivary cortisol was collected 4 times/day to determine diurnal decline.



Preliminary analysis revealed a positive relationship between acculturative stress and depression ( $p < 0.001$ ), but neither was related to social support. Less identification with the Mexican value of family support was associated with altered cortisol decline ( $p = 0.03$ ), but no relationship was observed between cortisol and depression or acculturative stress. In addition, satisfaction with received social support was negatively correlated with the endorsement of gender roles ( $p = 0.04$ ), a Mexican cultural value, and material success ( $p = 0.02$ ), an Anglo value. Thus, acculturative stress is a likely risk factor for depressive symptoms in pregnant Mexican-American women. However, identification with traditional Mexican cultural values may facilitate satisfaction with social support as well as be protective against the physiological changes associated with stress. This work suggests that the integration of traditional cultural values into culturally competent prenatal care for Mexican-American women may have beneficial effects on maternal health.

#### **FRI-117**

##### **SLEEP-DEPENDENT PROCEDURAL MEMORY IMPROVEMENT USING THE MOTOR SEQUENCE TASK**

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Procedural memory is essential to motor skill learning, such as riding a bike or typing. Within the field of sleep and memory research, a task known as the motor sequence task (MST) is often used to assess procedural learning. In this task, subjects type a 5-digit sequence over and over for 30 seconds, followed by 30 seconds of rest. They repeat this cycle for 4 blocks of 12 trials each for a total of 48 trials in 48 minutes. Previous studies, re-testing subjects across a variable time interval, showed improvement in performance shortly after learning. In our current study, we examine this improvement in performance to determine whether it reflects initial information processing and consolidation, or instead evidence of a buildup of cognitive or motor fatigue that masked true performance at the end of training. To understand the cause of this improvement, we are replicating this phenomenon, testing healthy subjects on 4 variations of the MST: 1) typing the same sequence for 48 minutes with no rest; 2) receiving visual feedback at the start of each block to provide a sense of restarting the task; 3) typing a sequence for 1 block, followed by a 12 minute break, then continuing to type the same sequence for 2 more blocks; or 4) typing 1 sequence for 1 block, introducing a novel sequence during the next block, then resuming the original sequence for the remaining 2 blocks. We will report our findings.

#### **FRI-115**

##### **THE EFFICIENCY OF VISUAL SELECTIVE ATTENTION IS MODULATED BY TASK DIFFICULTY AND REWARD**

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Visual selective attention prioritizes the processing of relevant information in order to facilitate goal-driven behavior. Physically salient and task relevant objects influence early visual selection

but so can non-salient task irrelevant objects if they have been previously associated with reward. This present study investigates the effects of task difficulty on the capture of attention by task irrelevant reward associations. In a training task, participants learned to associate particular colors with monetary rewards. One week later, participants completed a visual search task that required target identification among distracters. Targets (letters) and distracters (numbers) were arranged in a circle and presented inside differently colored circles that sometimes included the reward-associated color. A separate stimulus was also presented adjacent to the circle in a completely task irrelevant location. In high difficulty trials, targets and distracters were perceptually similar. In low difficulty trials, targets and distracters were less similar and easily distinguishable from each other. We have two predictions. First, based on previous work, we predict that the influence of reward associations will be greater for task-relevant items than task-irrelevant ones. Second, because previous studies have shown a greater influence of task irrelevant information in easy tasks, the effects of reward associations should be enhanced on low difficulty trials. Our findings would suggest that the extent to which reward associations capture attention depends on both task relevance and task difficulty.

## **OTHER SOCIAL SCIENCES**

### **FRI-122**

#### **THE EFFECTS OF EYEWITNESSES' AGE ON JURY DECISION MAKING**

Valeria Pereira, Judith Foy.

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The age of the eyewitness in criminal cases is a decisive factor that can influence the verdict of a jury in the courtroom in a misleading manner. In order to obtain an honest and reliable decision, it is necessary that a jury is not misled by the age of the eyewitness. In this study, 48 participants above 17 years of age were recruited through Facebook to serve as a mock jury. They were exposed to a trial description regarding a rape in which different ages of the eyewitness were randomly assigned. The eyewitness options were an 8 year old child, a 17 year old young adult, and a 70 year old elderly person. Participants then had to choose a guilt rating for the defendant on a scale of 1 to 7, with 1 being definitely not guilty and 7 being definitely guilty. There are studies that have focused on the same variables; however, the results they yield have not been consistent. Our findings coincided with studies that indicated that there was no significant difference between the guilt ratings given to the defendant when the eyewitness was a child, an elderly person, or a young adult. There are, however, studies that have found that the age of the eyewitness does have an effect on the guilt rating. The lack of significance in our results and the inconsistencies between similar studies suggest that jury decision-making is not a simple task and that there is much more to be studied in relation to this topic.

**SAT-121****EXAMINATION OF (RE)INTEGRATION PROCESS OF (SEX) TRAFFICKED WOMEN**

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Human trafficking is a direct violation of human rights, and as an international problem, has many actors involved. The actors work throughout the trafficking process from prevention, to coercion, to rescue, and to eventual reintegration. Reintegration is identified as the process of recovery with economic and social inclusion after a trafficking experience. This is accomplished by the empowerment of the trafficked women, developed from skills taught to the women to allow them to gain independence and self sufficiency. This study examines reintegration programs for women through various studies in Europe by exploring the variety of methods used by 3 different countries. We collected data based on a variety of interviews and previous studies, examining social questions about sex work, prostitution, and sex trafficking, including subsequent reintegration. Our study examined women's pre-trafficking conditions, migration/trafficking experiences, support needs, concerns, and future aspirations. By mapping post sex-trafficking experiences, a greater understanding of reintegration experiences and challenges can be gained and used to improve future aid. We have established through these interviews and literature reviews that, with a successful reintegration program, women were able to reestablish positive relationships with their families, find employment, improve overall psychological health, and develop lifelong skills. Important to this reintegration process is community activity. By taking an interdisciplinary approach, different entities involved with the recovery of a woman would be able to help her establish a place back in her society.

**POLITICAL SCIENCE/GOVERNMENT****SAT-122****DACA AND HISPANIC POPULATIONS IN NORTH TEXAS**

Maria Maciel, Victoria Lockwood.

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The Obama Administration issued a memorandum, the Deferred Action for Childhood Arrivals, DACA, in 2012 affecting immigrants all over the United States. This memorandum is often mistaken for the DREAM Act, an immigration reform bill that never passed. The purpose of this research is to synthesize and better understand the effects of this memorandum on DACA-eligible immigrants in North Texas, determine whether or not the policy is worth pursuing, and if this memorandum is the answer to a future successful immigration reform law. Based on the popularity of DACA over the past 2 years, it is presumed that if there are negative consequences in pursuing DACA, the benefits outweigh them. The data were collected by performing extensive literature reviews and conducting interviews of DACA-eligible individuals and 2 immigration attorneys in the Dallas area. The results thus far indicate that DACA has benefited many immigrants educationally and financially, although it has also introduced a new form of discrimination. Deferred action is the first step in the direction of a comprehensive immigration reform law, although by no means has it come close. It has drastically improved

the lives of people eligible to apply, although the question about its longevity remains a concern.

## **PSYCHOLOGY (GENERAL)**

### **FRI-123**

#### **SCHOOL STRESS, ACADEMIC PERFORMANCE, AND COPING IN COLLEGE FRESHMEN**

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The 2010 annual freshman survey from the University of California, Los Angeles found that incoming freshmen self-report as having lower levels of mental health than previous freshmen over the past 25 years. Lower levels of mental health have been found in research to correlate with higher levels of stress. If students have high levels of stress and ineffective coping skills this may negatively affect their performance. To understand how school stress, coping, and performance interact with each other, college freshmen from a mid-sized university in the Rocky Mountain region were asked to complete a stress inventory, a coping inventory, and a demographic survey. Results showed that stress and coping are significantly positively correlated, specifically emotional coping was significantly correlated with stress. Regression analysis showed that stress accounted for over a quarter of the variance in GPA when controlling for gender. These results suggest that stress may change a student's performance, and that freshmen may only know how to cope with stress in an emotional way.

### **FRI-124**

#### **THE DEVELOPMENTAL ORIGINS OF GENDER STEREOTYPES REGARDING GENERAL INTELLIGENCE**

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Our culture holds a broad, and potentially damaging, stereotype against women: they are less intellectually gifted than men. This stereotype against women's intellects is likely to have negative consequences for girls' and young women's career choices and expectations of success. Thus, it is important to investigate when children become aware of these broader stereotypes. In the current study, we investigated the development of gender stereotypes about intelligence by testing 5- to 7-year-olds on 2 implicit tasks. In the first task, children were told 2 stories, 1 about a really smart person and 1 about a really nice person (which served as a control). No hints as to the protagonists' gender were provided. After each story, children were shown 4 pictures (2 males and 2 females) and were asked to guess which of them was the person in the story. In the second task, children were shown pictures of pairs of people (1 male and 1 female) and were asked to guess which one of them is "really, really smart" or "really, really nice." We found that, between ages 5 and 7, girls became increasingly likely to associate being smart with males, suggesting they are beginning to assimilate the stereotypes of the culture around them. This research provides insights into the development of the stereotypes

against women's intelligence, thereby enabling parents and investigators to devise effective interventions to reduce the negative effect of such stereotypes on the development of young children.

#### **FRI-127**

##### **SHOALING BEHAVIOR: A LINK TO MAPPING STRESS RESPONSES IN ZEBRAFISH**

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Behavioral contextualization of linked responses, based on species-specific intrinsic reward may provide further clues for treatment of complex disorders where dopaminergic pathways are impaired. This study investigated dynamic relationships between environmental stressors and midbrain reward circuitry by examining changes in shoaling behaviors in zebrafish (*Danio rerio*). We hypothesized that environmentally or pharmaceutically induced changes in the neural pathways facilitating reward responses would decrease pro-social and increase anxiety behaviors. Sixty fish were either ostracized for 3 days, treated with a mixture of 220  $\mu$ M MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine), or treated with MPTP then ostracized. Treated fish were recorded in a novel tank environment with 4 untreated fish. Velocity (cm/ms), distance swam (cm), nearest neighbor distance (cm from nearest fish) and thigmotaxis (swimming within 2 cm of tank walls) were analyzed using ImageJ (National Institutes of Health). Statistical analyses of behavioral outcomes were conducted using excel and SPSS. Findings revealed that ostracized and MPTP treatment groups did not participate in pro-social behaviors without exhibiting changes in motor function. Similar motor function variation across treatment groups ( $P < X$ ) suggest that both conditions affect dopaminergic pathways in similar fashions. Spatial preference in nearest neighbor analysis showed a change in shoaling behavior in all treatment conditions ( $p < .04$ ). Further understanding of subsequent motor and endocrine pathways in diseases including depression, anxiety, autism, and Parkinson's disease, offer promising avenues for integrative science, medicine, and psychology.

#### **FRI-133**

##### **BEHAVIORAL TESTS TO ASSESS AFFECTIVE DISORDERS IN NEONATAL PIGLETS**

Angelina Jaimes<sup>1</sup>, Adrienne Antonson<sup>2</sup>, Rodney Johnson<sup>2</sup>.

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Similarities in porcine and human neuroanatomy make the pig a preferable model for human neurodevelopmental research. At present, little work has been done to develop behavioral tests for young piglets that can be used in place of human infant testing. Common areas of interest for detecting deficits in neurodevelopment include behavioral domains such as learning and memory, anxiety or stress response, sociability, and stereotypic behaviors. This study develops and validates 5 different behavioral tests related to these domains which can be used with neonatal piglets. Naturally farrowed piglets were placed in individual caging units at PD2. Piglets began testing at PD11 and experienced the following order of behavioral tests: an open field test for anxiety; a spatial T-maze task to determine learning and memory; a

consummatory, extinction-based frustration test; a sociability test that included measurements for general sociability and preference for social novelty; and a restricted repetitive behaviors test using an open arena with 4 different enrichment objects. These behavior measurements will be used in current research focusing on the effects of maternal immune activation during pregnancy on the neurodevelopment of the fetus. Infection in the mother during pregnancy may lead to dysregulation in normal brain development and therefore manifestations of aberrant behaviors in the offspring. These behavioral tests are intended to be sensitive to heightened anxiety and frustration, deficits in learning and memory, decreased social approach, decreased preference for social novelty, and increased restricted repetitive behaviors compared to controls.

### **FRI-125**

#### **THE ROLE OF LANGUAGE IN STORYTELLING: COMPARING SPANISH AND ENGLISH SPEAKERS**

Kenny Aspurez, Fernando Limon, Ruth Church.

*Northeastern Illinois University, Chicago, IL.*

Story telling is one of the oldest ways that information is transmitted from one person to another. What determines a good story? Many characteristics have been considered such as length of story, content of a story, and elaboration of detail. We asked whether monolingual English speakers differ from monolingual Spanish speakers in the way they recount story events. Twenty-one Spanish monolinguals and 22 English monolinguals watched 4 cartoon stories that differed in complexity. To control for effects of culture, we examined 24 English-Spanish bilinguals raised in the United States. Participants' ages ranged from 13 to 43 years. We analyzed the length of stories, the number of words used, and the number of dysfluencies produced during these story narrations. We found that Spanish monolinguals had significantly lengthier stories, larger word counts, and more dysfluencies than English monolinguals regardless of the level of story complexity or the age of the participant, suggesting a difference in the way that narratives are mentally represented across groups. Furthermore, this pattern was also found in English-Spanish bilinguals. The same individual when telling a story in Spanish produced significantly longer stories, larger word counts, and more dysfluencies than when they told the same stories in English. Preliminary analysis of the content of stories shows that narratives told in Spanish were far more elaborate and richer in detail than stories told in English. This research suggests that languages may differ in their grammatical structures and that these structures may reflect different cognitive representations and organization of experience.

### **SAT-123**

#### **COGNITIVE LOAD AND CODE-SWITCHING AMONG ENGLISH-SPANISH BILINGUALS DURING STORY TELLING**

Fernando Limon, Kenny Aspurez, Ruth Church.

*Northeastern Illinois University, Chicago, IL*

Approximately 16% of the population in the United States is Spanish-English bilingual and the number of bilinguals is increasing. This has prompted many to study bilingual processes in

linguistics and psychology. This research examines those cognitive processes underlying speaking 2 or more languages. Previous research showed that bilinguals show greater effects of performing under an experimentally induced cognitive load (had less working memory available) than monolinguals suggesting that bilinguals activate 2 language systems simultaneously while speaking. Our current research asks whether there is additional evidence provided in the language of our subjects further supporting the notion that bilingual individuals activate multiple language systems when speaking. Twelve bilingual, 24 Spanish-monolingual, and 14 English-monolingual participants performed 2 tasks simultaneously (a classic cognitive load paradigm): memorizing lists of numbers and retelling cartoons just viewed. The results presented here are an in-depth examination of the narrations of our bilingual and monolinguals. We examined code-switching in the bilinguals. Additionally, we looked at the narrations for language-specific syntax reflected in both speech and accompanying gesture. Preliminary results suggest that number of code-switches negatively correlated with memory. Moreover, we found that bilinguals show many more speech utterances combined with gestural phrases with a mix of language syntax (used both Spanish and English syntax) than either monolingual groups. These results suggest that although bilinguals use more memory space when speaking than monolinguals, they also create stories that are richer and more syntactically complex. We feel this has implications for how cognitive processes may underlay creative language tasks like story-telling.

#### **SAT-125**

#### **FACTOR STRUCTURE AND CONCURRENT VALIDITY OF SCORES ON THE MULTIDIMENSIONAL REVENGE ATTITUDE INVENTORY (MRAI-24)**

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Revenge can occur as a natural response to insult or injury, but this internal distress has not been adequately explored. The existing self-report measures of the revenge construct have limited psychometric properties. We examined the factor structure and psychometric properties of a newly-developed self-report measure of revenge, the Multidimensional Revenge Attitude Inventory (MRAI-24). In study 1 (N = 491) we examined configural and metric measurement variance of the 3 domains of the MRAI-24 (suicide ideation, revenge rumination, and desire for revenge) across 265 Hispanic (100 men, 165 women) and 226 Caucasian (101 men, 125 women) undergraduates. In study 2 (N = 122; 53 men, 69 women) we examined differential correlates for each MRAI-24 domain. In both studies, participants were 18 and older, and were recruited from a single university. In study 2, participants completed 3 concurrent self-report measures, including the Multidimensional Suicide Inventory-28 (MSI-28), the Suicide Anger Expression Inventory-28 (SAEI-28), and the Future Disposition Inventory-24 (FDI-24). Using exploratory structural equation modeling (ESEM) with robust estimator, the configural baseline data showed adequate fit estimates. Comparison of the metric (factor loadings) against the configural (baseline) models showed that the 3-factor model is invariant across the groups, chi-square  $\chi^2(63) = 52.76$ ,  $p = .82$ . Thus, data was combined for the

participants in study 2. Pearson correlations were computed to examine differential correlates for the MRAI-24 domains (scales). Taken together, this instrument has a stable factor structure and adequate psychometric properties to measure revenge.

#### **SAT-126**

##### **MIXED SMILES: AN ANALYSIS OF THE COHERENCE BETWEEN EXPERIENTIAL AND BEHAVIORAL RESPONSE FOLLOWING AMBIVALENT EMOTIONAL STIMULI**

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In 1972, Paul Ekman implied the 6 discrete emotions anger, happiness, surprise, disgust, sadness, and fear have distinct, universal facial expressions. We smile when we are happy and frown when we are sad. Past studies confirm that high levels of coherence exist between emotional experience and facial expression when subjects are shown unambiguously pleasant or unpleasant film clips. But what happens to the tie between emotional experience and facial response when the eliciting event stimulates ambivalent, mixed emotions? In this study, data collected from video recordings of individuals watching ambivalent film clips are used to examine the relationship between emotional experience and facial response when mixed emotions are elicited. Cross-correlations between data sources measuring positive and negative emotional response indicate low to moderate amounts of coherence between response systems. Contributors to coherence are being investigated, including the degree to which emotion is “mixed” at a given time, individual personality characteristics, and attitude toward various emotions. Furthering the understanding of response coherence and mixed feelings will shed light on various psychiatric disorders, where emotional dysfunction skews the normal emotional experience and response.

#### **FRI-126**

##### **WHERE'S DORA? YOUNG INFANTS' LOCATION MEMORY FOR HUMAN-LIKE OBJECTS**

Jazmin Landa, Renee Baillargeon, Maayan Stavans.

*University of Illinois at Urbana-Champaign, Champaign, IL.*

Findings suggest that infants as young as 2.5 months of age can represent and remember the location of a hidden object, contrary to the initial expectations of infant memory abilities shown in previous studies. When an object is hidden behind a screen, 9 month-old infants can remember many features of the object; when 2 objects are hidden behind 2 screens, however, the infants perform more poorly. This experiment examined whether 6-month-old infants showed improved memory performance in categorical representation trials using a human-like object and a non-human-like object, rather than focusing on the features of both objects. An anticipatory-looking method was used to determine whether infants can remember where each object was located. First, infants were presented with both objects: a Dora doll (human-like object) and a truck (non-human-like object). Each object was hidden behind separate screens, and a third matching object was presented (e.g., Dora doll or truck). Infants were then given 3 seconds in order to anticipate where the third matching object will be placed in order to match



1 of the 2 initial objects. Better understanding of infant memory can allow us to detect any cognitive development complications a young infant may encounter.

#### **SAT-124**

##### **THE IMPORTANCE OF DIFFERENT TYPES OF SOCIAL SUPPORT FOR REFUGEE MENTAL HEALTH**

Julia George-Jones<sup>1</sup>, Julia Hess<sup>1</sup>, Deborah Bybee<sup>3</sup>, Karen Wang<sup>1</sup>, Charlie Christian<sup>1</sup>, Brandon Baca<sup>1</sup>, Suha Amer<sup>1</sup>, Jessica Goodkind<sup>1</sup>.

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Refugees who have recently immigrated to the United States have typically survived numerous hardships and experienced difficulties acclimating to a new environment and culture. Thus, high rates of depression and other mental health problems among refugees are of critical concern. Social support from family members and members of one's ethnic community is related to lower levels of depression and PTSD in refugee populations, but research on the relationship between different kinds of social support and mental health in refugees from Iraq, Afghanistan, and the Great Lakes Region of Africa is lacking. The current study explores the relationship between social support, depression, and PTSD in these particular groups. The quantitative data we are analyzing comes from 34 refugees who completed standardized interviews that included measures of social support, depression, and PTSD. We are conducting correlations and regressions to examine the relationships between depression, PTSD, and social support from family, other co-ethnic community members, and community members not in respondents' ethnic group. Our qualitative data comes from semi-structured interviews conducted with the same refugees. The interviews were coded using nodes that represent themes or ideas. We are analyzing the nodes for social networks, mental health, and depression and performing queries and writing memos to explore instances where participants discuss social support, depression, and symptoms of PTSD. Our results will make important contributions to the body of research on social support, depression, and PTSD in refugees which will lead to further understanding and improving the mental health and well-being of these particular groups.

#### **PUBLIC POLICY STUDIES**

#### **SAT-132**

##### **ISSUE BRIEFS AS TOOLS FOR PUBLIC POLICY CHANGE TO ADDRESS COLLEGE DRINKING AND RELATED PROBLEMS**

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Excessive and underage drinking among college students in the United States is a significant public health problem, in part because of young people's easy access to alcohol. Two-thirds of Maryland college students reported drinking at private house parties, which creates environments that threaten the well-being of students and surrounding communities. Communities can use social host ordinances to regulate private house parties. Our hypothesis is that issue briefs, translational research tools for public policy change, can assist in the passage

of social host ordinances. This case study documents the development and use of an issue brief in support of a community campaign in collaboration with 2 universities to pass a social host ordinance. Quantitative (survey and administrative data) and qualitative (interview and focus group) methods provide materials for the issue brief. An issue brief was developed incorporating police calls for service data and results from a recent survey of drinking patterns and harm among local college students, as well as findings from key informant interviews and focus group research. The issue brief was inserted into a 10-step policy process designed to maximize and mobilize community involvement in the development and passage of the social host ordinance. Key strategic decision points on content and framing of the brief, and barriers and challenges experienced while developing it are reviewed. This presentation documents the conceptualization, creation, and dissemination of an issue brief in the context of a community mobilization campaign to reduce underage drinking at private house parties.

## **SOCIAL PSYCHOLOGY**

### **SAT-127**

#### **INTRAGROUP AND INTERGROUP DISCRIMINATION AND MENTAL HEALTH AMONG LATINOS**

Carlos Rosas, Heike Mahler.

*California State University San Marcos, San Marcos, CA.*

Racial/ethnic discrimination is defined as unfair treatment based on the race/ethnicity of the victim. The basis for discrimination varies across groups, and for Latinos includes skin color, level of acculturation, language spoken, immigration status, and place of birth. Research suggests that higher levels of racism are associated with higher levels of negative mental health outcomes. However, most studies have not distinguished between discrimination perpetrated by members of a different racial/ethnic group than the victim (intergroup) and discrimination perpetrated by members of the same racial/ethnic group as the victim (intragroup). The prevalence and effects on health of inter- versus intra-group discrimination among Latinos have not been widely studied. This study examined the prevalence of intragroup discrimination, and it explored the health effects of both intra- and inter-group discrimination among Latinos. The study took place at California State University San Marcos. Participants were Latino undergraduate students who completed standardized measures of inter- and intra-group discrimination, social support, and perceived stress. It was expected that participants would report a significantly higher number of intra- than inter-group discriminatory incidences. Further, it was expected that intragroup discriminatory acts would be perceived as significantly more stressful than intergroup discriminatory acts. Results showed that participants reported higher number of inter- than intra-group discrimination incidences. Similarly, participants reported higher levels of inter- than intra-group discrimination related stress. However, the differences were not statistically significant. Although the findings do not support the hypotheses, they suggest that intragroup discrimination may be more prevalent among a more diverse population.

**FRI-129****PREJUDICE REDUCTION THROUGH CONTACT THEORY AND COGNITIVE DISSONANCE**

Samantha White, Lauren Coursey, Jared Kenworthy.

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Over the past few decades, researchers have examined various methods of reducing prejudice. Although both contact research and dissonance research have each addressed prejudice reduction separately, no researcher has yet developed a way to combine cognitive dissonance and contact theory methods as a means of reducing prejudice. In this study, over 500 undergraduates from The University of Texas at Arlington completed a prescreening survey that measured attitudes toward Muslims. Thirteen men and 30 women that scored below average on Muslim attitudes were randomly assigned to one of two conditions: a high-choice condition (participants had a choice of choosing an out-group partner), or a low-choice condition (participants were assigned an out-group partner). Participants were then asked to fill out a demographic survey, fill out a schedule sheet for the partner interaction, and complete the main dependent variables. We expected that those who chose to work with an out-group member would reduce their prejudice more so than those who did not choose to work with an out-group member. Muslim attitude scales were compared between high-choice ( $M = 6.78$ ,  $SD = 1.24$ ) and low-choice conditions ( $M = 6.60$ ,  $SD = 1.85$ ), but there are not yet any significant differences,  $t(41) = -.257$ ,  $p = .190$ ,  $d = -0.0058$ . However, the data collection is ongoing, and currently the results are not yet significant.

**SAT-128****ENTITLEMENT AND WELL-BEING OF PUERTO RICAN STUDENTS**

Ana Martinez<sup>1</sup>, PR, Amanda Clinton<sup>1</sup>, Magdalena Zemojtel-Piotrowska<sup>2</sup>.

<sup>1</sup>*University of Puerto Rico, Mayagüez Campus, Mayagüez, PR*, <sup>2</sup>*University of Gdańsk, Gdańsk, PL*.

Entitlement is commonly defined as the sense that one deserves special treatment, and it has been linked to narcissism. This study aims to determine whether well-being is related to entitlement. The current study intends to answer this question using the following questionnaires: The Personal Well-being Index (PWI), Satisfaction with Life Scale (SWLS), Positive and Negative Affect Schedule (PANAS), Mental Health Continuum (MHC), and Entitlement Questionnaire & Belief in a Zero-Sum Game (EQ & BZSG), and comparing measures of entitlement and well-being. The aforementioned questionnaires were completed by 300 university students living on the southwest side of the Island of Puerto Rico, and correlational analyses were conducted. Preliminary results indicate a significant relationship between entitlement and well-being. Implications of this relationship are discussed.

**FRI-128****DECEPTION FACILITATION ACROSS COMMUNICATION MEDIA**

Brandon Gallegos, Jennell Higgs, Leslie Cramblet-Alvarez.

*Adams State University, Alamosa, CO.*

This current study examines deception facilitation across communication media. Three communication conditions (face-to-face, text-based computer mediated, and video-based computer mediated) were observed for instances of deception. Based on previous research, it was predicted that the text-based computer mediated communication condition would correspond to the highest rate of deception instances. This hypothesis was based on the media richness theory proposed in previous research, which describes less rich media as lacking the common cues that would allow deception detection. Contrary to the findings in recent literature, we found no significant interaction of communication media on self-reported deception. However, a trend was uncovered showing increased deception in the face-to-face condition. Further research is needed to evaluate the possible influences that may have led to these results.

**SAT-129****THE EFFECT OF IMPAIRED SELF-CONTROL ON WILLINGNESS TO SMOKE**

Modupe Odufuwa<sup>1</sup>, Jessica Alquist<sup>2</sup>.

<sup>1</sup>*South Plains College, Levelland, TX,* <sup>2</sup>*Texas Tech University, Lubbock, TX.*

This study was designed to test the hypothesis that people with impaired self-control will be less likely to report being willing to smoke than people without impaired self-control. Self-control is often defined as overcoming a dominant response in order to work toward a goal. Previous theoretical work has suggested that people may use self-control to engage in harmful behaviors in order to gain social acceptance. For example, most people don't initially like the taste of cigarettes and alcohol and may be using self-control in order to try them. Previous research has shown that people's self-control is temporarily impaired after a previous act of self-control. In order to test whether impaired self-control decreases the likelihood of smoking, participants will be randomly assigned to an impaired self-control condition or a control condition. Participants in the impaired self-control condition will be asked to type a paragraph as accurately as possible without using the letter E or the space bar. Participants in the control condition will be asked to retype the same paragraph as accurately as possible. Both groups of participants will then be given a vignette describing a situation where a coworker offers them a cigarette. Participants will be asked to report their likelihood of smoking in that situation. The data will be analyzed using a one-way ANOVA. We predict that participants in the impaired self-control condition will report being less likely to smoke than participants in the control condition.

## **SOCIOLOGY**

### **FRI-132**

#### **EXPLORING THE RELATION OF INDIGENOUS STUDENTS' IDENTITY FORMATION AND THEIR ASPIRATIONS TO HIGHER EDUCATION**

Eddie Triste, Manuel Barajas.

*California State University Sacramento, Sacramento, CA.*

Identity formation within the United States occurs at various instances throughout a person's lifetime. It occurs with interactions in family, in school, in cultural settings, in a community environment, and from the media. In particular, since the United States enacted the Bracero Program, Structural Adjustment Programs with Mexico, and the North American Free Trade Agreement (NAFTA), both migration from Mexico and identity formation have affected indigenous communities. In the past 30 years, Mexican-origin indigenous people have significantly increased. These diverse communities of indigenous people have distinct customs, communal values, culture, and in most instances the elders retain their indigenous language. However, little is known about the youth who grow up in the United States with an indigenous upbringing but within a Eurocentric educational and societal context. Many of these students are born to families that are undocumented, though the California Dream Act of 2012 provided opportunities to those seeking higher education and a better life for themselves and communities. This research is specifically interested in exploring the questions: How does indigenous students' identity formation affect their aspirations to higher education? How does their indigenous social capital (i.e., community ties and culture) help or hinder their academic achievement?

### **SAT-131**

#### **THE ANOMIE IN SOCIAL NETWORKING: FEELINGS OF ISOLATION THROUGH SOCIAL NETWORKING**

Ceilique Hatcher, Katy Pinto.

*California State University Dominguez Hills, Carson, CA.*

With Facebook being one way to keep up with the lives of our peers, how does that truly make users feel? Social networking has been recently criticized for causing feelings of isolation. The 2 sites we will focus on are Facebook and Twitter. By displaying the best parts of life, do social networking sites create feelings of social isolation among its users? We will analyze how social networking sites cause feelings of loneliness. In order to see how social networking sites have influenced young adults, we will pay close attention to the content of the sites. By using content analysis, we will look at the common trends in status posts, tone/attitude of the post, and pictures. We will be using qualitative methods rather than quantitative methods to measure participants' levels of loneliness on social networking sites. We hope to better understand the negative effects of social networking sites. Resources such as literature review, content analysis, and interviewing can show whether social networking creates a sense of loneliness and isolation within the participants. By doing this research, we will explain whether

the replacement of face-to-face contact with social networking sites causes even more of a barrier for those isolated. For this research, we will use the following methods: Daniel W. Russell's "UCLA Loneliness Scale", Likert Scale, content analysis, and interviews from volunteers.

#### **FRI-130**

##### **A CALL FOR CHANGE IN PUBLIC POLICY IN FAVOR OF SINGLE AFRICAN-AMERICAN MOTHERS LIVING IN ENGLEWOOD**

Dessiree Malone, Ruby Mendenhall.

*University of Illinois at Urbana-Champaign, Urbana, IL.*

In a May 23, 2014, Huffington Post article, Joseph Erbentraut challenges people not to believe everything they hear about Englewood, which is often referred to as Chicago's most dangerous neighborhood. Englewood has been stricken with high levels of violence, unemployment, and limited resources; however, it has the potential to rebuild. This study will examine 20 narratives from a larger sample of 93 narratives from low-income African-American mothers who live in and around Englewood. Aspects of grounded theory (open, axial, and selective coding) will be used to identify their perceptions of social structures (housing and education) and their suggestions for social change in Englewood, including public policy.

#### **FRI-131**

##### **RELATIONSHIP OF EXTENT OF PARTICIPATION IN COMPETITIVE FOOTBALL AND DEGREE OF PREJUDICE TOWARDS SEXUAL ORIENTATION IN COLLEGE-AGED MEN**

Manuel Ramirez, Jeremy Simmons.

*University of Texas at Austin, Austin, TX.*

Despite the cultural erosion of homophobia, several scholars suggest that contact/collision sports will remain bastions of antigay attitudes due to principles rooted in traditional masculine norms. Up to now, no study has examined the relationship between the extent of exposure to the values of competitive football and prejudicial attitudes towards gays. Therefore, the primary goal of this study is to investigate if being actively involved on a competitive football team is related to attitudes toward gays. This study also focuses on gender identity and the extent to which gender role identification relates to attitudes toward gays. The Modern-Homonegativity Scale-Gays (MHS-G) was used to assess anti-gay attitudes among 100 college, male undergrads at a large public university in the southwest. An online version of the MHS-G was used in addition to a demographic questionnaire and the Bem Sex Role Inventory (BSRI), which assessed the extent of identification with 20 masculine and 20 feminine personality characteristics. Our research team expects to find a statistically significant relationship between degree of participation in football and MHS-G scores. We also expect to find a statistically significant relationship between degree of participation in football and higher masculinity scores on the BSRI. This research suggests that competitive football organizations have taken minor steps to improve the antigay and discriminatory culture of the sport. It is important to understand how these issues can be addressed so that sexual minorities can feel more comfortable "coming out" and feel accepted on their collegiate and professional football teams.

# Graduate Poster Abstracts

## BIO/AGR/ENV LIFE SCIENCES

## BIOCHEMISTRY/BIOPHYSICS

### FRI-G2

#### **NMR STRUCTURE AND MODE OF ACTION STUDIES OF THE S-LINKED GLYCOPEPTIDE SUBLANCIN**

Chantal Garcia De Gonzalo, Wilfred van der Donk.  
*University of Illinois at Urbana-Champaign, Urbana, IL.*

The rapid development of bacterial antibiotic resistance not only decreases the effectiveness of known antibiotics but also increases the need for the discovery of novel drugs. Ribosomally synthesized and post-translationally modified peptide (RiPP) natural products are a rapidly expanding class of such compounds. Sublancin 168, produced by *Bacillus subtilis* 168, belongs to the glycocin family of RiPPs and contains a glucose moiety linked to a cysteine residue, an unprecedented post-translational modification assembled by a glycosyltransferase (SunS). Sublancin 168 has been shown to be extremely stable and has a narrow spectrum of activity with an unknown mode of action. Its extreme stability and unique structure have led us to hypothesize that sublancin has a novel antimicrobial mechanism of action. The solution NMR structure of sublancin has been solved for clues regarding its mechanism of action and provides an explanation for the previously reported high stability of sublancin 168. Various biochemical, microbiological, and genomic tools have been employed to characterize sublancin's activity. Data obtained from comparative genomic analysis and global gene expression using DNA microarrays has identified the PTS-glucose specific transport system as a possible mechanism by which sublancin could affect the cell. Current efforts include investigating sublancin's localization in the cell by fluorescent sublancin analogues. In addition, we are synthesizing sublancin analogues with a phosphorylated glycan to investigate the role of the sugar. A clear understanding of how this unique antibiotic exerts its antimicrobial activity may facilitate the development of new antibiotics.

### FRI-G7

#### **DEFINING THE BIOPHYSICAL STRUCTURE AND STABILITY OF H2A HISTONE VARIANTS HTAS-1 AND HTZ-1**

April Toledo, Raymond Esquerra.  
*San Francisco State University, San Francisco, CA.*

Histones compact DNA in cells by forming a protein-DNA complex known as the nucleosome core particle (NCP). How DNA is compacted affects how DNA is accessed for transcription, replication, and repair. Therefore, it is necessary to study the properties of histones. Understanding structure and physical stability will help us understand how histones play an

essential role in governing DNA chemistry. Nucleosome properties can be altered through the incorporation of histone variants that impact how and when DNA is accessed. This research will focus on 2 known H2A histone variants, HTAS-1 and HTZ-1, found in *Caenorhabditis elegans*. Their amino acid composition differs greatly from their isoform, specifically within regions that play important roles in NCP dynamics. HTAS-1 has 51% sequence identity to H2A, and HTZ-1 has 54% identity. The physical stabilities of HTAS-1/H2B and HTZ-1/H2B are being characterized and will be compared to H2A/H2B to further understanding of NCP dynamics. We hypothesize that the variant dimers will have a change in stability that will reflect DNA accessibility in their variant NCP. Histones were expressed in *E. coli* and purified using size exclusion and ion exchange chromatography. Equilibrium stabilities of histone monomers and dimers will be determined by urea-induced denaturation using circular dichroism. Studies will also be conducted in the presence of the co-solute trimethylamine N-oxide. The biophysical properties that will be defined with this research will provide insight into how HTAS-1 and HTZ-1 modulate nucleosome dynamics and DNA required processes.

#### **SAT-G10**

##### **IDENTIFICATION OF NOVEL INHIBITORS OF NEUTROPHIL EXTRACELLULAR TRAPS (NETS)**

Nancy E. Martinez<sup>1</sup>, Slava Ziegler<sup>1</sup>, Arturo Zychlinsky<sup>2</sup>, Herbert Waldmann<sup>1</sup>.

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Polymorphonuclear neutrophils are short-lived leukocytes that migrate to infected sites under the acute immune response where they phagocytose and degranulate to kill microbes. Neutrophils were found to form neutrophil extracellular traps (NETs). In this process, known as NETosis, the nuclear lobules disappear, the chromatin expands, and the DNA is expelled and is decorated with antimicrobial proteins. The signalling mechanisms leading to the formation of NETs are poorly understood. In addition, neutrophils are terminal cells and are not suitable for conventional analytical techniques, which complicate their study using genetic or other biological approaches. Here, we envisage a chemical biology approach to investigate the signalling processes regulating NET formation. The focus of this project is to identify the molecular targets involved in the NET formation process by using chemical inhibitors that may block this process at different stages. This approach may lead to the identification of novel therapeutic entities. To achieve this, a screen was first developed using isolated human neutrophils, and a commercial library was screened. Here, the inhibition of induced NET formation was analyzed using nuclear morphology and cell viability as readouts in a single protocol. Because of this screen, we could show that the Raf/MEK/ERK pathway is involved in NET formation through activation of NADPH oxidase and upregulation of anti-apoptotic proteins. In addition, the screening of a chemical library generated in the group enabled the identification of a novel compound class of inhibitors of NET formation. Further investigations to identify the molecular target of these inhibitors are ongoing.



#### **FRI-G4**

##### **CHARACTERIZATION OF CRYSTALLIZED BACTERIOPHYTOCHROME PHOTOCYCLE INTERMEDIATES**

Alba Katiria González Rivera, Katrina Forest.

*University of Wisconsin-Madison, Madison, WI.*

Bacteriophytochromes (BphP) are light-sensing histidine kinases that are part of a 2-component regulatory system. Photoconversion is characterized by a change in the photo-absorption profile resulting from a major structural change of the chromophore biliverdin within the protein. Excitation of the ground state Pr by 700 nm light promotes the transition into a second ground state Pfr. This process is reversible; exposure of Pfr to 750 nm light induces photoconversion to the Pr state. This photocycle has been extensively characterized in solution and by X-ray scattering from crystalline cryo-trapped intermediates. However, we are interested in characterizing the photoconversion of crystalline *Deinococcus radiodurans* BphP monomer without relying on cryotrapping. In our preliminary investigation, photoconversion was not observed in crystals, so we designed a variant of BphP, E185A, that we predict will disrupt crystal packing and allow photoconversion. Time-resolved spectroscopic studies of crystalline BphP-E185A will be undertaken by performing a visible-light scan on ground state BphP after excitation with ~700 nm light. This will help in identifying intermediate states of photoconversion that can be achieved in the crystal. Time-resolved X-ray crystallography will allow us to collect diffraction patterns of BphP crystals at specific time lapse intervals after photo-excitation. Using both spectroscopic and crystallographic techniques, we can structurally characterize the earliest intermediates in the transition from the Pr to the Pfr state.

#### **FRI-G1**

##### **INVESTIGATION OF RNA BINDING TO NANOPARTICLES FOR POTENTIAL USE IN GENE THERAPY SYSTEMS**

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Nanoparticles are defined as molecules that are 1 nm in size in at least 1 dimension, which contributes to their large surface area. Hydrotalcite, montmorillonite, halloysite, and graphene are nanoparticles that have garnered attention as potential drug delivery carriers in recent years. The low toxicity levels of these nanoparticles as well as their ability to interact with biomolecules, such as proteins and nucleic acids, is a key feature for gene therapy applications using nanotechnology. Studies have shown that single-stranded DNA, double-stranded DNA, and plasmid DNA bind well to these nanoparticles. Binding of RNA has not been extensively studied. With RNAi becoming an important gene therapy tool, finding suitable drug delivery vehicles for siRNAs is of crucial importance. In our studies, we have evaluated the binding efficiencies of different types of RNAs (ssRNA, dsRNA, and complex RNA structures) to different nanomaterials and compared them to DNA binding studies with the same nanoparticles. Furthermore, we also aim to characterize the mode of binding using X-ray diffraction and transmission electron microscopy. Our binding studies using hydrotalcite have shown similar binding efficiencies for ssRNA and ssDNA. The efficiencies were moderately greater than those

seen with dsRNA and dsDNA. Binding assays using montmorillonite revealed that binding of ssDNA was moderately stronger than that of ssRNA in the absence of added metal cations.

#### **FRI-G8**

##### **REDOX CONTROL OF PROTEIN ARGININE METHYLTRANSFERASE I (PRMT1) ACTIVITY**

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Elevated levels of asymmetric dimethylarginine (ADMA) correlate with risk factors for cardiovascular disease. ADMA is generated by the catabolism of proteins methylated on arginine residues by protein arginine methyltransferases (PRMTs), and is degraded by dimethylarginine dimethylaminohydrolase (DDAH). Reports have shown that DDAH activity is downregulated and PRMT1 protein expression is upregulated under oxidative stress conditions, leading many to conclude that ADMA accumulation occurs via increased synthesis by PRMTs and decreased degradation. However, we now report that the methyltransferase activity of PRMT1, the major PRMT isoform in humans, is impaired under oxidative conditions. Oxidized PRMT1 displays decreased activity, which can be rescued by reduction. This oxidation event involves one or more cysteine residues. We demonstrate a hydrogen peroxide concentration-dependent inhibition of PRMT1 activity that is readily reversed under physiological  $H_2O_2$  concentrations. Our results challenge the unilateral view that increased PRMT1 expression necessarily results in increased ADMA synthesis, but rather demonstrate that enzymatic activity can be regulated in a redox-sensitive manner. This also raises the possibility that PRMT1 could be a key player in the cellular oxidative stress response.

#### **FRI-G9**

##### **USE OF ANTIMICROBIAL POLYMERS AS A NOVEL ANTIFUNGAL APPROACH AGAINST *CANDIDA ALBICANS* BIOFILMS**

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The fungal pathogen, *Candida albicans*, is the fourth most common cause of nosocomial bloodstream infections worldwide. Increased drug resistance provided by formation of fungal biofilms limits the effectiveness of current antifungal drugs. We employed a new approach by using poly(phenylene ethynylene)-DABCO (PPE-DABCO), a non-toxic, photoactivated antimicrobial polymer, to determine its ability to enter and kill pathogens throughout fungal biofilm. PPE-DABCO can kill yeast in suspension cultures, but it is unclear how well it will penetrate thick biofilm structures. We added a lethal dose (20  $\mu$ g/ml) of PPE-DABCO or control Alexa Fluor 405 (AF405) at 100  $\mu$ M to *C. albicans* biofilms and measured diffusion of the compound into the film over 2 hours. The  $t_{1/2}$  of PPE-DABCO infiltration into the biofilm was 10 fold longer than AF405 infiltration when compared to non-biofilm diffusion. These results suggest PPE-DABCO interacts with the biofilm, but still allows for penetration. After 3 hours of binding, PPE-DABCO will be stimulated by 405 nm light, releasing reactive oxygen species. The killing efficiency of PPE-DABCO will be quantified by fluorescence of a DNA dye, DRAQ7. If greater fluorescence is measured in cells treated with PPE-DABCO than the untreated control,

killing ability will be confirmed. PPE-DABCO diffuses through *C. albicans* biofilm, indicating the electrostatic interaction as a positive characteristic for a compound diffusing through biofilm. Cell killing in *C. albicans* biofilm will continue to be studied, and if both are confirmed as expected, the traits of the compound can be used to further explore development of an effective, non-toxic anti-biofilm drug.

## BIOLOGY (GENERAL)

### SAT-G11

#### ACTIVATION OF ENOS PHOSPHORYLATION STATE AND NO PRODUCTION VIA ER- $\alpha$ AND ER- $\beta$ IN UTERINE ARTERY ENDOTHELIAL CELLS

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Uterine endothelial nitric oxide (NO) production is partly responsible for the maintenance of vasodilatation during physiologic states of high circulating estrogen levels such as pregnancy. Endothelial nitric oxidase synthase (eNOS) has several phosphorylation sites that correlate to its activity state and NO production. However, it is unknown if eNOS regulation depends on ER- $\alpha$  and/or ER- $\beta$ . We hypothesize that ER- $\alpha$  and ER- $\beta$  are capable of altering eNOS phosphorylation patterns and increase NO production. A series of experiments were set up. Endothelial cells were treated with the vehicle or increasing concentrations of E<sub>2</sub> $\beta$ . The cells were treated with E<sub>2</sub> $\beta$  for 0 to 30 minutes or were pre-treated with inhibitor, ICI-182, 780. We evaluated the eNOS phosphorylation changes at Ser635, Ser1177, and Thr495 via western blotting. Endothelial cells treated with E<sub>2</sub> $\beta$ , ATP, PPT (propylpyrazole-triol), and DPN (diarylpropionitrile) were also analyzed for total NO production. E<sub>2</sub> $\beta$  treatment increased stimulatory phosphorylations Ser635 and Ser1177 and decreased Thr495 phosphorylation. The increased in eNOS phosphorylation at Ser635 was blocked by ICI-182,780 pre-treatment. Surprisingly, E<sub>2</sub> $\beta$  and ICI-182,780 decreased the inhibitory phosphorylation at Thr495. Phosphorylation at Ser635 and Ser1177 were increased starting at 5 minutes of E<sub>2</sub> $\beta$  treatment, while the phosphorylation Thr495 was reduced after 30 minutes. Lastly, E<sub>2</sub> $\beta$ , ATP, PPT, and DPN treatments increase total NO production starting at 10 minutes and peaking at 30 minutes. These data support the hypothesis that E<sub>2</sub> $\beta$ -induced eNOS activation via its phosphorylation state in a dose and time-dependent manner although the inhibitory phosphorylation seemed to occur through an ER-independent mechanism. Our data also support the hypothesis that NO production is shown to increase by the activation of either ER- $\alpha$  or ER- $\beta$ .

### FRI-G11

#### A MULTILOCUS PHYLOGENY OF THE HOLARCTIC GROUND SQUIRREL, GENUS *UROCITELLUS*

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Squirrels (family Sciuridae) form a cosmopolitan group that colonized a range of habitats and environments. Within the Sciuridae, Holarctic ground squirrels (*Urocitellus*) comprise a genus

found predominantly in higher latitudes and altitudes of North America and Asia, including Alaska, Canada, and Siberia. However, despite decades of research on both the biogeography and socioecology of the group, the evolutionary relationships of the 12 species within the genus are poorly defined. In addition, the timing of colonization of the high-Arctic by 2 species, *U. undulatus* and *U. parryii*, remains unresolved. To better understand the phylogeny of *Urocitellus* and the number of Arctic colonizations, we used multilocus DNA sequence data (1 mitochondrial and 4 nuclear genes) and Bayesian species tree reconstruction. Despite some gene tree discordance, preliminary results suggest the Arctic was colonized twice. These independent events reflect the high adaptability of squirrels. Future research directions include sequencing additional loci and performing ancestral range reconstruction to more fully understand the evolutionary and biogeographic history of Holarctic ground squirrels and provide a rigorous temporal and spatial framework for future studies of adaptation in this diverse group.

#### **FRI-G10**

#### **MOLECULAR MECHANISMS OF NEURONAL SIGNALING BY MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I IMMUNE PROTEINS**

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Proteins of the major histocompatibility complex class I (MHCI) are best known for their role in the adaptive immune response. Recent studies show that MHCI proteins are also expressed by healthy neurons in the prenatal and postnatal brain and are unexpectedly critical for normal brain development and function. In the adult mouse hippocampus, MHCI limits synaptic transmission mediated by NMDA-type glutamate receptors and is required for NMDAR-dependent forms of hippocampal synaptic plasticity and hippocampus-dependent learning and memory. Although MHCI's binding partners in the immune response are relatively well-characterized, the molecular mechanisms by which MHCI performs these and other non-immune functions in neurons remain completely unknown. The extracellular domain of MHCI presents antigen while the cytoplasmic domain is dispensable for antigen presentation *in vitro* and has therefore long been considered non-functional. However, we and others have identified patches of conserved amino acid sequence in the MHCI cytoplasmic domain, hinting at as-yet unidentified functionality. Indeed, preliminary data from our lab is consistent with the possibility that the cytoplasmic domain is involved in non-immune signaling by MHCI in neurons. We are currently identifying and validating candidate binding partners for the MHCI cytoplasmic domain in neurons, using a combination of bioinformatic, molecular biological, electrophysiological, and biochemical approaches. Understanding the role of the MHCI cytoplasmic domain could provide insights into the molecular mechanisms by which MHCI influences circuit structure and function.

## CANCER BIOLOGY

### SAT-G14

#### USING BIOINFORMATICS TOOLS TO HELP DETERMINE IF HEAT SHOCK PROTEIN 70 (HSP70) IS A POTENTIAL BIOMARKER FOR HEPATOCELLULAR CARCINOMA

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Hepatocellular carcinoma (HCC) is the most common type of liver cancer in the world and patients generally will die within a year of its detection due to the lack of early diagnostic methods. As heat shock protein 70 (HSP70) is known to be overexpressed in HCC, it is important to determine if HSP70 can be a potential biomarker for the early detection of HCC. Protein-protein interaction (PPI) network databases were used to investigate whether HSP70 interacts with other known cancer-related proteins. If so, there is a high probability that HSP70 is specific to cancer and can be a potential biomarker for HCC. Once a correlation between HSP70 and HCC is found, then a homology analysis using proteins from the heat shock protein family is done in order to verify there are conserved regions across the protein family. An optimal biomarker has regions that are 90-100% conserved and can be also targeted by an antibody in the patient's sera. If a protein does not have highly conserved regions then it cannot serve as a good biomarker for cancer because there will be multiple mutations in the protein sequence that the antibody will not recognize. The results in this analysis will be used to help design wet-lab experiments for testing HSP70 as a possible biomarker and is expected to save valuable time and lab resources.

### FRI-G12

#### ROLES FOR EGFR AND IL-6 IN RHABDOMYOSARCOMA PATHOGENESIS

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Rhabdomyosarcoma (RMS) is a skeletal muscle-lineage, soft-tissue tumor, accounting for approximately 50% of all pediatric soft tissue sarcoma cases. Clinical treatments for high-risk RMS have not improved for 3 decades, arguing new genetic tools and insights are needed to probe and target RMS. Using a signaling network uncovered in a forward genetic screen using an RMS *Drosophila* model, we focus on evaluating the role of mis-regulated genetic networks in RMS pathobiology. One such pathway uncovered is the epidermal growth factor receptor (EGFR) pathway. Testing FDA-approved drugs that inhibit EGFR (e.g., Tarceva®) in RMS cell lines, we have found that Tarceva reduces RMS cell oncogenicity. Some RMS cell lines tested, however, show minimal to no response to Tarceva, suggesting the hypothesis that alternative/additional pathways facilitate RMS pathogenesis. Several prominent malignancies such as lung and prostate cancer have developed a mechanism to use both EGFR and IL-6 pathways to progress into a malignant phenotype, inducing proliferation, survival, and migration/invasion. We hypothesized that RMS exploits both EGFR and IL-6R pathways to enhance oncogenicity and questioned whether targeting EGFR and IL-6R in tandem would

result in an additive/synergistic decrease in RMS pathogenesis. Preliminary results of treating RMS cells with an anti-IL-6R monoclonal antibody (mAb) together with Tarceva demonstrates increased blockage of RMS oncogenicity than when treating with IL-6 mAb or Tarceva alone. Since humanized -IL-6R mAb (Tocilizumab®) is approved for the clinical treatment of various diseases (e.g., rheumatoid arthritis, ovarian carcinoma), we anticipate Tarceva/IL-6 mAb combination therapy might represent a new avenue to clinically target RMS.

### **FRI-G13**

#### **DEVELOPMENT OF A NOVEL NEURAL CREST EMT REPORTER LINE FOR *IN VIVO* SCREENING OF EMT AND CELL MIGRATION INHIBITORS**

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The epithelial to mesenchymal transition (EMT) plays a crucial role during development, and aberrant reactivation of EMT in tumor cells promotes metastasis. Mechanisms that control EMT remain incompletely understood, hampering efforts to target EMT in cancer patients. To identify upstream inducers and downstream effectors of EMT we have developed a novel zebrafish neural crest (NC) EMT reporter line, *Tg(snail1b:GFP)*, for *in vivo* screening of EMT and cell migration inhibitors. After screening a number of candidate kinase inhibitors for their ability to block NC migration in live *Tg(snail1b:GFP)* embryos, we found that the AXL receptor tyrosine kinase (RTK) inhibitor, HCI-2084, potently blocks hindbrain morphogenesis and cranial NC cell migration. Treatment of embryos at the 3-somite stage with HCI-2084 significantly decreases *twist1a* expression, a key regulator of EMT, blocks differentiation of *dlx2a*-expressing chondrogenic precursors, and instead promotes the differentiation of *mitfa*-expressing melanophore precursors that form adjacent to the neural tube. RNA-Seq analysis revealed that HCI-2084 treated embryos have a significant upregulation of retinoic acid (RA) signaling. Co-treatment of HCI-2084 with DEAB, an RA inhibitor, rescues the hindbrain and NC migration and differentiation defects caused by HCI-2084 treatment. We are currently investigating the potential role of AXL in NC cell migration and differentiation, and evaluating HCI-2084 as a possible therapy for neuroblastoma by using the zebrafish neuroblastoma pre-clinical model and human neuroblastoma cells *in vitro*.

### **SAT-G12**

#### **THE TUMOR SUPPRESSOR ROLE OF THE ARYL HYDROCARBON RECEPTOR IN COLORECTAL TUMORIGENESIS**

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Colorectal cancer (CRC) is the third leading cause of cancer-related mortality in the United States. It is estimated that perhaps 20% to 30% of all colorectal cancers can be attributed to genetics while the remaining cases can be attributed to environmental stimulation. Although

the pathogenesis of CRC-associated environmental stimuli is not clearly understood, dysfunction of intestinal innate immunity by these stimulations is thought to be integral in the pathogenesis. Recent studies have revealed that the aryl hydrocarbon receptor (AHR), a transcriptional factor and a mediator for environmental pollutants, plays an integral role in intestinal homeostasis through regulating intestinal innate immune cells. Therefore, we hypothesized that the AHR is involved in colorectal tumorigenesis. To examine this hypothesis, we performed a 2-stage colorectal tumor initiation-promotion assay using azoxymethane (AOM) and dextran sodium sulfate (DSS). Using this CRC model, we compared the susceptibility to AOM/DSS-colorectal tumorigenesis in an *Ahr* null and WT mice. We found that the susceptibility to AOM/DSS-induced colorectal tumorigenesis was significantly increased in *Ahr* deletion mouse model as compared to WT mice. The increase of AOM/DSS-induced colorectal tumors in the *Ahr* null mice was a consequence of enhanced AOM-tumor initiation and DSS-tumor promoting colitis. These results suggest that AHR plays a protective role in the AOM/DSS-induced CRC.

### **SAT-G13**

#### **PHYSICAL ACTIVITY DURING PREGNANCY CONVEYS PROTECTIVENESS AGAINST MAMMARY TUMORIGENESIS IN RAT OFFSPRING**

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Lifestyle factors such as physical activity and diet play a role in attenuating the incidence of breast cancer in women. Current research shows that exercise during pregnancy can convey long term health benefits to the offspring. The goal of this project was to determine if maternal physical activity during pregnancy could lead to reduced mammary tumor development in female offspring. Toward this goal, female rats were divided into 2 groups, sedentary (S) and exercise (E), with the exercise group given access to a running wheel during pregnancy. Female pups were weaned at 21 days of age, fed a high fat (HF) diet, and did not have access to a running wheel. At 6-weeks of age, pups were given a single injection of N-methyl-N-nitrosourea (MNU) intraperitoneally at 50 mg/kg. The study was conducted for 15 weeks and the developing tumors were palpated and measured with calipers. Endpoint analyses revealed that pups from dams with physical activity (exercise) had a substantially lower tumor incidence (42.86%) compared to pups from sedentary dams (sedentary) having 100% tumor incidence. Exercise pups had a higher frequency of tumors at 1.67 (S.E.  $\pm$  0.44) tumors/rat than sedentary 1.17 (S.E.  $\pm$  0.17). Interestingly, there was no histological difference in tumor grading between the 2 groups. These are the first data to demonstrate that short-term physical activity during pregnancy can lead to reduced tumor development in offspring. This study provides an important foundation for the possibility of behavior modification for the prevention of cancers.

## CELL/MOLECULAR BIOLOGY

### SAT-G17

#### **DETERMINING THE HLA HAPLOTYPES OF WOMEN AFFLICTED WITH TRIPLE-NEGATIVE BREAST CANCER**

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Triple-negative breast cancer (TNBC) is a highly aggressive breast cancer subtype that affects African and African-American (AA) women. It is characterized by the lack of expression of the estrogen receptor, progesterone receptor, and overproduction of the human epidermal-2 receptor. Absence of these receptors may be contributing to the poor prognosis for TNBC because these are targets for most effective breast cancer treatments. Poor prognosis for TNBC contributes to the growing health disparity in breast cancer mortality found for AA women. Previous studies demonstrated that women with African ancestry have the highest incidence rates for TNBC based on self-reporting of racial background; however, no studies have demonstrated a genetic link between African ancestry and TNBC. We predict that a link exists based on high incidence rates of TNBC for women presumed to have significant African genetic ancestry. In the United States, TNBC accounts for only 15 - 20% of all breast cancer and, of these, AA women comprise 32% and Latinas 25% of cases. Latinas are a human subpopulation with European, Native American, and African ancestry making them a suitable population for studying the genetic link between TNBC and African ancestry. At the genetic level, human ancestry can be studied by determining HLA haplotypes. The HLA haplotypes of 100 Latinas, 31 with TNBC, 34 with triple-positive breast cancer, and 35 unaffected controls will be determined. Determination of common HLA haplotypes in TNBC may contribute to the advancement of diagnosis and treatment of TNBC by demonstrating a genetic link among women diagnosed with this disease.

### SAT-G18

#### **ISOLATION, EXPRESSION, AND CHARACTERIZATION OF AZOREDUCTASE FROM *PSEUDOMONAS AERUGINOSA* STRAIN FRD1**

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*Pseudomonas aeruginosa* is one organism that has become increasingly antibiotic resistant causing severe lung infections, which are detrimental to patients, especially those with cystic fibrosis. The cystic fibrosis isolate *P. aeruginosa* FRD1 is a mucoid strain that can easily survive in the lungs on infection. Preliminary data shows that FRD1 is capable of surviving as well as decolorizing azo dyes when grown in dye-stress culture environments, suggesting the presence of azoreductase enzymes. Azoreductase not only reduces azo dyes, but has dual function through the activity of quinone reduction as well. This function of quinone reduction allows for the neutralization of reactive oxygen species (ROH). Our hypothesis is that azoreductase enhances the survivability of the bacterium when exposed to stressful environments, thereby enhancing FRD1 virulence and antibiotic resistance. Therefore, this study was to isolate and



express azoreductase for future functional comparisons of azoreductase gene(s) present in FRD1 to that of the known PAO1 non-mucoid strain in order to determine the role it may have for the pathogen. In conclusion, the results could support a novel mechanism associated with FRD1 virulence and antibiotic resistance possibly providing an avenue for the treatment of *P. aeruginosa* lung infections.

#### **FRI-G18**

##### **STRUCTURAL AND FUNCTIONAL CHARACTERIZATION OF HUMAN SMALL GLUTAMINE RICH TPR CONTAINING PROTEIN ALPHA**

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Steroid hormone receptors (SHRs) are ligand-dependent transcription factors which, upon binding hormone, translocate to the nucleus and regulate gene expression responsible for growth, development, and homeostasis of higher ordered eukaryotes. The Hsp90-Hsp70 chaperone machinery plays a crucial role for SHRs to achieve the hormone binding conformation. Human small glutamine rich tetratricopeptide repeat (TPR) containing protein  $\alpha$  (SGT $\alpha$ ) is a recently identified protein that has a characteristic Hsp90-binding TPR domain and is a key participant in the androgen receptor (AR) signaling pathway. We have demonstrated that SGT $\alpha$  binds to both Hsp70 ( $k_d = 6 \mu M$ ) and Hsp90 ( $k_d = 11 \mu M$ ). Yeast-based functional assays demonstrate that SGT $\alpha$  is a regulator of glucocorticoid (GR) and progesterone (PR) receptors but has no effects on estrogen and mineralocorticoid receptor signaling pathways. In addition to a functional effect, we have demonstrated SGT $\alpha$  association with GR and PR complexes by way of yeast 2-hybrid screening. Studies in the yeast reporter system demonstrate that SGT $\alpha$  expression can completely abrogate the regulation of receptor function by the cochaperone FKBP52. *In vitro* studies have shown no direct effect of SGT $\alpha$  on the formation of PR-Hsp90 complexes or on the ability of PR to bind hormones within complexes. A recent study suggested that SGT $\alpha$  antagonizes BAG6-mediated protein triage by promoting deubiquitination of substrates. Therefore, we hypothesize that the inhibitory effect of SGT $\alpha$  on receptor activity results from deubiquitination leading to a disruption of receptor recycling and activity. Future studies will be aimed at exploring the effects of SGT $\alpha$  on receptor ubiquitination.

#### **FRI-G16**

##### **THE ROLE OF THE TRANSCRIPTION FACTOR OCT1 AND ITS REGULATION IN STEM CELLS**

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Oct1 (*Pou2f1*) is a member of the POU family of transcription factors. Oct1 is ubiquitously expressed in embryonic and adult tissues with higher protein expression observed in stem cell compartments. Previous work in our laboratory has shown that Oct1 co-localizes with known stem cell markers in different tissues and that it is a determinant of somatic and cancer stem cell phenotypes. In order to determine the role of Oct1 in somatic stem cells and in tumor initiation and progression, we are using 3 mouse models where Oct1 is deleted in the stem cells of the colon, small intestine, and lung. Our preliminary data shows that Oct1 deletion in the

colon does not affect homeostasis but instead prevents regeneration. Oct1 is known to be highly modified post translationally. The functions of phosphorylation and glycosylation events in the Oct1 protein have been investigated, but the role of the 2 ubiquitination sites has not been determined. BRCA1 is an E3 ligase that has been shown to interact with Oct1. Because Oct1 protein, but not mRNA levels, are increased in stem cell compartments, Oct1 may be stabilized at the protein level in stem cells. Notch signaling is known to play an important role in stem cell maintenance in the intestine, and treatment of the breast cancer cell line HCC1937 with  $\gamma$ -secretase inhibitors shows a significant decrease in Oct1 protein levels. We hypothesize that Oct1 is stabilized by Notch signaling in stem cell compartments, causing accumulation of the protein and leading to regeneration.

#### **FRI-G14**

##### **IDENTIFICATION OF NOVEL SYNERGISTIC TARGETS FOR COMBINATION TREATMENTS WITH EICOSAPENTAENOIC ACID AGAINST INFLAMMATORY BREAST CANCER**

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Inflammatory breast cancer (IBC) is the most aggressive form of breast cancer, causing a disproportionate number of breast cancer related deaths. An incomplete molecular understanding of IBC hampers the development of therapeutic strategies and, as such, there is an urgent need to identify causative factors. We have reported that molecular mediators of inflammation such as COX-2 can promote IBC progression. A known inhibitor of COX2, eicosapentaenoic acid (EPA), is an anti-inflammatory compound that can inhibit tumor growth, but remains to be tested in IBC. To rationalize an EPA-based combination drug therapy in IBC, we sought to identify signaling pathways that, when inhibited, boost the cytotoxicity of EPA. We hypothesize the anti-tumor efficacy of EPA is enhanced in combination with inhibition of a novel kinase. To this end, we designed a synthetic, lethal, high-throughput screen that measured the ability of EPA to kill SUM149 IBC cells with concurrent silencing of specific genes. Our siRNA library targeted 939 cell-signaling-related genes, and we report that our screen had sufficient sensitivity to identify candidates that enhanced the cytotoxicity of EPA at an IC50 dose (Z-factor = 0.756). We further investigate the relevance of normalization methods for targeting gene discovery: Z-score (71 genes), B-score (13 genes), and regional normalization (57 genes). Candidate genes will be validated through *in vitro* cytotoxicity assays as a prelude to testing therapeutic relevance *in vivo* using preclinical IBC models. The successful completion of this study will provide preclinical evidence for an EPA-based, combination therapy for patients with IBC.

## **SAT-G20**

### **THE EFFECT OF *POLEROVIRUS* P0 EXPRESSION ON SKP1–CULLIN F-BOX E3 UBIQUITIN LIGASE TARGETING IN *NICOTIANA BENTHAMIANA***

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Potato leafroll virus (PLRV) is a +ssRNA virus that induces leaf rolling and phloem necrosis in plants. PLRV infection begins with the expression of P0, a multifunctional F-box protein that suppresses RNA-interference by degradation of argonaute (AGO1) to promote viral replication in host cells. While the interaction between P0 and AGO1 has been characterized to understand its role in suppressing RNA interference, conflicting reports have created controversy regarding the role of P0 in proteasome-mediated degradation. P0 is a potential F-box protein, being shown previously to interact with the SKP1 component of SKP1–Cullin F-box (SCF) E3 ubiquitin ligases. SCF E3 ligases target proteins with PEST motifs for degradation, which suggests that P0 may interfere with PEST targeting through its interaction with SCF E3 ligases. However, AGO1, a member of the AGO family that is the only confirmed target of P0, is degraded via the autophagy pathway instead of proteasome-mediated degradation. This apparent contradiction in P0 function may be resolved when analyzing other PLRV proteins. We have identified 2 PLRV proteins, RNA-dependent RNA polymerase (P2) and minor capsid protein (P5), that exhibit potential PEST motifs. The presence of these PEST motifs in P2 and P5 suggest they are targeted by SCF E3 ligase for degradation. Since P2 and P5 are essential for viral replication and transmission, P0 may alter SCF E3 targeting to preserve P2 and P5 expression in host cells. Our research may help clarify effects of P0 in both proteasome degradation and in AGO1 autophagy.

## **FRI-G21**

### **RIBOSOME PROFILING REVEALS PROTEOME DIVERSIFICATION VIA POTENTIAL ALTERNATIVE START SITES IN *TRYPANOSOMA BRUCEI***

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The diverse nature of the proteome has led to the discovery of mechanisms that can account for the disparities between the number of proteins compared to the relatively small number of genes. This is especially true in vertebrates, where mechanisms of alternative splicing such as intron retention and exon skipping can account for much of the diversity. However, outside of vertebrates, known mechanisms driving proteomic diversification in other eukaryotes are sparse. One species of interest is the human blood parasite *Trypanosoma brucei*, found to have minimal regulation at the transcriptional level. This lack of regulation opens the door to the possibility that post-transcriptional or post-translational regulation plays a crucial role in proteome diversification. One example is the use of alternative start sites within a gene's coding sequence to create separate protein products. A genome-wide analysis was performed to identify potential alternative start sites (PATSS) by mapping ribosome footprints to current annotations. These footprints are snapshots of mRNA being actively translated by the ribosome and can be used to create "peaks" or aggregates of reads, which indicate the presence of

PATSS. To determine the possibility that PATSSs function as translation start sites, we compared peaks across known translation start site AUGs and normal methionine coding AUGs. The goal is to use ribosome profiling in an effort to determine if PATSSs at downstream AUGs are truly alternative start sites and to use comparative analysis to gauge the wide-spread genetic functionality of the alternative start sites within *T. brucei*.

### **SAT-G23**

#### **C. ELEGANS HISTONE H2A VARIANT'S TRANSCRIPTIONAL ROLE DURING SPERMATOGENESIS**

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One key contributor to fertility is proper sperm development. Sperm development is managed by the packaging of chromatin, composed of DNA wrapped around histone proteins. How tightly DNA is wrapped around histones can affect how accessible genes are for activation. Canonical histones are replaced by specialized variants, which assist in regulating chromatin structure. During sperm development, core histone H2A is replaced by variants HTZ-1 and HTAS-1. HTZ-1 is 54% identical to H2A, expressed in all cell types, and present at 23% of all *Caenorhabditis elegans* promoters. While HTZ-1 is present throughout the male germ line, HTAS-1 is incorporated into sperm chromatin during a period of global transcriptional silencing. Previous data shows that both variants co-localize with each other during later stages of spermatogenesis, a time when spermatids are highly compacted. Despite their presence in spermatogenesis, the transcriptional role of these histone variants is not fully known. Using the *C. elegans* model system, we will study the localization of these two variants with regards to active and inactive chromatin during spermatogenesis. We hypothesize that while HTZ-1 will aid in gene accessibility for transcription, HTAS-1 will assist in transcriptional silencing. In studying H2A histone variants in spermatogenesis, we can better understand their function in gene regulation and identify their unique role in fertility.

### **FRI-G15**

#### **PUTATIVE PROTAMINES, SPCH-1/2/3, PLAY A ROLE IN FERTILITY**

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Male infertility is a significant medical concern for millions around the world. A major cause of male infertility is the improper compaction of sperm chromatin during spermatogenesis. Small proteins called protamines facilitate this compaction, yet their protein to protein interactions and exact contribution to fertility is unknown. Protamine identification and study is complicated by the fact they exhibit high sequence variability, resulting in little to no homology across species. Proteomic analysis identified 3 novel proteins, SPCH-1/2/3, enriched in the sperm chromatin of *C. elegans*. We hypothesize that SPCH-1/2/3 are *C. elegans* protamines that contribute to fertility through proper DNA compaction. Despite the high level of identity between SPCH-1/2/3 (88 - 99%), *spch-2* mutants produce progeny at only 33% of wild type, while *spch-1* and *spch-3* counts are similar to wild type. Further, *spch-3,spch-1* double mutants do not show reduced progeny numbers. These findings suggest that SPCH-2 contributes to

fertility. SPCH proteins likely contribute to fertility through compaction and packaging of sperm DNA. Antibody staining of fixed male germlines reveals SPCH localization around the condensed nuclei of mature sperm. Further, SPCH-1/2/3 are removed immediately after fertilization as the paternal pronucleus decondenses. Interestingly, mass spec analysis shows that SPCH-1/2/3 are highly phosphorylated (82 - 88%) at sites that differentiate between SPCH-1 and SPCH-2/3. This may be part of a mechanism for the cell machinery to distinguish between the 3 SPCH proteins. Removing the sites of differential phosphorylation using CRISPR will provide further evidence for the function of this modification.

#### **SAT-G24**

##### **EVALUATION OF THE *IN VIVO* ROLE OF A COLD-INDUCIBLE RNA BINDING PROTEIN (CIRP)**

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RNA binding proteins (RBPs) post-transcriptionally regulate gene expression at the mRNA level. Many RBPs associate with the regulatory sequences in the 5' and 3' untranslated regions of mRNA encoding, cancer-associated genes, increasing their expression. Furthermore, dysfunction of several RBPs is associated with cancer: they regulate target genes that promote cell growth, survival, and proliferation. Our current knowledge of RBPs and their role in regulating cancer-associated genes is largely based on *in vitro* studies. Our current study seeks to determine the *in vivo* role of cold-inducible RBP (CIRP) that is overexpressed in breast cancer. In cultured cells, CIRP promotes cell proliferation and survival, both hallmarks of cancer. Using mice expressing the human CIRP (hCIRP) transgene in the mammary epithelium, we compared proliferation and apoptosis during mammary gland development between wild-type mice and hCIRP mice. CIRP's effects on mammary tumor growth were also assessed using double-transgenic hCIRP/PyMT mice. Mice expressing Polyoma virus middle T antigen (PyMT) in the mammary epithelium develop tumors by ~7 weeks of age. Contrary to previous *in vitro* studies, our current data suggests that CIRP inhibits proliferation and slows tumor growth. These data may provide us with a more precise understanding of the *in vivo* function of CIRP.

#### **SAT-G19**

##### **IDENTIFYING CANDIDATE SUBSTRATES OF THE LEUCINE-RICH REPEAT KINASE 2 (LRRK2) BY MASS SPECTROMETRY-BASED PROTEOMICS**

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Mutations in human leucine-rich repeat kinase 2 (LRRK2) contribute to genetic forms of Parkinson's disease (PD) in people and related phenotypes in model organisms. However, the biologically relevant substrates for LRRK2 are not yet known, and to what extent they play a role in cell signaling. In this work, we ask: what are the *in vivo* effectors of LRRK2 phosphorylation in a fly model of PD? We apply phosphopeptide enrichment, peptide fractionation, and quantitative mass-spectrometry to interrogate the neuronal proteome for direct and indirect effectors of LRRK2. We use a transgenic fly model to express wild-type human LRRK2 (hLRRK2-WT) or a hyperactive kinase mutant of human LRRK2 (hLRRK2-mutant)

throughout the brain of the fly. We compared differences in protein abundance and phosphorylation of proteins. Increased phosphorylation on specific peptide sequences reveals candidate substrates for *in vivo* activity. Additionally, we present an *in vitro* kinase reaction of LRRK2 on peptides to discover direct sites of LRRK2 phosphorylation on specific proteins. The intersection of *in vivo* substrate candidates and *in vitro* substrates provides a list of potential bona-fide, biologically relevant substrates. These proteins may play a role in the signaling mediated by LRRK2 and provide insights into the mechanisms of LRRK2-related Parkinsonian phenotypes.

## **FRI-G22**

### **COMPARATIVE GENOMICS SHEDS LIGHT ON THE MYSTERY OF TRANS-SPLICING**

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One of the largest open mysteries of genomic/transcriptomic structure involves so-called spliced leader trans-splicing (SLTS), in which a short RNA tag transcribed from a single genomic locus, is added to the 5' end of gene transcripts of various genes. SLTS has been observed in diverse eukaryotes in a pattern strongly suggesting that SLTS systems have evolved independently many times. This striking convergence of molecular evolution suggests important functions for SLTS; however, no general function is known. Recent transcriptomic studies have revealed that many genes undergo widespread alternative trans-splicing (ATS), opening up the possibility that SLTS plays important roles in transcriptome diversification and/or regulation. One possibility is that ATS leads to alternative N-terminal protein isoforms by use of an internal alternative AUG as a translation initiation site. For instance, 2 trans-splicing isoforms of the isoleucyl-tRNA synthetase gene in *T. cruzi* encode proteins with different N-terminal cellular localization signals. Another possibility is that ATS plays roles in gene regulation, either by splicing at alternative 5' UTR sites to generate alternative 5' UTRs, or by disrupting the protein-coding sequence by splicing downstream of the functional start. We performed the first comparative genome-wide study of trans-splicing function by comparing TS and ATS patterns in orthologous genes between two deeply diverged trypanosome parasites. Our results indicate the functional importance of some cases of trans-splicing and provide the first estimates of the extent and mechanism of trans-splicing function in important human parasites.

## **SAT-G16**

### **DETERMINING THE ROLE OF THE HISTONE VARIANT HTZ-1 IN DNA TRANSCRIPTION AND GENE REGULATION IN *CAENORHABDITIS ELEGANS***

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Histones are the proteins that wrap DNA in order to condense it into a chromosome. Apart from the canonical histones H2A, H2B, H3, and H4, there exist histone variants. These variants have specific expression, localization, and function. For example, H2A.Z is ubiquitously expressed in all eukaryotes, localizes at promoter regions, and regulates transcription. H2A.Z

analog HTZ-1 in *C. elegans* is a well-conserved histone H2A variant that plays a role in chromosome segregation, genome integrity, and gene regulation. The incorporation of HTZ-1 histone variant into nucleosomes contributes to architectural changes in chromosomes. However, how an HTZ-1 histone variant leads to changes in chromatin structure and dynamics in *C. elegans* during transcription is poorly understood. We created recombinant *C. elegans* nucleosome and studied the role of HTZ-1 in gene regulation. We also created chimera proteins where we swapped domains of H2A with HTZ-1 to determine the roles of different domains in the accessibility of the nucleosomal DNA. We used restriction enzymes assay (REA) and fluorescence resonance energy transfer (FRET) to investigate the role of histone HTZ-1 *in-vitro*. We found that HTZ-1 nucleosomes increase DNA accessibility in comparison to H2A nucleosomes. We also found that the docking domain of HTZ-1 was responsible for an increase in stability of nucleosomes containing HTZ-1 protein. This implies that nucleosomes containing HTZ-1 variants are more accessible and more stable than nucleosomes composed of only wild-type histones.

### **SAT-G21**

#### **IDENTIFICATION OF 3'PRIMEUTR ELEMENTS THAT INHIBIT NONSENSE-MEDIATED DECAY**

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Nonsense-mediated decay (NMD) is an mRNA quality-control process that targets mRNAs containing premature termination codons (PTCs) for degradation and therefore prevents expression of potentially deleterious truncated proteins. The recognition of PTC is a quite complex process and is known to be influenced by the size of the 3' untranslated region (3'UTR). Hence, mRNAs with long 3'UTRs are usually targeted for NMD. However, many physiological mRNAs with long 3'UTRs seem to be resistant to NMD. The focus of this investigation is to determine how these mRNAs with long 3'UTRs evade NMD. In this study, we used plasmids expressing mRNA reporters containing the long 3'UTR of selected mRNA candidates under the control of a tetracycline-dependent promoter. After transfection in mammalian cells, the stability of these mRNAs was assessed by transcriptional induction followed by rapid transcription shutoff using tetracycline. Cells were harvested at different times after transcriptional shutoff, and mRNA levels were quantified by northern blot to determine mRNA half-lives. We identified 3'UTRs longer than 1,000 nucleotides that evade NMD. We performed extensive mutagenesis to narrow down elements responsible for NMD evasion. We demonstrated that several candidates contain *cis* elements that are sufficient to inhibit NMD and are located within the first 200 nucleotides downstream of the PTC. Further studies are necessary to decipher the mechanism by which long 3'UTRs evade NMD. Considering the crucial role of NMD in mRNA surveillance as well as gene expression, uncovering the mechanisms that allow mRNAs to evade NMD is essential to better understand NMD regulation.

## **SAT-G15**

### **MICROTUBULE ACTIVITY IN MITOTIC ENDOPLASMIC RETICULUM REORGANIZATION**

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The endoplasmic reticulum (ER) is the largest organelle in the eukaryotic cell and performs several functions to maintain cellular homeostasis including lipid synthesis and posttranslational modification. The ER maintains contact with several parts of the cell including the Golgi apparatus and the mitochondria by using microtubules as a scaffold. However, it is poorly understood how the ER interacts with the microtubule-based mitotic spindle during cell division. The ATPase spastin is a microtubule-severing protein that is associated with the ER, but its function during cell division has yet to be determined. We hypothesize that spastin is the protein that facilitates the ER's interactions with the mitotic spindle and controls the reorganization and division of the ER during mitosis. We will express and purify a recombinant wildtype, constitutively active and dominant negative spastin constructs, and inject them during the rapid mitotic divisions in the early *Drosophila melanogaster* embryo. We will assay the effects of each construct on the localization and movement of ER during mitosis. In addition, we will perform an RNAi-mediated knockdown of spastin in the early embryo and examine ER morphology and movement around the mitotic spindle during mitosis. We will also create a fluorescently tagged wild-type spastin construct and inject it into the embryo to determine localization of spastin during mitosis. These experiments should help us determine a molecular mechanism for ER movement and provide a better understanding of organelle inheritance during cell division.

## **SAT-G22**

### **NOVEL GENETICALLY ENCODED SMALL ILLUMINANTS (GESI) FOR DETECTION OF SPECIFIC PROTEIN TYROSINE KINASE ACTIVITY IN LIVING CELLS AND FOR HIGH-THROUGHPUT DRUG SCREENING**

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Protein post-translational modifications (PTMs) such as phosphorylation are essential for all levels of cellular regulations including oncogenesis. Thus, it is very important to have tools that can provide a spatiotemporal view of the function of PTMs in living cells. Green fluorescent protein (GFP) is limited due to its large size and may interfere with the function of host proteins. Our goal is to develop a new class of genetically encoded small illuminants (GESI) composed of 12 to 19 amino acids to track the PTMs in living cells. Using immobilized one-bead-one-compound (OBOC) combinatorial library screening, we recently developed short peptides that specifically activate the fluorescence of an organic dye, malachite green (MG), upon binding. In this 19-mer peptide library, we have 11-mer known Bcr-Abl tyrosine kinase substrate peptides placed at the N-terminus of a random octapeptide. The library was then treated with hydrofluoric acid (HF), and 4 beads that lost the fluorescence were physically isolated and sequenced. Then, these positive GESI peptide sequences were genetically cloned



at the C- and N-terminal portions of 3 different constructs such as N-LCK-Cerulean-GESI-C, N-Cerulean-GESI-C, and N-GESI-Cerulean and then transfected into K562 cells. MG was added to the culture medium, and confocal microscopy was performed. Co-localization of cerulean fluorescence and MG on the cell membrane in LCK-cerulean-GESI transfected cells was monitored. Gleevec (imatinib mesylate) is an anti-cancer drug that blocks Bcr-Abl tyrosine kinase. Cells treated with Gleevec showed no fluorescence for MG. Thus, GESI peptides can be used as potential sensors of PMTs in the cell.

### **FRI-G23**

#### **LEVELS OF COMPENSATION BETWEEN HISTONE H2A VARIANTS IN *C. ELEGANS***

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Sperm chromatin abnormalities or DNA damage can lead to male infertility. Histones, proteins that package DNA, are involved in tightening or loosening DNA for transcription. The DNA gets wrapped around a core of 4 different types of histones, one of which is H2A. Canonical H2A is replaced by different variants of H2A, each of which plays distinct roles in growth and development in *Caenorhabditis elegans*. One such variant, HTZ-1, is found in every cell of the developing embryo and is essential to normal development. HTAS-1, a sperm-specific histone variant, localizes with meiotic chromosomes and is found on mature sperm. In an *htas-1* mutant, there is an 18% decrease in progeny. Furthermore, the deletion of another H2A variant, *his-35*, shows a 35% decrease in progeny. *htas-1* and *his-35* double mutants show complete sterility. This data shows that HTAS-1 may partially compensate for HIS-35, suggesting that histone variants may share a similar role in fertility. We will ask whether HTZ-1 can compensate for HTAS-1 by inserting HTZ-1 into the location and time where HTAS-1 is normally expressed. By expressing HTZ-1 in the *htas-1;his-35* double mutant, we can quantify the progeny levels to determine the degree of rescue provided by HTZ-1 compared with HTAS-1. The results of this experiment would show whether histone H2A variants are similar enough in function to compensate for the loss of function of another variant during spermatogenesis.

## ECOLOGY/EVOLUTION

### FRI-G24

#### QUANTITATIVE TRAIT LOCUS ANALYSIS UNDER ENVIRONMENTAL STRESS IN AN INTERTIDAL COPEPOD, *TIGRIOPUS CALIFORNICUS*

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As natural habitats are exposed to increasing environmental changes, species must adapt to new conditions in order to survive. When *Tigriopus californicus*, a copepod adapted to the high intertidal zone, was challenged with high temperature and high and low salinity stress, we observed that more individuals from southern populations were likely to survive high thermal and salinity stress, while the northern populations have an advantage under low salinity. We hypothesized that some parts of the genome associated with survivorship would vary between crosses and between stressors, indicating a stress-specific response, while some loci would associate with more than one stressor, indicating a general or shared response. We generated 2 hybrid F<sub>2</sub> groups from 1 southern population (San Diego, California) crossed to 2 northern populations (Santa Cruz, California, and Friday Harbor, Washington). F<sub>2</sub> adults were assayed for tolerance to the three stressors and genotyped for 61 single nucleotide polymorphisms (SNPs) across the genome. Using quantitative trait locus (QTL) analysis, we examined the genetic loci associated with survivorship under each of these stressors for males and females. Putative QTL were found to differ between stressors and crosses, indicating that populations may employ different mechanisms for the same stress, and that different loci confer an advantage under different stressors. In a dynamic environment subjected to many stressors, a diverse range of stress responses may be advantageous and contribute to overall survivorship.

**FRI-G26****TRADITIONAL ECOLOGICAL KNOWLEDGE AND FINE-SCALE HABITAT CHARACTERISTICS OF PACIFIC LAMPREY *ENTOSPHENUS TRIDENTATUS* IN THE WILLAMETTE RIVER BASIN, OREGON**

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The Willamette River currently supports one of the last traditional Native American harvest sites of Pacific lamprey at Willamette Falls, and consists of a population that continues to persist given the greater losses in adjacent basins. To further address research and monitoring needs of all life stages, we studied 2 individual microhabitat associations of larval lamprey in the Willamette River Basin. Study objectives were to 1) estimate the substrate size most closely associated with larval lamprey abundance, and 2) estimate the influence of organic material upon larval lamprey abundance. We used a backpack electrofisher to sample larval lamprey in 6 wadeable Willamette River tributaries. In each tributary, we used a nested 2-pass sample design at a lower, middle, and upper reach (each reach composed of ten 1-m<sup>2</sup> quadrats). We collected a stream sediment core sample from each available quadrat area to examine ammocoete habitat quality and associations with larval lamprey CPUE (catch per unit effort). We used particle size sieve analysis to estimate dominant substrate size class per sample and measured organic matter by loss on ignition. Larvae were present in each reach and detected in 37% of the quadrats. Results indicate larval presence was strongly associated with habitats with predominantly medium fine sand (0.25 - 0.50 mm) substrate, while organic material was associated with larval presence. Our study indicates that substrate particle size was an important variable for larval lamprey habitat. To promote conservation of the Pacific lamprey, activities that promote natural river flow and distribution of fine sediment may be of benefit.

**FRI-G25****THE ZEBRAFISH VISUAL SYSTEM: MATHEMATICAL MODELING AND EXPERIMENTATION**

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Vision is a sensory modality that is fundamental to the biology of a tremendous diversity of animals. From hatching to senescence, fish depend on sight for essential behaviors such as foraging and predator evasion. In zebrafish, these functions are performed despite large changes in the shape of the eye during growth. It is not clear if these changes match the ecological conditions of each life history stage or are the product of developmental constraints. To help resolve this mystery, we combined mathematical modeling and experimentation to determine how the optics of the visual system change and affect behavior over the growth of zebrafish. Zebrafish exhibit an unconditioned behavior, the optokinetic response (OKR), where the eyes move to track horizontal motion of vertical stripes. Using measurements of the OKR, visual acuity and contrast sensitivity will be determined at 5 stages of growth (5, 10, 21, 44, and 90 days post-fertilization). We predicted that both visual acuity and contrast sensitivity increase as the fish grows. Using previous measurements of refractive index (RI), we determined how the lens of an adult zebrafish focuses light by applying a computational technique, ray tracing, that traces the path of light rays as they pass through the lens. To examine how anatomical

changes of the eye correlate with alterations in lens optics, we plan to obtain precise morphometrics from histological sections of the eye and use inverse optimization of ray tracing to determine the RI profile at each of the 5 stages considered by the OKR experiments.

#### **SAT-G26**

##### **NUTRIENT ENRICHMENT AND PLANT INTERACTIONS INFLUENCE NATIVE AND EXOTIC PLANT COMMUNITIES BUT ARE UNAFFECTED BY CLIMATE WARMING**

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Climate warming and nutrient enrichment may influence invasion success and alter community composition patterns. It is critical to experimentally evaluate the effects of these stressors on plant invasion success and their impact. We asked how nutrient addition and warming affect 1) native plant performance, 2) exotic plant performance, and 3) plant community composition patterns. We conducted a  $3 \times 2 \times 3$  factorial field mesocosm experiment with 4 replicates. We established mesocosms in 454L tanks with a soil/sand mix and added municipal water and 20 native snails. Mesocosms were randomly assigned to treatments: 1) plant origin: native (4 species), exotic (3 species), or mix (7 species); 2) nutrients: ambient or high (6 mg/L N); and 3) warming: ambient, low (+1 °C), or high (+2 °C) manipulated using solar water heaters. After 11 months, we harvested, sorted by species, and oven dried plant mass. Neither native nor exotic plant mass was affected by the other plant origins in ambient nutrients. However, native and exotic plant mass with high nutrients was lower in mix treatments compared to native or exotic plant treatments. This suggests that native and exotic plants reduce each other's growth. Exotic plant mass with elevated nutrients was higher than native plant mass in single origin communities (27-fold vs. 4-fold) and in mixed communities (16-fold vs. 3-fold). This suggests that exotic plants can take advantage of high resources; nutrient enriched ecosystems are more vulnerable to invasions. Overall, nutrient enrichment is the critical anthropogenic stressor that influences plant invasion success in this freshwater ecosystem.

#### **ENVIRONMENTAL SCIENCE/STUDIES**

#### **SAT-G27**

##### **KEY INDICATOR SPECIES *RANGIA CUNEATA* IN THE MISSION-ARANSAS NATIONAL ESTUARINE RESEARCH RESERVE: A PRELIMINARY ASSESSMENT OF ABUNDANCE AND DISTRIBUTION**

Maria Rodriguez, Wes Tunnell, Jana Gray.

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*Rangia cuneata* are brackish water clams that act as a key indicator species of freshwater inflow in Texas coastal watersheds. They are more abundant at the mouth of rivers where they enter into bays. The Mission-Aransas National Estuarine Research Reserve (MANERR), established in 2006, is one of the newest in the National Estuarine Research Reserve (NERRS) system. It is about 30 miles north of Corpus Christi, Texas, and its main purpose is to provide relatively natural settings for long term research. It is important to know abundance and distribution of *R. cuneata* to determine habitat quality in coastal watersheds. The objectives of this project were

to determine whether the clams are present in the MANERR and, if present, determine preliminary distribution and abundance. This study was conducted throughout June and July of 2013. The Aransas and Mission River systems were surveyed. A dredge was used every mile up the river from the mouth, and live and dead *R. cuneata* were enumerated when found. Once a bed of live clams was located, quadrat sampling was used. There were no beds found in the Mission system. In the Aransas River, however, 3 beds were found and surveyed. At each site, 5 quadrats were taken, and any extra clams found were measured and collected. The data collected did not yield a clear picture of abundance and distribution; however, *R. cuneata* were present in small refuge populations during the current extended drought. Future research should be conducted to determine more detailed abundance and distribution.

#### **FRI-G27**

##### **USING SOCIAL VALUATION TO ASSESS AND PROTECT ECOSYSTEM SERVICES IN THE MISSION-ARANSAS NATIONAL ESTUARINE RESEARCH RESERVE, TEXAS**

Mayra Lopez<sup>1</sup>, David Yoskowitz<sup>2</sup>, Susan Lovelace<sup>3</sup>, Michael Starek<sup>2</sup>, Jarrod Loerzel<sup>3</sup>.

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Ecosystem services (ES) are the benefits that humans derive from nature, which are necessary to live a full and healthy life. These services include, but are not limited to, food, shelter, storm protection, and recreation. Unfortunately, it is often difficult to value ES in a manner that conveys their importance. For this study, social valuation will be used to identify locations in the Mission-Aransas National Estuarine Research Reserve (MA-NERR) that are most important, in terms of ES. Social valuation is a method of valuating ES, which uses survey responses to rank ES. Survey takers will have the option of taking the survey over the phone, online, through the mail, or in-person. For the in-person surveys, a total of 12 sampling sites have been chosen within the MA-NERR. Surveys will be conducted between June and July of 2014. Data will be mapped using ArcGIS and analyzed using the USGS application Social Valuation for Ecosystem Services (SolVES). The final product will be a MA-NERR-focused report that identifies areas of importance on heat maps and ranks locations by ES importance. The overall goals of this study are to provide useful information to resource managers and policy-makers and to encourage public participation to provide a sense of democracy and legitimacy to the decision-making process.

#### **SAT-G28**

##### **CLIMATE CHANGE AND AMPHIBIAN COMMUNITIES IN PALOUSE PRAIRIE OF SOUTHEASTERN WASHINGTON**

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How will climate change in the Pacific Northwest affect landscape distribution and structure of amphibian communities in wetlands in Palouse Prairie and the Columbia River Basin? Given the importance of climate change to the future of biodiversity conservation, we addressed this question by sampling >7,200 amphibians in 90 wetlands (some repeated sampling) from 2009

to 2013 to develop algorithmic ecological models predicting amphibian distribution and abundance in this region. From individual models of 8 different amphibian species, we then derived a synthetic summary model of ecological factors predicting community structure and presence or absence of amphibians in the Columbia River Basin. This ecological process model suggests that future distributions and community structure will be strongly influenced by introduced predatory fish and continuing spread of invasive American bullfrogs in permanent water bodies. The flooding periodicity of small seasonal wetlands that are susceptible to premature drying under altered rainfall and temperature patterns will influence early breeding amphibians (e.g, long-toed salamanders and Pacific chorus frogs). The Columbia spotted frog, a species of conservation concern, may experience a range retraction toward the higher elevation foothills in adjacent Idaho. The ultimate fate of the state-endangered Northern leopard frog in the Potholes region of Moses Lake is uncertain, but its persistence in Washington appears partly dependent upon temperature-related dynamics with the introduced deadly chytrid fungus and managed flow regimes in the Columbia River. We conclude that data-driven models will facilitate projections of amphibian conservation issues under future climate change scenarios.

#### **FRI-G28**

#### **STABLE ISOTOPES IN PRECIPITATION, SURFACE, AND GROUND WATERS: RECORDING THE NORTH AMERICAN MONSOON IN ARIZONA, NEW MEXICO, AND UTAH**

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Data show that during the past 100 years the Navajo Nation has experienced increasing temperatures and decreasing precipitation. There has been historical variability in precipitation in the southwestern United States. In Arizona, New Mexico, and Utah, summer precipitation, also known as the North American monsoon, has ranged from weak monsoons, causing drought to develop, to strong monsoons, causing flooding. We propose to conduct research to better understand patterns and changes in the North American monsoon by measuring stable isotope ratios of water on the Navajo Nation. For several decades, hydrologists have recognized that stable isotope ratios of hydrogen and oxygen can be used to distinguish the origin of water in precipitation, surface, and ground waters. Stable isotopic research will provide unique and critical information that will help us understand how different oceanic water sources contribute to monsoon precipitation in the Navajo Nation and how monsoon precipitation contributes to surface, ground, and spring water sources. This work will address the following questions: Is there a mix of atmospheric water vapor sources contributing to monsoon precipitation in the Navajo Nation, and how does this vary geographically and with monsoon intensity? To what degree are different freshwater resources (streams, lakes, groundwater, and springs) derived from monsoonal precipitation, and which resources are likely to be the most sensitive to future changes in the monsoon? There is a need for quantitative data to interpret monsoonal precipitation changes and their effects on the Navajo Nation's changing climate.

## **SAT-G29**

### **PHOTOSYNTHETIC PICOPANKTON ASSEMBLAGES IN MESOTROPHIC TROPICAL RESERVOIR: TEMPORAL AND VERTICAL DYNAMICS OF PICOCYANOBACTERIA**

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Species composition, biomass, and dynamics of the picocyanobacteria in a tropical reservoir (Cerrillo, Puerto Rico) were studied from February 2012 to March 2013. Data were collected monthly in the limnetic and the littoral zones. Picoplankton was identified and quantified using flow cytometry and epifluorescence microscopy. A stable thermal stratification was observed during most of the year what allowed us to classify the reservoir as warm monomictic. Dissolved oxygen in the surface was relatively high; however, hypoxic conditions were present in the hypolimnion during the whole period of the study. The results suggested no differences in the composition and abundance of picoplankton between both stations. Superimposed to this spatial heterogeneity, a clear temporal variation related with the temperature and the hydrologic regime was observed. Cytometry analyses allowed the identification of 4 populations of picoplankton, indicating that picocyanobacteria groups (phycoerythrin-rich *Synechococcus* type) were dominant throughout the study, with maximal abundances ( $7.79 \times 10^3$  -  $25.7 \times 10^3$  cell/ml) although picoeukaryote were temporally important. Total chlorophyll-*a* (Chl-*a*) in the euphotic zone was higher, ranging from 2.13 to 38.55 ug/l. Fractionated Chl-*a* results show a relatively constant pattern ranging from 0.24 to 1.64 ug/l. The average contribution of APP to total Chl-*a* concentrations estimated by size fractionation during the study was 9.7%. Chl-*a* concentration reflected the annual variation in picoplankton, its concentration being higher during summer when solar radiation was also higher. The picoplanktonic community was structured basically, in accordance to temperature, nutrients, and light availability.

## **FOOD SCIENCES/TECHNOLOGY**

## **SAT-G30**

### **NUTRITIONAL AND PHYSICAL ACTIVITY SUMMER LEARNING YOUTH CURRICULUM**

Kattia Blanco, Katherine Cason.

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The Expanded Food Nutrition and Education Program (EFNEP) is a program that aims at informing and educating limited-resource children, youth, and families in developing and maintaining a nutritionally sound diet and a physically active lifestyle. Many of the intervention programs implemented through Youth EFNEP are created to be part of an existing school curriculum or as an after-school program. Currently, few programs exist that allow for easy transferability of these already existing programs to a summer camp setting. For this reason, a curriculum was developed to facilitate the implementation of a summer nutritional learning program that follows the Youth EFNEP core guidelines of nutrition and dietary quality, physical activity, food safety, and food resource management. Each lesson has a structured matrix that includes objectives, activities, materials, and evaluations based on the educational theory of

multiple intelligences and health promotion's social cognitive theory. Each lesson is then delivered through an age-appropriate medium such as posters, hands-on games, taste tastings, and physical activities. The curriculum will be pilot tested in Summer 2014 and implemented as part of a summer camp in Summer 2015. The pilot test will involve focus group discussions and interviews with participants, parents, and teachers. The data collected during the pilot test will be used to make further modifications to the curriculum. We expect that the final product will be adopted nationwide in summer camps by Youth EFNEP educators.

#### **FRI-G29**

##### **WEB-BASED NUTRITION EDUCATION INTERVENTION FOR AFRICAN-AMERICAN WOMEN USING THE THEORY OF PLANNED BEHAVIOR**

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African-American women (AAW) have been disproportionately impacted for decades by the obesity epidemic, which frequently leads to severe chronic diseases such as cardiovascular disease, diabetes, and hypertension. This raises the need to design a culturally tailored nutrition education program that combines a strong theory base and the use of technology and internet that is rapidly increasing amid young adult AAW. Little is known about the variables that motivate behavior change among AAW and the theory of planned behavior (TPB) can help us understand them by looking at the relationship between attitudes, intentions, and behaviors. According to TPB, behavioral intention is the most important determinant of behavior. The purpose of this study is two-fold: first, to explore with the TPB the beliefs and attitudes related to eating and physical activity behaviors in AAW ages 18 to 29 in South Carolina, and second, based on these results, to design a web-based nutrition education program specifically tailored to the needs of this population. The research will have a mixed methods exploratory sequential design which involves integrating qualitative and quantitative data. First, focus group results will be used to inform the design and content of the web-based intervention. Second, pre/post survey data will be collected during program implementation to measure the participants' intention to change their eating and physical behaviors. This approach will define a groundbreaking parameter for culturally-tailored interventions to promote behavioral changes among minorities with higher obesity risk and facilitate future incorporation of innovative learning technologies into nutrition education programs.

#### **GENETICS**

#### **FRI-G31**

##### **ATX-2, THE *C. ELEGANS* ORTHOLOG OF HUMAN ATAXIN-2, IS NECESSARY FOR CYTOKINESIS, ER MORPHOLOGY AND P GRANULE SEGREGATION**

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Spinocerebellar ataxia type 2 (SCA2) is a neurodegenerative disease caused by a polyglutamine expansion in human Ataxin-2. These mutations in Ataxin-2 lead to protein mis-folding and



aggregation causing Purkinje cell degeneration and loss of motor coordination. Human Ataxin-2 localizes to stress granules, important stores for RNAs and associated RNA-binding proteins under environmental stress. Although studies have suggested that Ataxin-2 may play roles in RNA metabolism and stress granule function, the cellular role of Ataxin-2 is unclear. Understanding the cellular functions of Ataxin-2 could provide new insights into SCA2 disease mechanisms. Our lab identified Ataxin-2 from isolated mammalian midbodies and the corresponding *C. elegans* ortholog, ATX-2, displayed defects in cytokinesis. In *atx-2*, RNAi-treated embryos cytokinesis defects, spindle orientation, and ER morphology defects are observed. In the absence of ATX-2, the ER structure collapses resulting in aggregates of ER throughout the cytoplasm. To determine where ATX-2 localizes during the cell cycle, we have created CRISPR and Mos-1 single-copy insertion constructs for 2 of the identified ATX-2 isoforms. Lastly, P granule segregation defects have been observed in 70% of the ATX-2-depleted embryos suggesting that ATX-2 may play a role in RNA regulation and localization during development. We hypothesize that ATX-2 may play a role in mediating the targeting and regulation of RNAs localized in the midbody or mediating the local translation of these RNAs throughout the cell cycle. We will present our current understanding of the cellular functions of ATX-2 in the *C. elegans* embryo.

#### **SAT-G31**

#### **CDC42 REGULATES ENDOTHELIAL CELL POLARITY AND ADHESION VIA THE ACTIN CYTOSKELETON**

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Understanding and ultimately controlling blood vessel formation lays the foundation for development of pro- and anti-angiogenic therapies. GTPases have been shown to control basic mechanisms of vessel morphogenesis. Here, we aim to elucidate the mechanisms by which the small Rho-GTPase and classical polarity determinant Cdc42 regulates blood vessel formation, development, and maintenance. Using the conditional Cre-LoxP gene ablation approach, we show that loss of Cdc42 in embryonic endothelium *in vivo* leads to rapid lethality due to vascular failure resulting from defects in vessel tubulogenesis and vessel maintenance. In Cdc42<sup>-/-</sup> mutant embryos, endothelial cells (ECs) show compromised cytoskeletal organization and rapid loss of cell polarity. In addition, mutant ECs display irregular distribution of cell-cell adhesion proteins and reduced cell extracellular matrix (ECM) adhesion. We propose that Cdc42 controls cell polarity and EC-EC and EC-ECM adhesion by regulating cytoskeletal anchoring of adhesion points. Specifically, Cdc42 directs actin filament attachment to cell adhesions via regulation of non-muscle myosin II actin crosslinking. Current work is aimed at determining how Cdc42 regulates vascular development in different types of blood vessels and the molecular signaling that occurs downstream of Cdc42.

**FRI-G32****GENETIC BASIS OF OCTANOIC ACID RESISTANCE IN *DROSOPHILA SECHELLIA*: FUNCTIONAL ANALYSIS OF A FINE-MAPPED REGION**

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*Drosophila sechellia* is a species of fruit fly endemic to the Seychelles Islands located northeast of Madagascar off the coast of Africa. Unlike its generalist sister species *D. simulans*, *D. mauritiana*, and *D. melanogaster*, *D. sechellia* evolved to specialize on a single plant species, *Morinda citrifolia*. Specialization on *M. citrifolia* is surprising because the fruit of the plant contains toxic compounds, primarily octanoic acid (OA), that are lethal to all *Drosophila* species except *D. sechellia*. Although the ecological and behavioral adaptations to this toxic fruit are known, the genetic bases for the evolution of the resistance phenotype is not. Prior work characterized a genomic region on chromosome 3R containing 18 genes shown to contribute to OA tolerance. To determine the specific gene(s) involved in OA resistance in this region, we knocked down individual genes with RNA interference (RNAi) in *D. melanogaster*. RNAi knock-down flies were tested for resistance to OA using a Cox proportional hazard model. Here, we identified a pair of neighboring genes, *Osiris 6* and *Osiris 7*, where ubiquitous knockdown of these genes leads to an increase in OA sensitivity. Using tissue specific knockdown, we further identified the specific tissue contributing to OA tolerance. This study sheds light on the genetic basis for ecological adaptation to a toxic host within *Drosophila* and insect-host specialization more broadly.

**FRI-G30****CROSS-TISSUE REGULATORY VARIANTS MAPPED IN HUMAN ADIPOSE AND SKELETAL MUSCLE TISSUE EXPLAIN MISSING HERITABILITY OF TYPE-2 DIABETES AMONG POPULATIONS OF EUROPEAN AND MEXICAN DESCENT**

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Top signals from genome-wide association studies (GWAS) on type-2 diabetes (T2D) are enriched for expression quantitative trait loci (eQTLs) identified in skeletal muscle and adipose tissue. We therefore hypothesized that such eQTLs might account for a disproportionate share of the heritability to type-2 diabetes (T2D) estimated from all SNPs interrogated through GWAS. To test this hypothesis, we applied mixed linear models to the Wellcome Trust Case Consortium (WTCCC) T2D GWAS dataset representing subjects from the United Kingdom (1,924 cases, 2,938 controls) and to 2 additional datasets representing Mexican Americans from Starr County, Texas (837 cases, 781 controls) and Mexicans from Mexico City (967 cases, 343 controls). We estimated the proportion of phenotypic variance attributable to the additive effect ( $V_a/V_p$ ) of all variants interrogated in these GWAS as well as from a much smaller set of variants identified as eQTLs in human adipose, skeletal muscle, and lymphoblastoid cell lines (LCLs). The narrow-sense heritability explained by all interrogated GWAS SNPs in each of these

datasets is greater than the heritability accounted for by GWAS-significant SNPs (~10%) with GWAS SNPs explaining over 50% of phenotypic variance in the WTCCC, Starr County, and Mexico City datasets. The estimates of  $V_a/V_p$  attributable to cross-tissue eQTLs is greater in the WTCCC dataset and among lean Hispanics whereas adipose eQTLs significantly explain heritability among Hispanics with BMI  $\geq 30$ . These results support an important role for regulatory variants in the genetic component of T2D susceptibility, particularly for eQTLs that elicit effects across insulin-responsive peripheral tissues.

## **SAT-G32**

### **THE IMPACT OF FORENSIC DNA TESTING IN HUMAN TRAFFICKING CASEWORK: A REVIEW IN HISPANIC COMMUNITIES**

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In his 2013 Easter Message, Pope Francis is credited with calling human trafficking the “most extensive form of slavery in the 21st century”. This horrendous crime afflicts people of all ages, races, and sex worldwide. Victims of human trafficking are hidden in houses, illegal establishments, factories, farms and other places around the world. Children are at a higher risk for human trafficking into the sex industry. These victims are commonly obliged to participate in prostitution and are sexually exploited. Approximately 18,000 foreign nationals are trafficked into the United States each year; moreover, the number of U.S. citizens trafficked within the country is even higher. The University of North Texas Center for Human Identification (UNTCHI) collaborates with the United States government to help identify the remains of victims found along the Mexican border. DNA-PROKIDS, an international humanitarian effort to identify children who have been victims of human trafficking and to reunite them with their families, also works closely with UNTCHI to begin the long battle to combat human trafficking with DNA technology. Using autosomal STRs, Y-STRs, mitochondrial DNA, and databasing innovations, all common tools in forensic DNA analysis, identification of these victims is now more plausible. These techniques have proven to be successful for identification of human trafficking victims in countries like El Salvador, Guatemala, Honduras, and Mexico. Here we present a review of the impacts that forensic DNA typing and databasing have had in major crimes that have affected the Hispanic community throughout the world.

## **MARINE SCIENCES**

## **FRI-G35**

### **THE VALUE OF HABITAT DIVERSITY IN MARINE RESERVES: SPINY LOBSTER USE OF THE INTERTIDAL ZONE AT THE SANTA CATALINA ISLAND MARINE PROTECTED AREA**

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Marine protected areas (MPAs) are a relatively new approach to managing exploited marine species. However, in order for MPAs to be effective, a diversity of habitats that incorporate all necessary ecosystem services for targeted species must be included in their design. The

Southern California spiny lobster (*Panulirus interruptus*) is an exploited species for which MPAs have been designed. Previous work suggests this species forages within the intertidal zone at high tide; however, the relative importance of this habitat in the early design of MPAs was not considered. As part of a study to test the efficacy of a longstanding MPA on Catalina Island, California, snorkel and scuba surveys recording abundance, size, and gender were conducted along transects within the MPA and outside at high tide. Intertidal habitat composition was also assessed at low tide using GIS to create photographic transects based off of spatial reference points which were then classified manually. It was hypothesized that spiny lobster demographics were greater in the MPA. It was also hypothesized that demographic patterns were higher in the intertidal zone relative to the subtidal at high tide. Results suggest current demographic parameters are higher outside of the reserve due to more suitable intertidal habitats for foraging. These results provide insight on how MPAs should require ecosystem-based management that incorporates fine-scale habitat types utilized throughout the lifetime of managed species.

### **SAT-G35**

#### **USING GIS TO MODEL THE IMPACTS OF CLIMATE CHANGE ON *MYTILUS CALIFORNIANUS* COVER**

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Abiotic processes play a key role in determining the distribution of intertidal species, including the California mussel (*Mytilus californianus*). Climate change could alter these processes, including the impact of temperature regimes, wave force, and relative sea level, leading to potentially dramatic shifts in species distribution. Increased temperatures result in desiccation stress, limiting mussel fitness and survival. Increased wave force can increase mussel distribution by reducing desiccation stress, as well as increasing larval recruitment, but can also result in disturbance events including bed tear outs. Landscape variation, such as tidal height, can help explain the relative influence of these environmental factors on mussel distribution. The purpose of this study is to quantify the relationships between temperature, wave force, tidal height, and mussel bed cover. Utilizing abiotic and biotic data collected within an intertidal boulder field near the Bodega Marine Laboratories in California, we interpolated values for the 4 variables across the entire boulder field using GIS. We will use marine geospatial ecology tools (MGET) to create a generalized linear model (GLM) designed to model variation in mussel cover as a function of our 3 abiotic variables. We expect all 3 abiotic factors to be significantly related to mussel bed cover. This model can then be used to predict how the distributional limits of the mussel bed will shift according to climate change projections and increase our understanding of how the physical landscape influences intertidal species distribution, as well as provide insight as to how climate change will impact these communities.

**FRI-G33****BUILDING ISLAND RESILIENCE AGAINST CLIMATE CHANGE THROUGH A COMMUNITY-LED WATERSHED, CORAL REEF, AND FISHERIES REVIVAL EFFORT IN GUAM**

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Coral reefs are essential coastal ecosystems for many tropical islands and their societies, providing immense ecological, economic, and cultural benefits. In order to build resilience against global stressors such as climate change and sea level rise, island communities must address local stressors impacting these ecosystems. A community-based effort called the Humåtak Project works to build resilience against environmental stressors by restoring coastal watersheds, coral reefs, and near-shore fisheries in the United States territory of Guam. The project addresses a major local environmental stressor, accelerated erosion, which is caused by poor land-use practices. Erosion is associated with the loss of native forests and the resulting sedimentation on coral reefs which smothers and kills corals and destroys essential fish habitat. Community groups contribute hundreds of volunteer hours each year to restore the degraded environment. Tree seedlings are planted to reforest bare-soil areas, and sediment filter socks are installed along eroding hillsides. Observations of restoration plots indicate that vegetation is greatly increasing, and hillside slumping is decreasing. Soil analysis 21 months after restoration treatments indicates soil accumulation is greater around trees and sediment filter socks than at reference plots. Water quality and coral data are being collected to evaluate the effectiveness of and further refine erosion control measures. The Humåtak Project also builds awareness of environmental issues among community members through educational outreach events and social media. Findings of this research will be used to promote effective watershed restoration practices as well as improved mitigation strategies intended to offset adverse impacts to aquatic resources.

**SAT-G33****ASSOCIATIONS BETWEEN DEMERSAL FISHES AND STRUCTURE-FORMING INVERTEBRATES IN TEMPERATE WATERS ON THE CONTINENTAL SHELF OF THE PACIFIC NORTHWEST**

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Plans are under way to deploy wave energy capture devices off the coast of the Pacific Northwest as a solution to the region's ever-growing demand for energy. Implementation of wave energy fields could have far-reaching effects on structure-forming invertebrates which are slow-growing, fragile, and sensitive to siltation. Impacts on these invertebrates could, in turn, have adverse effects on associated fish species by reducing available or preferred habitat. We aim to evaluate the extent to which fishes associate with the structure-forming invertebrate community at sites that may be impacted by wave energy generation. Video footage was collected for this study by the remotely operated vehicle (ROV) Hammerhead from Gray's Bank, Washington, and Siltcoos Reef, Oregon, in late summer 2011. We characterized the proximity between 660 individual fishes and 907 structure-forming invertebrates in the study area. More than 75% of individual fishes were within one body length of an adjacent invertebrate. Chi-

squared tests suggest a difference in associating groups of fishes between soft-sediment and hard-bottom habitat. Furthermore, regression testing showed significant relationships between structure-forming invertebrates and fish in only the soft-sediment habitat; however, the relationships observed were weak. Ultimately, the hard substrate provided by wave energy structures in a soft-bottom environment may be more important to demersal fishes than structure-forming invertebrates.

#### **FRI-G34**

##### **LARVAL SETTLEMENT AND REPRODUCTIVE PATTERNS IN THE BROODING CORAL, *LEPTASTREA PURPUREA***

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Coral reefs are highly diverse marine ecosystems of ecological, economic, and cultural value. With the expected negative effects on reefs from global climate change including rising sea temperatures and ocean acidification, the identification of resilient coral species has become increasingly important. *Leptastrea purpurea* is an encrusting coral that is found throughout the Indo-Pacific and Red Sea. While most corals are broadcast spawners that release sperm and eggs to be fertilized in the water column, some corals brood planula larvae within their bodies after internal fertilization. *L. purpurea* appears to brood planula larvae on a continuous basis within the parent colony as observed during histological analysis. The planula larvae show incredible resilience under a wide range of stressful conditions, as well as the ability to successfully settle and metamorphose after 180 days. Various compounds were tested to identify a settlement cue for *L. purpurea*, and our results suggest that a microbial cue associated with the parent colony may induce settlement and metamorphosis. Understanding the settlement cues and reproductive biology of this coral is important to our broader knowledge of this resilient coral species in the reef environment.

#### **MICROBIOLOGY**

#### **FRI-G37**

##### **SPATIOTEMPORAL DISTRIBUTION OF ARSENIC AND IRON REDUCING BACTERIA IN A MODEL SOIL ARSENIC-IRON ENVIRONMENT**

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The consumption of arsenic-contaminated ground waters has become a global public health problem. To most organisms, arsenic is toxic. However, prokaryotes have evolved arsenic detoxification (via *ars* genes) in order to cope with this metalloid. Moreover, certain microbes can also use arsenic (i.e., arsenate) as an alternative electron acceptor for anaerobic respiration, encoded by *arr* genes. In subsurface soil environments, aerobic-anaerobic cycling (redox) plays a critical role in the arsenic geochemistry cycle. Anaerobic -arsenic reduction leads to the removal of mineral-bound arsenic, thereby increasing dissolved arsenic and ultimately arsenic contamination of water sources. Little is known about spatiotemporal distribution of

arsenate- and Fe-reducing bacteria along these redox gradients. An *arr* biosensor, green fluorescent protein (GFP) integrated into *arrAB* gene cluster, in *Shewanella sp.* ANA-3 was constructed to determine the spatiotemporal distribution of arsenic metabolism and impacts on redox cycling within a model soil arsenic-iron environment. Our approach is to add the *arr-gfp* reporter strain to arsenic-iron coated sand molded into spheres to simulate redox gradients that occur within natural soil aggregates. The modeled soil aggregates are monitored over time in a flow cell pumped with artificial groundwater. This system allows for abiotic and biotic manipulations that impact arsenic cycling in the environment. Cores taken through the aggregates are being analyzed for arsenic and iron, using a confocal microscope to localize bacteria expressing the *arr* pathway. This study will elucidate the ecological distribution of metal-reducing bacteria and impacts of redox gradients on arsenic release from soils.

#### **SAT-G41**

#### **DESERT WASTELAND OR OASIS: THE EFFECTS OF HOST CELL ENVIRONMENT ON *ALPHAVIRUS* INVASION, REPLICATION, AND SPREAD**

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Members of the *Alphavirus* genus are positive-sense RNA viruses that have been isolated from around the world. In addition to their large geographic range, *Alphaviruses* also have a diverse host range: birds, humans, and fish. Typically, *Alphavirus* transmission requires an arthropod vector, the predominant vector being the mosquito. To proliferate, the virus must invade and hijack host cell machinery. In the mosquito, *Alphavirus* establishes a persistent infection and replicates without causing disease; however, once transmitted to the vertebrate host, symptoms and disease ensue ranging from arthritis and arthralgia to encephalitis and subsequently death. Based on the difference in *Alphavirus* pathogenicity, we hypothesize that host cell environment determines *Alphavirus* invasion, replication, and spread, specifically due to the different host factors of arthropod (vector) and vertebrate (host) cells. To test this hypothesis, we investigated both the biochemical properties of the *Alphavirus* virion and host cell environment. Approaches include focused ion beam scanning electron microscopy (FIB-SEM), bioinformatics, and infection assays. FIB-SEM is being used to track morphological changes that occur within vector and host cells during infection. Current literature and bioinformatics were used to highlight conserved factors required for *Alphavirus* infection. To investigate the temporal difference of infection onset between vector and host, infection assays were done with virus containing a fluorescence marker. Preliminary data suggests the difference in *Alphavirus* pathogenicity between vector and host is due to specific host factors. Future research is under way to identify the specific arthropod vector and vertebrate host factors that aid or antagonize viral infection.

**SAT-G44****ANTIMICROBIAL EFFECTS OF SILVER(I) CYANOXIMATE-COATED SURFACES ON BIOFILM FORMATION OF HUMAN PATHOGENS**

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Post-surgical medical implant infections caused by bacterial biofilms are the most common cause of patient morbidity and hospitalization costs. To prevent such infections, metal complexes are being incorporated into medical implant materials, leading to the reduction in the infection rate while not introducing a toxic effect to the human cells and tissues. Silver (Ag) has shown to exhibit strong antibacterial properties by reacting with bacterial DNA or inactivating enzymes of bacterial electron transport chain. We have synthesized 8 novel silver(I) organic complexes of cyanoximes designated as Ag(ACO), Ag(BCO), Ag(CCO), Ag(ECO), Ag(PiCO), Ag(BIHCO), Ag(BIMCO), and Ag(BOCO). These compounds are non-antibiotic, water insoluble, and UV/visible light resistant. To quantify biofilm inhibition in these silver complexes, we selected 3 human pathogens representing different infection profiles: *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *Streptococcus mutans*. The compounds at the concentrations of 0.5%, 1%, 2.5%, and 5% were embedded into the polymeric light-curable acrylamide composite commonly used in dental practice, and applied onto the surface of 96-well plates. Quantitative 96-well plate crystal violet biofilm assays showed that *P. aeruginosa* and *S. aureus* biofilm growth was inhibited completely in the presence of 0.5% to 5% of the compounds, with the most efficient inhibition by Ag(BOCO) and Ag(BIHCO). *S. mutans* showed complete inhibition of biofilm growth at 0.5% of AgMCO and AgPiPCO. Thus, we show that several silver(I) cyanoxime complexes efficiently prevent biofilm development of both Gram-negative and Gram-positive human pathogens and, therefore, present a great potential in medical applications as non-antibiotic antimicrobials.

**FRI-G42****PEPTIDOGLYCAN REMODELING AND FLAGELLAR ASSEMBLY IN *BACILLUS SUBTILIS***

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Peptidoglycan is a polymer that forms a mesh-like structure that surrounds the plasma membrane of bacteria. In Gram-positive bacteria, the peptidoglycan is thick, and remodeling of it is necessary in order for bacteria to insert and rotate propeller-like flagella. Autolysins are enzymes that bacteria utilize to remodel the peptidoglycan for growth and cell division. Here we find that CwlQ, a poorly studied autolysin in *Bacillus subtilis*, is required for motility, and fluorescence microscopy has revealed that the flagella break from the cell body in these mutants. Here we discuss why CwlQ is required for flagellar stability and how flagellar stability is related to fundamental aspects of bacterial cell envelope synthesis and turnover.



**FRI-G41****PHYSIOLOGY OF *CLOSTRIDIUM PERFRINGENS* IN RESPONSE TO AZO DYE EXPOSURE**

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*Clostridium perfringens*, a strictly anaerobic microorganism and inhabitant of the human intestine, has been shown to produce the azoreductase enzyme. This enzyme reduces azo dyes from various products that we consume into aromatic amines, which are carcinogenic in nature. This study serves to fill a gap in the literature regarding the unknown effects of azo dyes on the physiological state of this important bacterium. A variety of common azo dyes with varying characteristics were examined for their effects on the generation time and kinetics of reduction under varying nutrient conditions. Effects of azo dyes on the cell wall were also examined to understand cell permeability to these dyes and proteins. It was found that the presence of azo dyes increases *C. perfringens* generation time (slows growth). A microarray study examining the effects of azo dye exposure on *C. perfringens* transcript levels was completed to further study the detrimental effects of azo dyes on this bacteria. *C. perfringens* is capable of reducing a large variety of azo dyes of different sizes and polarities, suggesting the presence of multiple azoreductase enzymes. In addition, these studies have also shown that, when exposed to sulfonated azo dyes, *C. perfringens* translocates proteins across the cell wall, one of which is hypothesized to be an azoreductase enzyme. An antibody against the azoreductase was generated to confirm protein translocation results. The results of this study will serve to provide an important link between the azo dyes and the physiological state of *Clostridium perfringens* cells.

**FRI-G44****PARALLEL GENE SILENCING USING RNA INTERFERENCE**

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Filamentous fungi can produce up to 100 grams per liter of cellulase under optimal fermentation conditions but, in order for fungi to reach their true potential as producers of recombinant proteins, the activity of their extracellular proteases must be drastically reduced. An effective way of silencing gene expression is by manipulating the highly conserved pathway of RNA interference (RNAi). A combinatorial silencing construct was designed using 30 bp segments from 11 protease genes as well as 3 alpha glucosidase genes flanked by constitutive *trpC* (tryptophan) promoters. The 30 bp segments were chosen so that the DICER enzyme would cut each of the segments and load the Argonaute complex, thus silencing each of the target mRNAs in parallel. When this construct was tested in *Aspergillus nidulans*, there was a large-fold difference in the target mRNAs when the transformants were grown in a media without a nitrogen source and a peptone carbon source. There is also the lack of a halo around the transformants when grown on a 1% skim milk agar plate. Moreover, glucoamylase assays showed a 60% activity reduction, suggesting that both targeted pathways' starch and protein degradation were significantly silenced. However silencing these pathways was not complete. Proteosecretome analysis using LC-MS/MS of silenced and non-silenced strains showed that, in

both cases of silencing glucoamylase genes or targeting proteases, certain proteins were not secreted into the medium while new proteins appeared suggesting a compensation mechanism that bypasses the silenced genes.

#### **SAT-G36**

##### **GOING WITH THE FLOW: THE ELECTROCHEMICAL GRADIENT AND ITS ROLE IN THE CELLULOSIC ETHANOLOGEN *CLOSTRIDIUM PHYTOFERMENTANS***

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*Clostridium phytofermentans* is a cellulosic microbe capable of breaking down and fermenting multiple carbohydrates to ethanol as its main product, making it attractive for biofuel production. ATP is generated through fermentation when acetate is produced. However, acetate levels are low compared to ethanol, suggesting that additional energy conservation mechanisms may be used by *C. phytofermentans* to improve growth energetics during fermentation of carbohydrates to ethanol. In a previous study, transcriptional microarray data indicated increased expression of certain membrane-bound proteins under some growth conditions: an Na<sup>+</sup> F-type ATPase, an Na<sup>+</sup> V-type ATPase, and an ion-translocating ferredoxin NAD<sup>+</sup> oxidoreductase (Rnf-FoR), possibly capable of translocating Na<sup>+</sup>. We hypothesized that *C. phytofermentans* is able to produce ATP via the F/V type ATPases by an ion motive force, driven by Na<sup>+</sup> and/or H<sup>+</sup> ions, that is generated through the activity of the Rnf-FoR. In order to test this hypothesis, two approaches were used. First we examined the effects of cell growth of the ETH2120 Na<sup>+</sup> ionophore and TCS protonophore. Second, protein sequence comparisons were employed. Results showed that both ETH2120 and TCS prevented cell growth suggesting that *C. phytofermentans* relies on both a sodium motive force and a proton motive force. Sequence comparison indicate conserved amino acid subunits involved in Na<sup>+</sup> binding in both *C. phytofermentans* F-type and V-type ATPases. Additionally, a second V-type ATPase was found to have conserved H<sup>+</sup> amino acid subunits, which might explain *C. phytofermentans*' susceptibility to both ionophores. However, the ion used by Rnf-FoR is unknown.

#### **FRI-G40**

##### **UNCOVERING INTERACTIONS BETWEEN SEGMENTED RNA VIRUSES AND THE RNA DECAY MACHINERY**

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Successful infection of a host requires that transcripts generated by RNA viruses avoid the host cellular RNA decay machinery. Recent work has implicated viral RNA stabilization strategies as possible contributors to cytopathology and pathogenesis. Previous work in our laboratory has largely focused on strategies for how positive-sense RNA viruses ensure the stability of their transcripts. Little is known how transcripts from segmented, ambisense RNA viruses like Junin virus (JUNV) and Rift Valley fever virus (RVFV) interface with the cellular RNA decay machinery. Notably, individual JUNV viral RNA segments appear to have differential RNA stabilities in infected cells. This suggests that differential RNA stability may indeed be playing an important

role in infections by segmented viruses. Since many elements that regulate RNA stability are located in the 3' untranslated regions (UTR) of transcripts, we have focused on this key region of the various JUNV and RVFV mRNAs to determine the underlying mechanism for the observed differential stability. We are currently assessing how RNAs containing these viral 3' UTRs interface with the major enzymatic activities in mRNA decay in deadenylation, exonuclease, and decapping assays using cytoplasmic extracts that we previously developed. Interestingly, many of the JUNV 3' UTR segments interact strongly with an ~55 KDa cellular protein by UV cross linking. We are currently characterizing this protein and its relationship to JUNV biology.

### **SAT-G43**

#### **NITROGEN CYCLING IN THE SUBSURFACE: MICROBIAL ROLES**

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Arid-land caves are likely to be extremely nitrogen-limited, but almost nothing is known about how microbes in subsurface environments obtain this essential element to meet cellular demand. The depth of caves beneath the surface may represent a critical factor affecting microbial nitrogen cycling in these environments. We hypothesize that, in shallow lava caves, water infiltrating from the surface after precipitation events represents the major input of organic and inorganic nitrogen into these environments. Surface water likely results in the exchange of nutrients that influence bacterial and archaeal community structure in shallow lava caves. Percolation of water and nutrients from a precipitation pulse event would affect deep arid-land carbonate caves much more slowly. To obtain nitrogen in deep, carbonate caves, microorganisms could use nitrate in the host rock for assimilatory biochemical pathways, or a respiratory electron acceptor. However, the latter process leads to losses of bioavailable N through production of N<sub>2</sub>O and N<sub>2</sub>, which can only be replaced by N<sub>2</sub> fixation or weathering. We hypothesize that there will be a correlation between cave depth, mineralogy, and the relative distribution of nitrogen cycling genes in organisms found in carbonate and lava caves. We propose a metagenomic study of ferromanganese deposits (FMD) collected from 2 deep carbonate caves in Carlsbad Caverns National Park, NM, and microbial mats found on basalt rocks from 2 lava caves in El Malpais National Monument, NM. Taxonomic composition and nitrogen cycling functional genes will be compared among sites and study locations.

### **SAT-G38**

#### **KSHV INFECTED ENDOTHELIAL CELLS REQUIRE GLUTAMINOLYSIS FOR SURVIVAL**

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The etiologic agent of Kaposi's sarcoma (KS), the most common tumor of AIDs patients, is Kaposi's sarcoma-associated herpesvirus (KSHV). Our lab is interested in how latent KSHV infection alters host cells to induce cancer. Increased glycolysis and glutaminolysis are hallmarks of cancer and are required for the survival of many tumor cells. Our lab has shown that endothelial cells, the main cell type of KS tumors infected with KSHV, require increased glycolysis for survival. Using global metabolomic analysis of KSHV-infected endothelial cells, we

found that latent KSHV infection significantly induces several host metabolic pathways commonly reprogrammed in cancer cells. Importantly, levels of both glucose and glutamine were elevated. In cancer cells, glutamine-derived carbon replenishes the tricarboxylic acid cycle (TCA) intermediates depleted by increased glycolysis. Therefore, we hypothesized that induction of glutaminolysis by KSHV is likely to be required for the survival of latently infected cells through replenishment of the TCA cycle. Glutamine starvation, as well as drug inhibition of glutaminolysis, led to a significant increase in KSHV-infected cell death as compared to mock-infected cells under the same treatment conditions. The majority of the infected cell deaths recorded in the absence of glutamine is rescued upon addition of TCA cycle intermediates (pyruvate or alpha-KG), demonstrating that glutamine is required to replenish the TCA cycle. Overall, these data indicate that KSHV infection induces and requires glutamine metabolism for the survival of infected cells. This work suggests that viral induction of host metabolic pathways may contribute to the induction of KS tumors.

### **SAT-G39**

#### **FUNCTIONAL ANALYSIS OF REV BINDING REGION 2, A STRUCTURAL ELEMENT OF THE EIAV REV RESPONSIVE ELEMENT**

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Retrovirus replication depends on a number of RNA-protein interactions that mediate key steps in the virus life cycle. In lentiviruses, export of incompletely spliced viral RNA to the cytoplasm requires interactions between the viral Rev protein and a viral sequence known as the Revresponsive element (RRE). In equine infectious anemia virus (EIAV), Rev binds 2 regions in the RRE, Rev-binding region-1 (RBR-1) and Rev-binding region-2 (RBR-2). RBR-1 is sufficient to mediate RNA export and overlaps an exonic splicing enhancer that binds the alternative splicing factor SF2/ASF shown previously to be functionally competitive with Rev. RBR-2 is structurally similar to other lentiviral RRE structures required for export, and is required for EIAV Rev high affinity binding to the RNA; however, the functional significance of RBR-2 is unknown. Here, we used a Rev-dependent nuclear export assay and a Rev dependent EIAV virus gene expression assay to assess the role of RBR-2 in Rev dependent nuclear export and virus gene expression. There was no significant difference in export activity with or without RBR-2, whereas deletion of RBR-1 resulted in complete loss of nuclear export. Deletion of RBR-2 also had no effect on SF2/ASF inhibition of Rev activity in transient assays, suggesting RBR-2 does not provide a competitive advantage to Rev in the presence of SF2/ASF. Further, deletion of RBR-2 from the Rev dependent Gag/Pol expression construct did not result in any change to EIAV virus gene expression or virus production. These results indicate RBR-2 is not involved in Rev-mediated nuclear export.

**FRI-G38****BACTERIAL SIDEROPHORES IN THE UNDERWORLD: CHARACTERIZATION OF POTENTIAL SIDEROPHORE-PRODUCING CAVE BACTERIA ISOLATED FROM LECHUGUILLA AND SPIDER CAVES, CARLSBAD CAVERNS NATIONAL PARK (CCNP)**

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Determining how bacteria acquire and cycle iron in the subsurface remains an unanswered question of subterranean ecology. Bacteria have the ability to live in caves which are aphotic environments with low nutrients, including low amounts of iron. One way that cave bacteria acquire needed iron may be through the secretion of ferric iron-selective siderophores, which are low-molecular-weight compounds. These compounds are known to be used by surface bacteria to acquire ferric iron. In this study, we investigated potential siderophore production in Lechuguilla and Spider Caves in Carlsbad Caverns National Park (CCNP). We hypothesize that cave bacteria are using siderophores to acquire ferric-iron that they used for critical cellular processes. CCNP caves contain a variety of cave secondary minerals that may or may not contain iron. One cave secondary mineral is ferromanganese deposits (FMD) that are found on the cave walls and ceilings. We analyzed previous cultures inoculated with FMD and other secondary minerals from Spider and Lechuguilla Caves and subcultured 171 sub-cultured bacterial isolates. These isolates were characterized by catalase and oxidase testing, Gram staining, and tested for siderophore production. The majority of isolates tested positive for catalase and oxidase and were mixed cultures based on Gram stain analysis. Interestingly, 63% of the cave isolates tested positive for siderophore production. The presence of isolates that produce siderophores supports our hypothesis that cave bacteria are using siderophores to acquire iron. These studies will shed light on the production of siderophores in subsurface, low nutrient environments.

**FRI-G36****MICROBIAL AND HOST IMMUNE SYSTEM CROSS-TALK IN THE GASTROINTESTINAL TRACT OF PRAIRIE VOLES**

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The human intestinal tract contains trillions of resident bacteria. These bacteria play a crucial role in maintaining the health of their hosts. Intestinal bacteria might not only be important for intestinal health, but also for immune and nervous system functions beyond the intestine. We aim to explore the interactions between the bacteria and the host immune system in the intestinal tract of prairie voles. This study investigates how changes in the intestinal bacteria early in life can influence the development of the mucosal immune system including the epithelial barrier. Parental prairie voles received antibiotics in drinking water *ad libitum* for 6 weeks during gestation and lactation, while control voles received unadulterated water. The bacterial-mucosal immunity interactions were analyzed using real-time PCR, histological staining, intestinal permeability assay, and flow cytometry. We have identified differences in the epithelium development between treated/untreated adolescent voles. It is possible that

using probiotics might restore the cross-talk between the host-immune system. Future studies will be directed toward understanding the probiotic mechanisms and the role of the gut microbiota in neonatal immune system development, as well as studying changes in behavior in the highly social prairie voles.

#### **SAT-G40**

##### **TRANSCRIPTIONAL REGULATION OF *HIL*A IN *SALMONELLA ENTERICA* SEROVAR TYPHIMURIUM**

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*Salmonella enterica* serovar typhimurium is one of the most common foodborne pathogens in the world. It typically infects orally, traveling through the gastrointestinal tract until it reaches the Peyer's patch in the distal ileum of the small intestine. Once there, it activates its *Salmonella* pathogenicity island (SPI-1) Type 3 Secretion System (T3SS), a needle-like complex used to inject effector proteins into the host cell leading to bacterial invasion and inflammatory diarrhea. In order to evade immune detection, the SPI-1 T3SS must be tightly regulated. Research has shown that the regulation of this system is extremely complex, and it is mediated by different environmental signals through global regulatory systems. Many of these signals act through a single regulatory protein, HilA, which transcriptionally activates a multitude of structural and effector proteins required for a functional SPI-1 T3SS. PhoP and Hha are 2 global regulatory proteins that are known to repress *hilA*, but how that repression occurs is yet to be discovered. In this work, we transcriptionally fuse a suite of truncations of the *hilA* promoter region to the reporter gene *lacZ* to evaluate the regions required for regulation. PhoP and Hha are both able to repress transcription of *hilA* when the entire *hilA* promoter region is present. In shorter promoter regions, that repression no longer occurs, narrowing down the region necessary for regulation by these 2 proteins.

#### **SAT-G42**

##### **DOWNREGULATION OF CCR7 BY HIV-1 VPU IMPAIRS MIGRATION WITHIN PRIMARY CD4+ T CELLS**

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The human immunodeficiency virus type 1 (HIV-1) and acquired immunodeficiency syndrome (AIDS) pandemic has been the cause of over 60 million infections and 25 million deaths worldwide. Therefore, a better understanding of host-pathogen interactions is necessary for the eventual design of new therapeutics. In particular, the HIV-1 accessory protein Vpu is a small 81 amino acid (16 kDa) type I integral membrane phosphoprotein that is unique to HIV-1 and some simian immunodeficiency viruses (SIVs). To date, Vpu has been shown to antagonize 4 host proteins: CD4, BST-2, CD1d, and NTB-A. Each one of these actions promotes the counteraction of a particular mechanism of host innate immunity. Using flow cytometry,

immunoprecipitation (IP), immunoblotting, immunofluorescence, and molecular biology techniques, we reveal an additional target of Vpu: the chemokine receptor CCR7. CCR7 plays a crucial role in the homing of T cells to peripheral lymphoid organs for the assembly of immune responses. Our findings show that replication-competent HIV-1 down regulates CCR7 from the surface of infected CD4<sup>+</sup> T cells. Additionally, Vpu did not affect the endocytosis rate of CCR7 and seemed to sequester CCR7 within the trans-Golgi network (TGN). Total levels of CCR7 remained constant within HIV-infected cells, suggesting that Vpu does not degrade CCR7. Critically, cells infected with HIV were impaired in their ability to migrate towards CCR7's cognate ligand, CCL19. Therefore, rather than antagonizing a specific innate immune mechanism (as is the case for other targets of Vpu), down regulation of CCR7 hinders the functionality of T cells in a general manner.

### **SAT-G37**

#### **THE *VACCINIA* VIRUS K1 PROTEIN INHIBITS NF- $\kappa$ B ACTIVATION AT A POST-NF- $\kappa$ B NUCLEAR TRANSLOCATION STEP AND PLAYS A ROLE IN VIRAL PATHOGENESIS**

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Inflammation is an innate immune response to injury or microbial infection. When acute inflammation occurs, leukocytes migrate to the damaged region to aid in clearing bacteria and viruses. Nuclear factor kappa B (NF- $\kappa$ B) is a transcription factor that stimulates the inflammatory response by inducing pro-inflammatory gene expression. Inactive NF- $\kappa$ B, a p65-p50 heterodimer, is in the cytoplasm of every uninfected cell, and is associated with its inhibitory factor, I $\kappa$ B $\alpha$ . Upon an inflammatory stimuli, I $\kappa$ B $\alpha$  undergoes proteosomal degradation and NF- $\kappa$ B translocates to the nucleus, binds to DNA enhancer elements, and activates the transcription of its target genes. *Vaccinia* virus (VACV), the prototypical member of poxviruses, encodes 10 different inhibitors of NF- $\kappa$ B activation. One such inhibitor is K1, which was published to inhibit virally induced NF- $\kappa$ B activation by preventing the degradation of I $\kappa$ B $\alpha$ . However, we now find a distinct K1 inhibitory mechanism for TNF, PMA, and MyD88-induced NF- $\kappa$ B activation via luciferase reporter assays. In this case, K1 does not inhibit I $\kappa$ B $\alpha$  degradation. We have observed that K1 allows NF- $\kappa$ B nuclear translocation and DNA-NF- $\kappa$ B interactions, but inhibits NF- $\kappa$ B-dependent transcription. In addition, we found that the K1 protein is important for *Vaccinia* virus virulence in an intranasal mouse model as mice infected with a VACV lacking the K1 protein show complete survival and fewer signs of illness compared to mice infected with WT VACV. Increasing the knowledge of how viruses modulate the host environment to promote infection is beneficial as new therapies and recombinant vaccines could be developed.

### FRI-G43

#### **EVOLUTION AND DISPERSION OF INSERTION SEQUENCES IN *ACINETOBACTER BAUMANNII* RECOVERED FROM A CLINICAL SETTING BETWEEN 1983 and 2006**

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*Acinetobacter baumannii* is a multiple drug resistant (MDR) nosocomial pathogen that can cause various diseases. The ability of this bacterium to survive for long periods on inanimate surfaces and its MDR makes it a successful microorganism that is capable of causing outbreaks. In 1980 and 1990, most of the *A. baumannii* isolates were susceptible to carbapenems. However, in recent years it has increased in drug resistance to almost all available antibiotics to treat its infections. In order to understand genetic plasticity, MDR evolution, and the important role of insertion sequences (IS) in this bacterium, we decided to study IS that are associated with resistance genes. A total of 48 *A. baumannii* isolates with different resistance profiles recovered in a clinical setting of Buenos Aires between 1983 and 2006 were included in the study. Total DNA was extracted and used to perform PCR amplification reactions. To determine the relatedness of the isolates, pan-PCR assays were carried out, exposing the presence of 6 different pan-PCR amplification patterns. Amplifications of IS related to antibiotic resistance were performed. A predominance of IS125 (93.75%) followed by IS*Aba1* (64.58%) and IS26 (62.50%) was observed. IS*Pa14* was present in 26 of the isolates (54.17%), while IS*Pa12* was not found. A lower content of IS was observed in the oldest isolates in comparison to the ones recovered in 2006 that are all MDR. These results support the hypothesis that IS play a crucial role in the development of antibiotic resistance in *A. baumannii*.

### NEUROSCIENCE

#### **SAT-G46**

#### **TRANSLATIONAL CONTROL OF LEARNING AND MEMORY DEFICITS IN TUBEROUS SCLEROSIS COMPLEX**

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Tuberous sclerosis complex (TSC) is an autosomal genetic disorder found in 1 in 6,000 individuals and results in systemic tumor formation, autism, and epilepsy. TSC is caused by a mutation in one of the tumor suppressor genes, *TSC1* or *TSC2*, which function to incorporate inputs into the mammalian target of rapamycin signaling complex-1 (mTORC-1). Neuronal mTOR signaling functions to induce protein translation during the enhancement (LTP) or reduction (LTD) of synaptic strength. Adult *TSC2*<sup>+/-</sup> mice demonstrated reduced protein translation and reduced LTD at the synapse. We recently demonstrated an mTOR-independent mechanism that works through heightened ERK and metabotropic glutamate receptor 5 (mGluR5) signaling which drives salient TSC phenotypes. An mTORC1 independent plasticity implies that mTORC-1 inhibitors such as rapamycin will be ineffective in treating the neurological manifestations of TSC. Dissecting an alternate mechanism is thus necessary to push an effective TSC therapy forward. In this study, we propose that heightened ERK signaling



causes increased activation of RNA polymerase III (pol III) transcriptional activity, driving the expression of micro-RNAs (miRNAs) and hence downregulation of important protein translation factors at the synapse. To test this hypothesis, we are quantifying a number of pol III target gene transcripts in the hippocampus of adult TSC mice. We will test the role of heightened pol III activity in the neurological phenotypes associated with TSC using electrophysiological recordings in the mouse hippocampus and pol III inhibitors. The outcome of this project will be a novel suite of therapeutic targets to treat the neurological deficits associated with TSC.

#### **FRI-G46**

##### **THE EFFECTS OF *WITHANIA SOMNIFERA* ON RAT BRAIN CORTEX GABA<sub>A</sub> RECEPTORS MICROTRANSPLANTED INTO *XENOPUS* OOCYTES**

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*Withania somnifera* (WS), also known as ashwagandha, is an adaptogenic plant which has been used for thousands of years in Ayurvedic medicine. Experimental evidence has shown that WS has pharmacological effects on the central nervous system (CNS), showing anti-convulsive, anti-anxiolytic, and stress reducing properties. These pharmacological effects suggest that WS might function through GABAergic pathways. Indeed, recently, it was found that WS has GABA-mimetic activity probably through direct interaction with GABA<sub>A</sub> receptors. Though these are promising results, the main pharmacological activity and molecular mechanisms through which WS works are still unknown. To further elucidate the electrophysiological properties of WS on mammalian brain GABA<sub>A</sub> receptors, we prepared rat brain cortex membranes and microtransplanted them into *Xenopus* oocytes. We evaluated, 24 to 48 hours later, the electrophysiological effects of distinct WS root powder preparations (decoction, infusion, and dissolved solution, 3 commonly used preparations in traditional Ayurvedic medicine) on GABA<sub>A</sub> receptors. The mode of extraction seems to play a critical role in the composition and activity of the extracts. Our results show that the optimal WS preparation, infusion, had an EC value of 4.68 mg/mL (p-value = 3.81). Here we demonstrate a dose-dependent effect of WS root on GABA<sub>A</sub> ionotropic receptors. In addition, we were able to observe complex effects of WS as a GABA agonist and a partial inhibitor. Our data supports a complex modulatory effect on the CNS by WS.

#### **SAT-G45**

##### **THE EFFECTS OF *WITHANIA SOMNIFERA* ON NEUROTRANSMITTER RECEPTOR GABA<sub>RHO1</sub>**

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*Withania somnifera* (WS) is an herb traditionally used in Ayurvedic medicine for its adaptogenic properties. WS has been reported to have antistress, cognition facilitating, and anti-

inflammatory effects. Recently, WS was shown to have potential as a treatment for Alzheimer's disease by helping reduce plaque pathology in a mouse model. In the central nervous system, WS has been implicated in GABAergic pathways. Yet the mechanisms by which WS acts at the cellular level are unclear. We therefore aimed to test the effects of a WS root infusion, a commonly used form of WS treatment, on neurotransmitter receptor GABA<sub>A</sub>  $\rho$ 1 subtype (GABA <sub>$\rho$ 1</sub>) activity. GABA <sub>$\rho$ 1</sub> is an extra-synaptic receptor responsible for generating a tonic hyperpolarizing conductance that modulates the excitability and integration of synaptic activity, processes important for learning and memory. GABA <sub>$\rho$ 1</sub> synthetic cRNA was generated from pig retinal cells and microinjected into *Xenopus* oocytes to express functionally active homomeric ionic receptor channels. Electrophysiological properties of membrane receptors were then recorded after treatment with WS at varying concentrations. Here we report a novel finding of the dose-dependent activation of GABA <sub>$\rho$ 1</sub> by WS at a high affinity EC50 value of 0.081 ( $p = 1.64$ ). Our results provide an important target for the development of pharmacological treatments for neurological disorders associated with GABAergic pathways.

#### **FRI-G45**

#### **CA<sup>2+</sup>-PERMEABLE AMPA RECEPTORS IN THE MEDIAL PREFRONTAL CORTEX IN CUE-INDUCED REINSTATEMENT OF COCAINE SEEKING**

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Recent studies have focused on the role of corticostriatal circuits in vulnerability to cocaine relapse. Of interest to us is the bimodal modulation that the medial prefrontal cortex (mPFC) exerts on the nucleus accumbens (NAc). Previous studies have described the role of the pre-limbic (PL)-mPFC projections to the core of the NAc in driving cocaine seeking whereas infralimbic (IL)-mPFC projections to the NAc shell inhibit this behavior after extinction training. A key adaptation that has been observed in the NAc after forced abstinence is the accumulation of calcium permeable AMPA receptors (Cp-AMPA). The presence of Cp-AMPA receptors in response to cocaine-associated cues has not been investigated in the mPFC. We used the intravenous cocaine self-administration reinstatement model in rats to study the role of Cp-AMPA receptors in the mPFC in drug-seeking behavior. We prepared rat mPFC coronal brain slices (300  $\mu$ m) either 15 mins or 24 hrs after cue exposure and performed voltage-clamp recordings. Current-voltage relationship plots were used to calculate AMPA rectification index (RI). Our results show a decrease in RI in the PL-mPFC suggesting less Cp-AMPA receptors only 24 hrs after cue exposure. In the IL-mPFC, we observed an increase in the RI suggesting an increase in the levels of Cp-AMPA receptors. These results point at the 24 hr timepoint as the onset of these AMPA adaptations in the mPFC. Therefore, we propose that these adaptations are increasing responsiveness to drug-associated cues, and the behavioral correlate of these changes is an increase in cocaine seeking in our cue-induced reinstatement task.

## SAT-G48

### CLEARANCE MECHANISMS OF POLY-Q-EXPANDED HUNTINGTIN AGGREGATES

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Huntington's disease (HD) is a fatal degenerative brain disease caused by an abnormal lengthening of a CAG repeat encoding glutamine tract (poly-Q) in the Huntingtin (*Htt*) gene. The pathological hallmark of HD is characterized by the formation of protein aggregates and the selective degeneration of spiny neurons in the striatum. Importantly, it has been demonstrated that longer polyQ repeats are directly linked with increased formation of aggregates in cell and animal models of HD. We employ *Drosophila melanogaster*, commonly known as the fruit fly, to investigate the dynamics of aggregate formation and clearance of the human exon1-Htt-poly-Q-tagged with eGFP. By generating transgenic flies with variable lengths of polyQ, we have established *Drosophila* HD models where aggregates form robustly in an age- and polyQ-length dependent manner. We determined that clearance of mutant Huntingtin poly-Q aggregates is mediated by macro-autophagy, the catabolic process that signals dysfunctional cellular components for lysosomal degradation. Autophagy is initiated by trafficking of ubiquitinated proteins to the autophagophore by Ref(2)P, the fly homologue of human P62. We report an alteration in the autophagosome formation mechanisms in a poly-Q-length dependent manner. These results suggest a potential role of the autophagic flux in the clearance of polyQ aggregates and provide potential therapeutic targets for poly-Q diseases. Future work involves testing the function of the autophagosome scaffolding players in regulating the dynamics of mutant Huntingtin poly-Q aggregate formation. We expect to observe an aggressive protein aggregation in brains deficient of molecules regulating autophagosome initiation.

## NUTRITIONAL SCIENCES

## FRI-G48

### NUTRITION ENVIRONMENT SURVEY DEVELOPMENT FOR ELEMENTARY SCHOOL SETTINGS

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To address childhood overweight issues, interventions have targeted the school environment. These may include school meal offerings, nutrition education, or healthy eating promotions involving teachers, principals, food service workers, and community workers. Resources, attitudes, barriers, and perceived benefits of such changes can impact their adoption. With no current reliable survey to measure all of these variables, our objective was to create a school environmental survey that allows for baseline nutrition environment assessment of elementary schools in order to design and evaluate healthy interventions. Preliminary surveys based on previous studies were developed for elementary school principals, teachers, community

workers/health educators, and food service directors/managers. After being exempted by the Institutional Research Board, a panel of reviewers were identified to cover the breadth of occupations and perspectives (n = 7) for content and face validity. Feedback from individual panel members was gathered through interviews and written comments. Comments were summarized and consensus reached on changes. Recommended question changes primarily reflected formatting concerns. The Community Worker/Health Educator Survey was revised to exclude any overall school policy questions and to include their own teaching of nutrition or health. The food service manager and teacher survey changes primarily reflected changes in federal or local health policies or food procurement/service refinement. Overall, development of a baseline survey that assesses the nutrition environment, school wellness policies, and nutrition education may help researchers, public health officials, and school workers have a starting foundation for planning and evaluating healthy environmental changes in elementary school settings.

#### **SAT-G49**

#### **SAUDI ARABIAN STUDENTS IN THE U.S. USE NATURAL HEALTH PRODUCTS MORE SO THAN OTHER UNIVERSITY STUDENTS IN THE U.S.**

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Natural health products (NHP) are derived from organisms and may include supplements and herbal/traditional remedies. Published research indicates females use NHP more than males. In 2013 we reported Native/Aboriginal students use NHP more than non-native students. Less is known about Saudi students. We hypothesize there are gender and ethnic differences in NHP use. Students from Wayne State University (n = 560; 193 males and 367 females) participated in a cross-sectional online-survey of NHP with a sample of 64 Saudi students. A  $\chi^2$  test detected group differences. Multiple logistic regression models (MLR) predicted variables of NHP use. The alpha-level was 0.05, and data were analyzed with SPSS Software 22. Of 560 surveyed students, 353 (63%) used NHP, while 207 students (37%) did not. There were differences in NHP use among student nationalities: Saudi vs. non-Saudi, p = 0.003; Hispanic vs. Middle Eastern, p = 0.025. There were no differences in NHP use between students: male vs. female and Middle Eastern vs. non-Middle Eastern. Predictors of NHP use were freshman (95% OR = 0.43, CI = 0.22 - 0.88, p = 0.02) and sophomore (95% OR = 0.46, CI = 0.25-0.84, p = 0.01) compared to 3<sup>rd</sup>, 4<sup>th</sup>, and graduate-level years. Additional predictors include age: young age (18 y  $\geq$  to 25 y) (95% OR = 0.41, CI = 0.24-0.69, p = 0.001)] vs. older age (26<sup>+</sup> y). There is significant use of NHP among Saudi and Hispanic students in the United States. Predictors of NHP use are grade level (freshman and sophomore) and young age (18 y  $\geq$  to 25 y). Future work should clarify differences of NHP use by Latin American students vs. Hispanic students.

## OTHER AGRICULTURAL SCIENCES

### FRI-G50

#### A GPCR-FOCUSED INVESTIGATION OF THE *R. MICROPLUS* TRANSCRIPTOME

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*Rhipicephalus microplus*, also known as the southern cattle tick, has been found in tropical and subtropical regions all over the world, including Mexico. It is a vector for parasites responsible for cattle diseases that can lead to decreased weight, anemia, loss of milk/meat production, and death. The cattle tick was eradicated from the United States in the early 20<sup>th</sup> century; however, the ease for tick-carrying animals to cross the border, cattle importation from Mexico, and the cattle tick's growing resistance to acaricides are becoming causes for concern since reinfestation of the United States might occur. The objective of this project is to develop a bioinformatics pipeline for identifying possible G-protein coupled receptors (GPCRs), utilizing sequence length and number of helices. A series of Python scripts were written to analyze the cDNA sequences reverse-transcribed from the transcriptome of the synganglion of the cattle tick. Using these scripts, possible protein coding regions are obtained from the cDNA and are input into the Transmembrane Hidden Markov Model web server. The protein sequences identified by the scripts as potential GPCRs were run through a stand-alone version of Pfam, a database of conserved protein domain families, which classified the submitted proteins by comparing them to the Pfam library of Hidden Markov Models. This output and a sequence similarity search by BLASTX resulted in 28 probable GPCRs. All protein coding regions for the synganglion were run through Pfam for comparison (72 GPCRs were identified) and for identifying the encoded proteins.

### SAT-G50

#### *RALSTONIA SOLANACEARUM* BACTERIOCIN DIVERSITY AND SPECIFICITY WITHIN THE SPECIES COMPLEX

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Bacterial wilt, caused by members of the *Ralstonia solanacearum* species complex, is an economically important vascular plant disease affecting many important agronomic plants including potato, tomato, banana, and pepper. Humans have globally distributed *R. solanacearum* strains but, for unknown reasons, different strains rarely occur in the same field and have never been found in the same plant. In the stems and rhizospheres of whole tomato plants, a North American strain (K60) outcompeted both a tropical Asian strain (GMI1000) and a cool temperate Race 3 strain that causes potato brown rot (UW551). The North American strain also inhibited growth of other *R. solanacearum* strains in culture. The inhibitory activity was secreted, heat-labile, degraded by proteinase K, larger than 50 kDa, and had no activity against

tested non-*R. solanacearum* bacteria. We hypothesize that the inhibition is caused by bacteriocins, proteinaceous toxins produced by bacteria to inhibit the growth of similar or closely related bacterial strains, which may mediate competition among *R. solanacearum* strains in the field. Five Tn5 mutants of strain K60 had fully or partially lost the ability to inhibit growth of Race 3 on plates. Four of the 5 mutants had Tn5 insertions in genes encoding diverse Rhs domain proteins of around 65 kDa. The K60 genome encodes 21 putative Rhs proteins, which are cell surface or secreted toxins. Characterization of these genes is under way to better define the role of bacteriocins in competitive fitness within the *R. solanacearum* species complex and their potential application to control bacterial wilt disease.

## OTHER BIOLOGICAL SCIENCES

### SAT-G52

#### IDENTIFYING A PHARMACOPHORE FOR THE ESTROGEN RECEPTOR $\alpha/\beta$ HETERODIMER TO DECIPHER ITS BIOLOGICAL ROLE

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Estrogen plays an important role in the normal development and growth of the mammary gland. The binding of 17 $\beta$ -estradiol (E2) and other estrogenic compounds to the estrogen receptor (ER) leads to its dimerization and consequent genomic transcription and cascade of biological activities. ER $\alpha$  and ER $\beta$  have been shown to exhibit a yin-yang relationship in regulating breast cancer cell growth: ER $\alpha$  promotes cell growth while ER $\beta$  inhibits it. At the receptor level, ER $\beta$  appears to negatively regulate the proliferative role of ER $\alpha$  through the formation of ER $\alpha/\beta$  heterodimers. The objective of this study is to identify natural estrogenic compounds which promote the formation of ER $\alpha/\beta$  heterodimers, thereby activating ER $\beta$  while dampening ER $\alpha$  activity, which might have a protective effect in breast cancer. We initially screened 37 phytoestrogenic compounds from 4 flavonoid subclasses in a 2-step screening process that includes activation of ER gene transcription using an ER-dependent reporter assay and dimerization using the bioluminescent resonance energy transfer (BRET) assay where 6 slightly selective ER $\alpha/\beta$  heterodimer-inducing compounds were identified. *In silico* studies were then performed to identify the pharmacophore that confers ER $\alpha/\beta$  heterodimer specificity in order to design high affinity ligands. Further characterization of these compounds will allow us to decipher the biological role of the ER $\alpha/\beta$  heterodimer.

### FRI-G52

#### A BIOINFORMATICS APPROACH TO IDENTIFY POTENTIAL ENHANCER ELEMENTS FOR GENES EXPRESSED IN THE MUSHROOM BODY NEURONS IN *DROSOPHILA*

Carolina Guerra, Raymond Ford, Ming-Ying Leung, Kyung-An Han.

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Bioinformatics is an interdisciplinary science that focuses on the management and interpretation of data obtained from complex biological phenomena using mathematical models, computational algorithms, and statistical methodologies. In this project, we combine

several existing bioinformatics software for identifying DNA motifs with other computational tools to develop a new approach for finding potential enhancer elements of a set of genes related to learning and memory in *Drosophila*. Through the use of web scraping scripts, we collected data of interest from the HHMI Janelia Farm Research Campus and FlyBase to construct 6,931 FASTA files containing the DNA sequence data for *D. melanogaster*. Using 6 different DNA motif discovery software, 18 conserved motifs were identified among the DNA sequences driving mushroom body expression. The FASTA files for all Janelia Farm lines were computationally searched to determine if any of the discovered motifs were present in these sequence data. This information can be used to identify potential enhancer elements for the genes expressed in the mushroom body gamma neurons, which are responsible for learning and memory. With these results, we can further identify additional genes expressed in the gamma neurons which mediate dopamine and octopamine signals that are involved in neuropsychiatric disorders including ADHD, autism, schizophrenia, Parkinson's disease, and drug abuse/addiction. This study would ultimately help understand the underlying pathological mechanisms.

#### **SAT-G51**

##### **STRUCTURAL OPTIMIZATION OF THE RAC GTPASE INHIBITOR EHOP-016**

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Recently, we discovered EHop-016 as a novel small molecule inhibitor of Vav2-Rac1 interactions in MDA-MB-435 metastatic cancer cells at low micromolar concentrations. By inhibiting Rac, EHop-016 reduced lamellipodia formation, cell migration, and metastasis. Preliminary *in vivo* experiments in xenograft mice implanted with MD-MBA-435 demonstrated that EHop-016 reduced tumor growth and metastasis. Nevertheless, the therapeutic index (*in vitro* activity in tumor cells vs. toxicity against epithelial cells) is quite low. Therefore, there was a need to develop new derivatives of EHop-016 in order to further optimize the activity, reduce the toxicity, and improve physicochemical parameters. EHop-016 consists of 3 major building blocks and, via synthesis and testing of novel derivatives, the carbazole group was demonstrated to be important for maintaining inhibitory activity. Molecular docking was utilized to aid in the design of additional new compounds with modifications in the central core and the pending morpholine group. Compounds with promising binding energies and favorable physicochemical parameters were synthesized and tested for activity. The synthetic procedures and the analysis of the structure activity relationships will be presented. The presented improved inhibitors of Rac activity could possibly be used for treatment of metastatic breast cancer

**FRI-G81****ENVIRONMENTAL AND ANTHROPOGENIC INFLUENCES IN DENGUE INCIDENCE: A CASE STUDY FROM YUCATÁN STATE, MÉXICO**

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Vector-borne diseases are an important issue for communities around the world. Among these, dengue fever is a major vector-borne disease in Yucatán state, México, with thousands of cases reported annually. The dengue fever vector in the Yucatán Peninsula is *Aedes aegypti*, a tropical/subtropical mosquito that flourishes in urban areas. It reproduces easily in artificial water containers. Studies have shown that dengue cases increase with increased rainfall. Understanding spatiotemporal variations in dengue distribution in specific geographic areas could help improve disease prevention and forecasting. We studied the relationship between dengue incidences and meteorological and other environmental data and mapped cases per population in the Yucatán Peninsula. We hypothesized that areas with high urban pixels and rainfall would influence dengue occurrence. To test for these influences and potential forecasting, we collected data per municipality on dengue cases from the Sistema Nacional de Información de Salud (SINAIS) and geographic/demographics from the Instituto Nacional de Estadística y Geografía (INEGI) for 2011. Meteorological data were obtained from 7 airports in the Yucatán Peninsula and interpolated utilizing spatial analyses. Geospatial analyses were used to create an unsupervised land cover classification map for urban pixels extraction. Multivariate regression analyses showed that seasonal changes (rainy/dry) had a statistical significant association with dengue incidences ( $P < 0.05$ ;  $\beta = -7.9$ ), whereas temperature, rainfall, urban pixels, and population did not show significance ( $P > 0.05$ ). Overall, these preliminary results suggest seasonal influences on dengue incidences. Further investigation will be needed to identify specific associations with these climatic and physio-environmental factors to improve disease prevention and forecasting.

**FRI-G51****HUMAN-INDUCED PLURIPOTENT STEM CELL *IN VITRO* MODELS OF DIFFERENTIATION ALLOW FOR THE PREDICTION OF CARDIAC AND SKELETOGENIC TERATOGENS**

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<sup>1</sup>*University of California, Riverside, Riverside, CA,* <sup>2</sup>*University of California, San Diego, La Jolla, CA.*

Within the past decade, human-induced pluripotent stem cells (hiPSCs) have become the center of concentrated research efforts in pharmaceutical and toxicological assessments. As hiPSCs are highly similar to human embryonic stem cells (hESCs) in genetic and epigenetic regulation of gene expression, proliferation ability, and differentiation capacity, hiPSCs have been identified as a promising alternative to hESCs in *in vitro* toxicity evaluations such as the embryonic stem cell test (EST). Originally murine-based, the EST is a well-established assay that evaluates embryotoxicity of compounds by measuring cell viability and capacity of ESCs to differentiate into functional (i.e., beating) cardiomyocytes following treatment. At present, EST



teratogenicity screens featuring hiPSC-derived cardiac and non-cardiac tissue endpoints have not yet been reported, though numerous screens with hESCs have been successfully carried out. This study investigated the robustness and predictive capacity of the hiPSC-based EST featuring cardiac and bone tissue endpoints. Cells were treated with compounds possessing established toxicity assessments: 5-fluorouracil (5FU), retinoic acid (RA), and penicillin G (non-teratogenic; negative control). Differentiation inhibition was measured via beating and calcium assays for cardiac and bone endpoints, respectively. Cell viability was measured by MTT assays for both tissue endpoints. Day 10 changes in cardiac and osteogenic gene expression were assessed by qPCR analysis. Dose-dependent cell death, differentiation inhibition, and down regulation of gene expression were observed in 5FU and RA in both tissue endpoints. Results demonstrate that cardiac and bone endpoints in the hiPSC-based EST are comparable to the hESC-based EST in their predictive capacity for toxicological analysis.

## PHARMACOLOGY

### SAT-G54

#### **CANNABINOID RECEPTOR FUNCTION ON BONE MARROW-DERIVED DENDRITIC CELLS**

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Dendritic cells (DCs) are professional antigen-presenting cells that are indispensable in the linking of innate and adaptive immune responses. Each distinct DC subset has its unique set of surface markers and different abilities to respond to environmental stimuli and process antigen. Mammals express at least 2 types of cannabinoid (CB) receptors, Cannabinoid receptor 1 (CB<sub>1</sub>) and Cannabinoid receptor 2 (CB<sub>2</sub>). The role of the CB receptors on DC development, function, and susceptibility to exogenous cannabinoid compounds such as  $\Delta^9$ -tetrahydrocannabinol ( $\Delta^9$ -THC) has not been characterized. The objective of the present study was to determine CB receptor function in the development and maturation of DC subsets from mouse bone marrow. Bone marrow was extracted from femurs and tibias of WT (C57bl6) and KO mice and stained for DC markers. Our results indicate that the percent of DC populations, determined by CD11c expression, composes ~38% of freshly isolated bone marrow cells in WT mice and ~48% in KO mice. We also found that KO bone marrow has a higher percent of MHC I<sup>+</sup> cells. On the other hand, WT mice demonstrated a slightly higher percent MHCII<sup>+</sup> cells. Monocyte DCs followed by CD103 were the major CD11c<sup>+</sup> subpopulations identified in mice bone marrow. Monocyte DCs and their MHC I expression were significantly higher in freshly isolated bone marrow of KO mice. Bone marrow cells isolated from KO mice were able to induce a T cell response in the absence of LPS stimulation. Our findings suggest a possible role of CB receptors in DC maturation and subset development.

**SAT-G55****ACTIVATED PROTEIN C PROMOTES CO-ASSOCIATION OF PROTEASE-ACTIVATED RECEPTOR 1 AND SPHINGOSINE-1-PHOSPHATE RECEPTOR 1 AT THE PLASMA MEMBRANE**

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This research aims to understand how the GPCRs, PAR1 and S1PR1, mediate cytoprotective signaling in endothelial cells. APC is an anti-coagulant protease that also functions as an agonist for PAR1 to promote cytoprotective signaling. APC was used previously as a therapy for the treatment of sepsis but has been withdrawn due to increased bleeding events associated with its anti-coagulant properties. Sepsis is a systemic inflammatory reaction caused by a bacterial infection that has a high mortality rate and severe tissue edema. However, there are currently no drugs approved by the FDA for the treatment of sepsis. This project aims to dissect the mechanism of APC-mediated cytoprotective signaling with the goal of identifying new targets for the development of drugs that can be used for the prevention and treatment of sepsis. Our hypothesis is that PAR1 and S1PR1 are co-associated, and together promote biased cytoprotective signaling that leads to endothelial barrier stabilization and reduced permeability. To complete these studies, we utilized a variety of cell and molecular biology techniques as well as biochemical assays and cultured human endothelial cells. These techniques include bioluminescence resonance energy transfer, confocal immunofluorescence microscopy, and co-immunoprecipitation. Preliminary results show evidence that PAR1 and S1PR1 associate at the plasma membrane and that this association is mediated by APC treatment. We expect that this co-association occurs endogenously in cultured endothelial cells. These results provide the background for the identification of PAR1 small molecule biased agonists that mimic APC-mediated cytoprotective signaling, potentially leading to therapeutic targets for sepsis treatment.

**FRI-G54****XYLAZINE AS A DRUG OF ABUSE: TOXIC EFFECTS TO ENDOTHELIAL CELLS IN COMBINATION WITH COCAINE AND HEROIN**

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The use of xylazine in Puerto Rico and worldwide as a drug of abuse and its combination with cocaine and/or heroin has increase in recent years. Xylazine is approved by the FDA for animal use only. Clinical findings reported that xylazine users presented limb skin lesions, ulcerations, and greater physiological deterioration than heroin users only. The aim of this study was to assess the cytotoxicity of xylazine on endothelial cells, as this is the first tissue affected upon administration. Human umbilical vein endothelial cells in culture were treated with xylazine, cocaine, heroin, and their combinations from 10 nM to 400  $\mu$ M at exposure periods of 24, 48, and 72 hours. IC<sub>50</sub> was determined applying a fluorometric assay for viability determination. The Annexin V assay was also implemented as well as activation of caspases 8 and 9 in order to determine apoptosis as the cell death mechanism. Results indicated IC<sub>50</sub> values at 24 hours as

follows: xylazine 62  $\mu$ M, cocaine 202  $\mu$ M, heroin 278  $\mu$ M, and the combination of the three drugs 55  $\mu$ M. Similar  $IC_{50}$ s was observed at 48 and 72 hours. The Annexin V positive results as well as the positive activation of caspases 8 and 9 strongly suggest apoptosis as the cell death mechanism. The study demonstrated that xylazine inhibits endothelial cell proliferation at lower concentrations than cocaine and heroin. These findings support that xylazine use increases the toxicity of cocaine and heroin when used in combination and induce cell death by apoptosis.

### **FRI-G53**

#### **DIETARY SUPPLEMENTS INFLUENCE ACTIVITY OF ACID-SENSING ION CHANNELS**

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Dietary supplements and nutraceuticals have been the focus of research to identify novel therapeutics for a variety of pathologies, including the prevention of long-term consequences from stroke and pain reduction. Ion channels offer a growing group of molecular targets for treatment, which include the acid-sensing ion channels (ASICs). Acid-sensing ion channels (ASICs) are sodium channels that are sensitive to changes in extracellular pH, specifically those changes following injury and ischemia. The ASICs are trimeric channels with large extracellular domain, transmembrane domain, and intracellular N and C termini. These channels are expressed most prominently in the peripheral and central nervous system. Their role in physiology is yet to be fully understood, but these channels have been implicated in pain sensation and centrally in the neurodegeneration following ischemic stroke. We identified an over-the-counter dietary supplement (DS) that shares a similarity with guanidine compounds that selectively modulate acid-sensing ion channels. Thus, we hypothesize that this dietary supplement inhibits channel activity in acid-sensing ion channels. We used whole-cell patch-clamp electrophysiology. Our preliminary data show that DS decreased the ASIC1a pH sensitivity by shifting the observed proton activation profile to the right, and it reduced peak current amplitude of the channel. Furthermore, we observed a change in the ASIC1a steady-state desensitization profile. Future experiments will focus on determining the influence of DS on other acid-sensing ion channel subtypes and identifying the DS binding site with the protein structure.

### **PHYSIOLOGY/PATHOLOGY**

### **FRI-G55**

#### **MIR-155 IS A KEY REGULATOR OF MICROGLIA BEHAVIOR IN RESPONSE TO NEUROINFLAMMATION**

Macarena Aloj, Wei Su, Dongyoon Kang, Bryce Sopher, Stephanie Hopkins, Gwenn Garden.

*University of Washington Seattle, Seattle, WA.*

Neuroinflammation is observed in acute and chronic central nervous system (CNS) injury, including traumatic brain injury and neurodegenerative diseases. Microglia are a specialized population of resident myeloid cells that mediate CNS innate immune responses to disease

relevant stimuli. Previously we described a novel mechanism by which p53, an ROS responsive transcription factor, modulates microglia behaviors *in vitro* and *in vivo*, promoting pro-inflammatory functions and suppressing the downregulation of the inflammatory response and tissue repair. We demonstrated that p53 negatively regulates the anti-inflammatory transcription factor c-Maf through 2 micro RNA (miRNA)-mediated pathways in cultured neonatal microglia and a macrophage cell line. One regulator of c-Maf expression is miR-155. To evaluate the regulative role of miR-155 in microglia activation, we used both neonatal and adult microglia cultures from miR-155 (*mbic*) knockout mice. However, since it is not known if miR-155 also plays roles in development, a more applicable model to study adult microglia behavior can be achieved by deletion of miR-155 in adult cells. Therefore, to assess the role of miR-155 in modulation of adult microglia activation phenotypes, we successfully developed an adeno-associated virus (AAV) serotype 2 vector to introduce CMV-Cre into floxed-miR155 (miR-155<sup>flx/flx</sup>) microglia. We observed the effect of chronic or transient deletion of miR-155 on several microglia responses to inflammatory signals, including altered expression of markers of classical activation phenotypes, phagocytosis of apoptotic cell bodies, and cytokine release. Taken together our preliminary findings support the hypothesis that p53 influences microglia function in response to inflammatory signals through miR-155 mediated modulation of c-Maf expression.

## ZOOLOGY/ENTOMOLOGY

### SAT-G56

#### A PHYLOGENY OF THE BURROWING WATER BEETLE (COLEOPTERA: NOTERIDAE) INFERRED FROM COMBINED MOLECULAR SEQUENCE AND MORPHOLOGICAL DATA

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The Noteridae (Coleoptera: Adephaga), commonly called the burrowing water beetle, is a small family of aquatic beetles comprised of 17 genera and approximately 260 species. Despite being globally well-dispersed and common in aquatic beetle collections, the Noteridae have received little attention from the entomological community, with a few weak studies of the systematics of the family. Here we address this problem by constructing a phylogeny of the Noteridae based on both molecular sequence and morphological data. The phylogeny is inferred from the analysis of sequences of four gene fragments, Cytochrome c oxidase I (COI) mtDNA, Histone 3 (H3) nDNA, 12s rDNA, and 16s rDNA, and 35 adult morphological characters. A taxon sampling of 70 species is used, including representatives of all noterid genera and outgroups. Resulting trees based on the different analyses are provided. Phylogenetic relationships of genera, character evolution, and future studies within the Noteridae are presented and discussed.

## COMPUTER/INFORMATION SCIENCES

### FRI-G56

#### EXPERIMENTAL EVALUATION OF LEARNING ALGORITHMS AND TEXT REPRESENTATION FEATURES TO CLASSIFY MEDICAL QUERIES IN BRAZILIAN PORTUGUESE

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The objective of this research is to develop an automatic method to classify medical queries to direct the question to the appropriate medical specialist. The questions were submitted by Brazilian medical professionals to RedeNUTES at the Universidade Federal de Pernambuco in Recife, Brazil; the dataset contains 2,481 questions and 33 classes. We evaluated several machine-learning algorithms including support vector machines, k-nearest-neighbors, naïve Bayes, and decision trees. We also experimented with 2 types of representations: word frequencies and binary indicators of word appearances. Preliminary results indicate that support vector machines in combination with binary indicators yield the most accurate results. The significance of developing an automatic method that correctly identifies medical queries would allow improved health care in remote areas and faster identification of health trends.

## EDUCATION

### EDUCATION RESEARCH/ADMIN. (EXCEPT EDUC./SCHOOL PSYCHOLOGY)

### FRI-G57

#### OKAY, TIME TO FILL-OUT OUR RUBRICS: THE EFFECTS OF SELF-EVALUATION ON STUDENTS' LEVELS OF ENGAGEMENT

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Engagement is a crucial factor for succeeding academically and reaching high levels of attainment in the classroom. Students' levels of engagement are highly correlated with students' self-efficacy beliefs which are important to identify in order to understand behaviors that may be impacting student engagement and learning. Self-assessment is a useful tool to identify self-efficacy in the classroom and to motivate students to modify behaviors to increase engagement and academic success. Self-assessment tools can empower students to understand the criteria for judging success and guide their own learning in a more individualized manner. This study examines the effects of self-evaluations in students' levels of engagement in the classroom. Utilizing an action-research approach to education, we created and applied self-assessment rubrics to a curriculum for our students to self-assess their levels of engagement in two secondary mathematics II classrooms in Salt Lake City, Utah. Over the course of a semester, we observed, recorded, and analyzed the students' self-evaluations to examine trends in student engagement-level and how they related to certain positive and negative behaviors and classroom dynamics (i.e., phone use, cultural relevancy, instructional strategies, etc.). The findings in this study suggest self-assessment plays an important role in increasing students'

levels of engagement in the classroom. Through self-assessment, students may be able to recognize factors that affect their engagement and disengagement in the classroom, which can then be conducive to building and reinforcing behaviors to increase engagement and attainment in the classroom.

#### **SAT-G57**

##### **INCREASING CAMPUS KNOWLEDGE OF WASTE GENERATION AND REDUCTION TECHNIQUES**

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The campus waste diversion rate, recyclables removed from the traditional waste stream (e.g., landfills and incinerators), at Wayne State University (WSU) has been low in past years. In 2012, the Office of Campus Sustainability at WSU shows a low diversion rate (19%). Prior research has shown a correlation between knowledge and environmental attitudes. We hypothesize that there will be an increase in the diversion rate among different university's buildings throughout a Green Warrior Project (GWP) initiative. The study will measure 8 high-population buildings on the WSU campus. The GWP seminars will be presented to students, staff, and faculty at 4 buildings, and the other 4 buildings (control groups) will not receive the GWP. The data will be collected once a month during spring, summer, and fall 2014 terms. A one-way ANOVA test will be used to analyze the different independent groups with the alpha level set at 0.05. Data will be analyzed with SPSS Software 22. We expect increases in the diversion rate among different university buildings and that the groups of university buildings that receive the GWP will show greater diversion rate than the control building groups. The expected increase in the campus diversion rate will yield new opportunities to further investigate the effects of the GWP. The evidence-based efficacy resulting from GWP seminars conducted will allow a clear assessment of the correlation between diversion rate and waste reduction education. Future work will include assessment of additional areas of solid waste reduction such as food waste in the dining halls.

## **ENGINEERING**

### **BIOENGINEERING/BIOMEDICAL ENGINEERING**

#### **SAT-G58**

##### **META-ANALYSIS OF GENETIC SIGNALING PATHS: FIRST IDEAS AND RESULTS**

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Establishing the role of different genes in the development of cancer can be a daunting task starting with the detection of genes that are important in the illness from high throughput biological experiments. These experiments belong to the "... omics" denomination, as in genomics, proteomics, metabolomics, and the like. Furthermore, it is safe to say that even with a list of potentially important genes, it is highly unlikely that these show changes in expression

in isolation. A biological signaling path is a more plausible underlying mechanism. This work attempts the simultaneous analysis of multiple microarray experiments to build a mathematical network problem. A preselection of genes is carried out with a multiple criteria optimization framework previously published by our research group. First results are presented in cervical cancer and lung cancer.

#### **SAT-G59**

##### **CLICK-CHEMISTRY-BASED MOLECULARLY RESPONSIVE HYDROGEL AS BIODEGRADABLE SCAFFOLDS FOR 3-D CELL CULTURE**

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In order to better understand how cancer grows and metastasizes, researchers are interested in the development of platforms to model the environment of tumor tissue and enable the study of the effects of cancer cell-secreted molecules on cell replication, extracellular matrix remodeling, and cell migration leading to metastasis. Due to their tissue-like properties, hydrogels have the ability to serve as such model systems by providing a 3-dimensional scaffold in which cancerous cells could be cultured and studied. The goal of this work is to develop a hydrogel system that is molecularly responsive, can be synthesized at physiological conditions, and could be used as a model for the study of cancer cell growth. In order to achieve this goal, we focused on 1) the development of an aptamer complex to be used as a crosslinker within the hydrogel network that is responsive toward the cancer cell-secreted protein vascular endothelium growth factor (VEGF), 2) the development of methods for the synthesis of hydrogels under mild conditions via copper-free click chemistry, and 3) the integration of cell adhesive properties to the hydrogels through a cyclo-arginine-glycine-aspartic acid (cRGD) peptide that mimics fibrin and collagen. In doing so, a hydrogel that is molecular responsive, nontoxic, and capable of encapsulating cells is fashioned in order to serve as a 3-dimensional platform for their study.

#### **CHEMICAL ENGINEERING**

#### **FRI-G60**

##### **IDENTIFYING IMMUNE RESPONSES OF VERY-LATE ANTIGEN-4 INTEGRIN RECEPTORS THROUGH FLUORESCENCE LIFETIME USING A RETROFITTED FLOW CYTOMETRIC SYSTEM**

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Very late antigen-4 (VLA-4) belongs to a family of heterodimeric integrin adhesion receptors. Integrins expressed on immune cells mediate that cell-cell and cell-matrix interactions are important for immune responses. Integrin-mediated adhesion is regulated by cell signaling through conformational changes that include integrin extension. However, studies of integrin conformation are hampered by heterogeneity in the receptor population where multiple states are difficult to assess using traditional methods. Here we distinguish VLA-4 conformation after

signaling using a FRET protocol and fluorescence lifetime in a flow cytometer. The human U937 cell line stably transfected with formyl peptide receptor (FPR) was used in this study. Cells were stained with a VLA-4-specific ligand donor (LDV-fluorescein) bound to the VLA-4 headgroup. The membrane was stained with a fluorescent lipid acceptor (PKH-26). The integrin conformational change was induced by treating cells with FPR ligand (formyl-Met-Leu-Phe-Phe). Previously, this model system showed changes in the fluorescent intensity consistent with a bent integrin at rest and a partially extended integrin after activation. We used radio frequency modulated laser light to elicit a sinusoidal waveform in both the side-scatter (SSC) and fluorescence channel (FL1). The time-lapse between both waveforms provides the phase angle that is proportionate to the fluorescence lifetime. The addition of FRET acceptor shortened average fluorescence lifetime of the donor from  $4.00 \pm 1.00$  ns to  $3.35 \pm 1.25$  ns (per 1,000 events recorded) that supported our intensity data. Currently, we are focusing on activation-induced conformational changes. Using this novel technology, we are anticipating a distribution of fluorescence lifetime that corresponds to individual integrin states.

#### **FRI-G59**

##### **ROLL-TO-ROLL SYNTHESIS OF VERTICALLY-ALIGNED CARBON NANOTUBE ELECTRODES FOR ELECTRICAL DOUBLE LAYER CAPACITORS**

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Electrochemical double layer capacitors (EDLCs) have emerged as promising solutions for high power/high energy applications. The unique properties of carbon nanotubes (CNTs) such as high electrical conductivity; electrochemical, mechanical, and chemical stability; high surface area; and low mass density, make them suitable candidates for EDLC electrodes. Vertically-aligned, multi-walled CNTs (VACNTs) have been considered for use in EDLCs due to their facile synthesis and the ability to control the ion-accessible surface. Chemical vapor deposition (CVD) has emerged as a practical and reliable method for VACNTs production, offering versatility in terms of controlling CNT characteristics and relatively low temperature requirements ( $<1,000$  °C); however, technological advances are limited by the lack of continuous and scalable synthesis methods. Three primary factors limit continuous manufacturing of nanomaterials: substrate size determined by reactor geometry, requirements of complex catalytic substrate preparation, and high operating temperatures that are incompatible with traditional current collectors (e.g., Al foil). In this work, we present a scalable roll-to-roll process for synthesizing forests of VACNTs on inexpensive Al foil ribbons which are continuously drawn through a CVD reactor operating at ambient pressure and a relatively low growth temperature (600 °C). EDLC electrodes comprising VACNT forests synthesized in continuous and stationary CVD processes are directly assembled into supercapacitor cells, which yield high power densities (1,270 W/kg) and energy densities (11.5 Wh/kg). These devices exhibit very low internal series resistance due to their intimate contact with the current collector and excellent cycle stability with no loss in performance over multiple thousands of cycles.



## **ELECTRICAL/ELECTRONICS/COMMUNICATIONS ENGINEERING**

### **SAT-G61**

#### **A MICROCONTROLLER-BASED SYSTEM FOR IMPROVING THE LEARNING PROCESS OF UNDERGRADUATE STUDENTS IN THE AREA OF CONTROL SYSTEMS**

Juan Felipe Patarroyo, Gerson Beauchamp, Carlos Bolívar.

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Many class projects in control systems are developed using high-level simulation tools and data acquisition boards. The results using this method have been excellent so far. However, we have identified a new need: students need to learn how to implement digital control systems directly with microcontrollers since the current approach hides several important features of the implementation that are needed in professional practice. A proposed solution to this problem is to create a Texas Instruments C2000 microcontroller-based development board capable of reading several types of sensors and activating several types of actuators. The proposed boards will have protection for overvoltage or bad connections. The system will be autonomous in the sense that, once programmed, no external computer will be needed. To enhance the learning experience and decrease the implementation time of projects, we are developing a set of C language libraries to facilitate the implementation of control systems in several control environments: digital control, fuzzy logic, robotics, and state-variable feedback. The effectiveness of this approach against other methods such as Simulink® and LabVIEW® will be demonstrated through pedagogical experiments with several groups of undergraduate students. Also, we will evaluate the learning curve for each of the participants in the learning process.

### **SAT-G62**

#### **SATELLITE GROUND STATION SOFTWARE – DATABASE**

Enrique Torres, Hien Vo.

*Ana G. Méndez University System, Gurabo, PR.*

The satellite ground station is an important component of the CubeSat nano-satellites. The ground station must have a database to store, log, and register the data transmitted by the CubeSats in low-Earth orbit. The database will log and register the data obtained and will store telemetry data for every component of the CubeSat that the on-board computer was programmed to fetch in addition to the data that the QB-50 project specified for this mission: whole orbit data (WOD) and science data (SD). The WOD is basic data to indicate if the main components of the CubeSat are working properly. The SD is data the scientific device or payload obtained during the mission. The WOD and SD datasets are strictly structured and can be stored in the database as either raw or processed data. We used MySQL and Qt software, which was used to develop the satellite ground station software. Our objective is to have a functional database to store all the CubeSat data needed to interact with the existing satellite ground station software and the Mission Control Center.

**FRI-G62****DESIGN AND IMPLEMENTATION OF A FUZZY LOGIC CONTROLLER USING OPERATIONAL AMPLIFIERS**

Nicolas Cobo, Rogelio Palomera.

*University of Puerto Rico, Mayaguez Campus, Mayaguez, PR.*

Fuzzy logic has made possible the control of non-linear systems that are difficult to model mathematically with conventional methods, or for which the existing model is very complicated. The methodology is based on a set of rules, described in human language, established by an expert in the system that is to be modeled. These sets of rules are then translated into relatively simple mathematical steps, which allow the realization of a physical controller. The practical implementation of the physical system can be performed in different ways. In all cases, the system's blocks and subcircuits should execute the necessary algorithms such as input/output membership functions, minima and maxima comparisons, and defuzzification methods. This work proposes a hardware implementation using only discrete components that can be found in most basic electronics laboratories. This permits an economic, embedded assembly that provides a real-time response when compared with the response obtained with a software solution. Also, it offers to the user and students a tool for prototyping and getting proofs of concept for different applications.

**SAT-G80****EXPLOITING SENSOR ARRAY MOTION FOR AUGMENTATION OF CO-PRIME LINEAR ARRAYS**

Juan Ramirez Jr., Jonathan Odom, Jeffrey Krolik.

*Duke University, Durham, NC.*

We combine concepts from synthetic aperture processing and non-uniform linear array theory. Our objective is to use array motion to synthesize an array that can achieve the performance of a filled, uniform linear array (ULA), but with fewer sensors than required for spatial Nyquist sampling. The class of physical arrays we use for synthesis are co-prime arrays constructed by nesting under-sampled ULA's with co-prime, inter-element spacings. In particular, we use array motion to fill in missing co-array spacings. For co-prime  $M$  and  $N$ , a physical array of  $M + 2N - 1$  sensor elements plus modest array motion is used to achieve a filled co-array corresponding to approximately  $2MN$  sensor elements. This facilitates spatial spectral estimation via non-adaptive beamforming over an extended aperture with low sidelobe performance.

**FRI-G61****SCALABLE ADDRESS GENERATION PATTERNS FOR 2-DIMENSIONAL FOLDING SCHEMES IN RADIX-2 FFT IMPLEMENTATIONS**

Felipe Minotta, Manuel Jimenez.

*University of Puerto Rico, Mayaguez Campus, Mayaguez, PR.*

The fast Fourier transform (FFT) is the main block in many communication systems and signal processing applications as it provides the frequency spectrum of any signal. Hardware implementations of this operation are highly regarded as they provide improved performance

characteristics with respect to software-based sequential implementations. This work proposes a method for scaling the level of parallelism in an FFT core with radix-2 butterflies when implemented in hardware. Our approach was based, mainly, in  $2f$  memory blocks, an address generator, and  $f$  radix-2 butterflies using a 2-dimensional folding scheme. The number of butterflies,  $f$ , is also called the vertical folding factor and determines the level of parallelism. The main challenge was the development of a block capable of generating the addressing patterns of permutations regardless of the folding factor, size of the FFT, and numeric format. The addressing patterns were found, validated, and expressed mathematically in Kronecker products as stride-2 permutations and then implemented in hardware. We made comparisons between our core and commercial benchmarks, obtaining positive results in terms of performance and consumed resources. The expected successful outcome of the core lies in the fact it does not need dedicated permutation hardware between stages. Instead, an address generator controls the data flow and order. Using this scheme, the impact on consumed resources is significantly mitigated when the number of points of the FFT core is increased. As a result, we obtained a fully scalable FFT core with adjustable latency, number of points, and numeric format using this approach.

## ENVIRONMENTAL ENGINEERING

### FRI-G63

#### VALIDATING THE USE OF A SILICA PRECURSOR TO MITIGATE NANO-SIZED METAL PARTICLE TOXICITY IN THE RESPIRATORY SYSTEM

Cruz Ortiz Jr.<sup>1</sup>, Tara Sabo-Attwood<sup>1</sup>, Jun Wang<sup>2</sup>, Chang-Yu Wu<sup>1</sup>.

<sup>1</sup>University of Florida, Gainesville, FL, <sup>2</sup>The University of Oklahoma Health Sciences Center, Oklahoma City, OK.

Nano-sized particles in welding fumes pose a significant risk to occupational health and safety. Baseline welding fumes were generated inside an American Welding Society (AWS) chamber with a metal inert gas (MIG) welder using stainless steel wire as a metal filler. The experimental particles were generated by introducing tetramethylsilane (TMS) via the welding torch to produce amorphous silica encapsulated (ASE) nano-metal particles. Recent studies found that using TMS during stainless steel welding can reduce  $\text{Cr}^{6+}$  emissions by more than 90%. The ultimate goal of this study is to validate whether the encapsulation technology will mitigate the cytotoxic effects of metal fumes by limiting their bioavailability in the respiratory tract. To first assess the potential utility of amorphous silica as a non-toxic coating agent, human small airway epithelial cells (SAEC) were cultured and exposed to amorphous silica nanoparticles for a period of 24-hours with dosages that ranged from 0.1 to 200  $\mu\text{g}/\text{cm}^2$ . Preliminary results show that amorphous silica is non-toxic to SAEC at a dose of up to 200  $\mu\text{g}/\text{cm}^2$ . Similar studies are currently being performed on laboratory generated welding fume particles with and without silica coating. Transmission electron microscopy (TEM) imagery revealed nano-sized primary fume particles ranging in size from 10 - 100 nm. The increase in particle size due to ASE may help reduce respiratory track deposition. Overall, these observations collectively support future investigations to use ASE to minimize the toxicity associated with exposure to nano-sized metal particles.

**FRI-G64****SPATIOTEMPORAL ANALYSIS OF RELATIONSHIPS BETWEEN PHTHALATES CONTAMINATION IN KARST GROUNDWATER SOURCES AND TAP WATER**

Vilda Rivera, Ingrid Padilla.

*University of Puerto Rico, Mayagüez Campus, Mayagüez, PR.*

The northern karst region of Puerto Rico has a long and extensive history of contamination and high potential for exposure and significant adverse health impacts. Phthalates have been detected in groundwater sources in the northern karst system and are being evaluated as one of the causes for the extremely high rates of pre-term births in Puerto Rico. These are among the highest rates in the United States and the world. This study aims at determining the link between phthalate contaminations in karst groundwater systems and that found in tap water. The work evaluates detection frequencies and concentrations of Di-2-ethyl-hexyl-phthalate(DEHP), Di-ethyl-phthalate(DEP), and Di-n-butyl-phthalate(DBP) in groundwater and tap water samples. The analysis integrates historical data collected from regulatory agencies and data from current field measurements involving samples and analysis of groundwater and tap water from residential homes. Geographic information system technology is used to develop spatiotemporal relationships between groundwater and tap water contamination and determine the extent and possible routes of exposure to the contamination. Results show historically, phthalates are detected in 3% (analyzed only for DEHP) of groundwater samples, with concentration ranging up to 23.66 ug/L. Detection frequencies of DEP, DBP, and DEHP in tap water are 42%, 29%, and 48%, respectively, with concentrations ranging up to 89.10 ug/L. Higher detection frequencies and concentrations in tap water indicate additional sources of pollution between the groundwater source and the point of use. Future work will develop statistical correlation models between groundwater and tap water and assess additional sources of contamination.

**INDUSTRIAL/MANUFACTURING ENGINEERING****SAT-G64****EFFECT OF FLY ASH AND NANOSILICA ON CONCRETE COMPRESSIVE STRENGTH AT EARLY AGE**

Nitza García Berrios, O. Marcelo Suárez, Luis Zapata, Mauricio Cabrera.

*University of Puerto Rico, Mayaguez Campus, Mayaguez, PR.*

The replacement of cement by mineral admixtures in concrete has been of interest in the construction industry. Nevertheless, several potential replacements have shown a drop in concrete's compressive strength at an early age due to slower reaction. Fly ash class F, for example, follows such a pattern. Hence, a viable option to compensate for this loss is mandatory. This project investigates the use of nanosilica to compensate the loss of compressive strength by accelerating the hardening process. Also the use of such nanoparticles is expected to improve the microstructure interface between cement paste and the aggregate by making it more uniform and compact. A statistical, experimental design involving mixtures of Portland cement, fly ash, and nanosilica, in addition to water-to-binder ratio as an external

factor is proposed to this end. This design allows the estimation of a cubic regression model that properly accounts for the mixture components within a constrained experimental region. In this work, the results are discussed based on the chosen experimental design. The interaction terms that significantly affect the response variable were identified. As future work, an optimization problem to maximize concrete's compressive strength will be developed to look for an optimal mix that satisfies all the restrictions.

## **MATERIALS ENGINEERING (INCLUD. CERAMICS/TEXTILES)**

### **FRI-G65**

#### **INDUCING CRYSTALLIZATION OF POLY(3-HEXYLTHIOPHENE) NANOWIRES BY WELL-DEFINED NUCLEATION SITES**

Daniel Acevedo-Cartagena, Yue Zhang, Alejandro Briseño, Ryan Hayward.  
*University of Massachusetts Amherst, Amherst, MA.*

Device efficiency is important for energy generation from renewable sources in order to preserve the environment and improve quality of life. Solution crystallization of conjugated polymers promises a facile way to fabricate nano-scale structures with desirable properties for improving organic-based electronics, especially solar cells. The addition of well-defined nucleation sites to a supersaturated solution can induce crystallization and allow for control over structural features. We identified conditions in which homogenous nucleation of a model semicrystalline polymer, poly(3-hexylthiophene), P3HT, is suppressed, allowing for controlled crystallization into nanowires on addition of well-defined nucleation sites. The hysteresis window between crystallization and melting temperatures of P3HT nanowires is tuned using concentration, molecular weight of the polymer, and solvent quality. We show that, in this manner, short P3HT nanowires ("seeds") can be extended, though obtaining well controlled extension into linear structure remains an open challenge. In a similar fashion, graphene or graphite coated substrates were found to be excellent nucleating agents for growth of nanowire films.

## **MECHANICAL ENGINEERING**

### **SAT-G65**

#### **ORIENTATION-DEPENDENT IMPACT BEHAVIOR OF POLYMER/EVA BILAYER SPECIMENS AT LONG WAVELENGTHS**

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<sup>3</sup>*California State University Northridge, Northridge, CA.*

Multilayer foams of varying densities are of great interest for the reduction in structural damage and injuries generated by dynamic forces. In the present work, the effect of sample orientation on the impact behavior of bilayer specimens made by bonding a 1 to 2 mm thick dense polymer layer (polyurea) to a 10 mm thick EVA foam was investigated. The peak dynamic force was found to be dramatically different, by as much as 30 to 40%, depending on which face

of the bilayer specimen bore the impact. The transmitted impact force was lowest when the dense polymer layer was in contact with the force transducer and the foam was directly hit from the top by the falling indenter. This study is the first to report these unusual observations: dramatic differences in the peak dynamic force by flipping the bilayer specimen in the low strain rate regime, the reduction is accompanied by higher dynamic stiffness and consequently lower overall specimen displacement; and the peak force is reduced without significantly increasing the duration of the impulse. This should encourage research leading to newer armor designs that are effective against dynamic loads with impulse durations in the 1 to 100 ms range. Since such impacts are ubiquitously encountered, results presented here have the potential to impact our daily lives in a significant way.

## HEALTH

### MEDICINE (E.G., DENTISTRY, SURGERY, OPTOMETRY, VETERINARY)

#### FRI-G66

#### UROPATHOGEN FREQUENCY AND *E. COLI* ANTIBIOTIC RESISTANCE AS MEASURED BY ROUTINE URINE CULTURE

Cristy Miles, Abijit Shinde, David Jaeger.

*Aayu Clinics, Chicago, IL.*

Dysuria is a common complaint in primary care settings. The majority of these cases can be attributed to urinary tract infections (UTI). There is a plethora of data to support an empirical diagnosis of *E. coli* UTI in females presenting with classic symptoms. Empirical treatment guidelines offer a choice, with the most frequent antibiotics used including trimethoprim/sulfamethoxazole (TMP/SMX), ciprofloxacin, and nitrofurantoin. This retrospective chart study seeks to determine 1) urine culture results in a whole population presenting with dysuria, and 2) the antibiogram (antibiotic susceptibility profile) of *E. coli* in our patient population. The study was performed at a single urgent care clinic which routinely orders urine cultures on all patients presenting with dysuria. A chart review was performed with a total of 954 urine culture results. The culture results data was collected in aggregate. For 388 cultures, *E. coli* was the pathogen and, for these, the antibiogram was recorded. The numbers were totaled and averaged. For 388 *E. coli* cultures, we found an antibiotic resistance to TMP/SMX of 22.2%, Ciprofloxacin of 5.6%, and Nitrofurantoin of <1%. Our study data supported currently accepted uropathogen frequencies with *E. coli*, and *S. saprophyticus* being the most common pathogens. The antibiogram of *E. coli* supports the use of Nitrofurantoin for appropriate patients has a first line treatment and, as mentioned in the discussion, discourages the use of TMP/SMX and ciprofloxacin in uncomplicated UTI patients.

## PHARMACY

### SAT-G66

#### **A PROPOSAL FOR AN INDIVIDUALIZED PHARMACOGENETIC-GUIDED WARFARIN DOSAGE REGIMEN FOR PUERTO RICAN PATIENTS COMMENCING ANTICOAGULATION THERAPY**

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Warfarin is the standard-of-care in oral anticoagulation; its clinical use is challenging due to significant inter-individual dosing variability. This study was aimed at predicting individual warfarin doses in Puerto Rican patients commencing anticoagulation therapy, using a pharmacogenetic algorithm and pharmacokinetic-pharmacodynamic (PK-PD) simulations. A retrospective, observational, pharmacogenetic study was conducted in 138 male patients on warfarin from the Veterans Affairs Caribbean Health Care System (VACHS) in Puerto Rico, who constituted the derivation cohort. Participants were genotyped for common *CYP2C9* and *VKORC1* variants. A pharmacogenetic algorithm for 3-day initial dosing that included preemptive genotypes, target INR, age, BSA, co-medications, admixture, co-morbidities, and vitamin K intake was derived and explained approximately half of the dose variability ( $R^2 = 0.48$ ). Predicted initial doses were fractioned over the first 3 days to reduce risk of overshooting the target INR range. Predictability was assessed by using WinNonlin® one compartment/indirect response PK-PD simulations. Individual genotype-adjusted PK-PD simulations of INR responses fell within the target range in 92% of cases, confirming good predictability. Pharmacogenetic algorithms that incorporate clinical, INR measurements, admixture, and genetic factors to predict initial dosing over the first week of therapy were developed and tested in a cohort of Puerto Rican patients on warfarin. The adoption of a pharmacogenetic-driven approach to predict initial doses in Puerto Rican patients commencing warfarin therapy is expected to improve the safety of warfarin initiation and subsequent clinical management of high-risk patients at the VACHS anticoagulation clinic in Puerto Rico. Further studies are warranted to validate these findings and determine superiority of the pharmacogenetic approach over current practices.

## MATHEMATICS & STATISTICS

### APPLIED MATHEMATICS

#### SAT-G68

##### EXPLORING THE DYNAMIC INPUT OF BLOOD INSULIN CONCENTRATIONS WITH PERIODIC AND IMPULSIVE SUBCUTANEOUS INSULIN INJECTIONS

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Insulin is a pancreatic hormone that is essential to maintain the plasma glucose level within a normal range. Diabetes mellitus is characterized by hyperglycemia which is caused by either no insulin production (type-1 diabetes) or inadequate insulin production (type-2 diabetes). Type-1 diabetics are unable to produce their own insulin and, therefore, require exogenous insulin infusion in order to keep the glucose levels under control. Currently, the state-of-the-art technology for insulin administration is automated injection into subcutaneous tissue through insulin pumps in an impulsive fashion. In this study, we extend existing differential equation models to impulsive differential equation models, and we investigate the impacts of the periodic and impulsive injection of insulin analogues into subcutaneous tissue and the subsequent absorption of insulin into the blood stream. Comparisons reveal that fast-acting insulin analogues cause a sharp spike in blood insulin concentrations following the impulsive injections, whereas slow-insulin analogues generate a smoother response. It is revealed that the joint adjustment of the dose of insulin and the frequency of impulsive injections can sustain insulin concentrations within a satisfactory level.

#### FRI-G68

##### FAST NORMALIZED CUT WITH LINEAR CONSTRAINTS AND ITS APPLICATIONS

Ivan Ojeda-Ruiz, Ren-Cang Li.

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Several methods are used to process images in many fields including clustering, image segmentation, and medical imaging. In this study, we use a category of methods called graph-cut. In these methods, graphs determining the relation between several objects are divided in one or more pieces in order to solve a variety of problems. Most of these methods are “unsupervised”, which means any information known about the data objects is not used. In some of the applications listed above, some prior knowledge could be given. Using this prior knowledge can be the key to optimizing the speed of the methods. We present a novel algorithm that exploits prior information in order to optimize the speed of the process. We tested this algorithm and compared it to other methods, and the results show faster convergence. The study has shown this algorithm can provide better results to a general class of optimization problems which have a larger number of applications and can impact many fields positively. We also explore several variations of the same problem.



**FRI-G67****SOLUTIONS TO NONLINEAR PARTIAL DIFFERENTIAL EQUATIONS USING NONLINEAR SYSTEMS OF RICCATI AND ERMAKOV**

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The convection-diffusion process and the diffusion-reaction processes are fundamental in describing a wide variety of problems in physical, chemical, biological, and engineering sciences. In particular in this poster, we consider the Burger's equation that models gas dynamics and traffic flow and Fisher's equation that models spatial population growth and gene selection. In our presentation, we find explicit solutions for Burger's equation with non-constant coefficients (non-autonomous). Our method consists in finding solutions for a non-autonomous linear heat equation first and then transfers these solutions to the non-autonomous Burger equation using Hopf-Cole transformation. Implicitly, our method requires to solve nonlinear systems than include nonlinear Riccati and Ermakov equations. Using a similar approach, we present travelling wave solutions for a modified Fisher equation but, in this case, we present our own transformation.

**SAT-G67****HOW ROBUST ARE PROPOSED MITIGATION STRATEGIES TO MISSPECIFICATION OF AGE-RELATED CONTACT RATES? - AN EXAMPLE FROM THE CONTROL OF INFLUENZA (A/H1N1) SPREAD**

Romarie Morales<sup>1</sup>, Jay Taylor<sup>2</sup>.

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The research objective is to find the best mitigation strategies for fast spreading influenza (A/H1N1) virus by identifying the right levels of aggregation (age-windows) to incorporate into an informational, mathematical model of the disease. A simple extension of the susceptible-infected-recovered (SIR) age-structure model of influenza transmission is used to illustrate the use of the dynamic optimization methodology. We used the interior point method approach which allows a more effective inclusion of real life constraints (i.e., limited vaccines) to assess the potential discrepancies in the age structure component. Our results show light on the growing concern that contact matrices, which determine how disease is spread within and between age groups, are formulated without ample data collection or specificity. If we apply a contact matrix that does not originate from the country of study, we expect to see an intervention policy that differs greatly from the policies implemented when a more accurate matrix is used. This work will motivate the collection of data regarding current individual contacts per day in different countries.

## MATHEMATICS (GENERAL)

### FRI-G70

#### FACTORIZATION PROPERTIES OF LEAMER MONOIDS

Ashlee Kalauli, Roberto Pelayo.

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The Huneke-Wiegand conjecture has prompted much recent research in commutative algebra. In studying this conjecture for certain classes of rings, García-Sánchez and Leamer construct a monoid  $S_{r,s}$  whose elements correspond to arithmetic sequences in a numerical monoid  $\Gamma$  of step size  $s$ . These monoids, which we call Leamer monoids, possess a very interesting factorization theory that is significantly different from the numerical monoids from which they are derived. In this poster, we offer much of the foundational theory of Leamer monoids, including an analysis of their atomic structure, and investigate certain factorization invariants. Furthermore, when  $S_{r,s}$  is an arithmetical Leamer monoid, we give an exact description of its atoms and use this to provide explicit formulae for its delta set and catenary degree.

## OPERATIONS RESEARCH

### SAT-G70

#### SOLUTIONS TO DETERMINISTIC AND STOCHASTIC RAILWAY VEHICLE ROTATION PROBLEMS

Kyle Smith<sup>1</sup>, Ivan Avramidi<sup>1</sup>, Lorie Liebrock<sup>1</sup>, Ralf Borndorfer<sup>2</sup>, Christian Ratsch<sup>3</sup>.

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Train scheduling that implements regularity and rotation is a nontrivial integer programming problem. It is formulated using hypergraphs and solved using an integer programming approach with data from Deutsche Bahn in the deterministic case. When stochastic time delays are considered, the programming problem is much more complex and presents additional challenges. Methods for solving the stochastic time delay problem are implemented to reflect a more realistic viewpoint. Solving these problems gives better efficiency of existing infrastructure along with a more objective approach to scheduling trains.

## STATISTICS

### FRI-G71

#### DIMENSIONALITY REDUCTION TO OPTIMIZE CLASSIFICATION ON FUNCTIONAL DATA

Shirley Y. Huanca Ochoa, Edgar Acuna.

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Over time and with the continued advancement of technology in statistics, we have the need to develop new methods to extract meaningful information quickly and efficiently from large datasets such as sets of functional data. Variables are treated theoretically using the definitions

and properties of curves; computationally, through data mining techniques, variables are treated as high-dimensional vectors. It is in this sense that the application of some methods of feature selection and functional principal components are selectable prior to any analysis of such data, because both techniques show a representation of finite size for each curve, thus overcoming the problem of high dimensionality. This paper presents a methodology that consists of using the techniques described above, consecutively obtaining the functional principal components in different datasets, which have been previously subjected to the application of feature selection techniques. This is done in order to compare the effectiveness of minimizing the error rate of misclassification in the datasets studied, comparing it with application to a unique technique of functional principal components. Therefore, we conclude that our methodology is valid.

#### **SAT-G71**

##### **MATHEMATICS ANXIETY AND ITS EFFECTS ON HISPANIC STUDENTS**

Luis Fernandez, Xiaohui Wang.

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Mathematics anxiety is a feeling of apprehension, fear, tension, and discomfort when an individual is presented with a mathematical task. Mathematics anxiety has been shown to interfere with an individual's learning, performance, and choice of college major and career. Researchers have yet to agree on the prevalence and effects of math anxiety. This study investigated which groups of college students (overall or by major, classification, or sex) seem to suffer higher levels of mathematics anxiety and compared determining factors, education levels of family members, school status, or work status. The data was obtained from predominantly Hispanic undergraduate students ( $n = 1,923$ ) who took elementary algebra or intermediate algebra (which are regarded as remedial mathematics courses) between fall 2011 and spring 2012 at the University of Texas Pan-American. A mathematics anxiety score was obtained from a 20-question survey with 5 levels of agreement and was analyzed using statistical methods: ANOVA, t-tests, and correlational analysis.

#### **PHYSICAL SCIENCES**

##### **CHEMISTRY (EXCEPT BIOCHEMISTRY)**

#### **FRI-G74**

##### **SYNTHESIS OF A FLEXIBLE MOLECULAR HETEROCAPSULE THAT REVERSIBLY BINDS GUEST MOLECULES**

Edzna Garcia Ramirez, Linda Gutierrez-Tunstad.

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This study concerns the synthesis and characterization of a covalently linked and conformationally flexible resorcin[4]arene heterocapsule that has the ability to trap guest molecules. Resorcin[4]arene cavitands, container molecules with an enforced cavity, are of interest because of their 8 hydroxyl groups that can be functionalized to tailor guest binding. This field of supramolecular chemistry has become of great interest, because of the many

potential applications of guest encapsulation such as in separation technologies and toxic remediation. Previous attempts to synthesize our heterocapsule met with difficulty because of the presence of many side products which made separation and purification difficult. We hypothesize that templation will facilitate the synthesis of our heterocapsule by driving its formation because of favorable interactions that stabilize the heterocapsule. Our heterocapsule will be synthesized from 2 different resorcin[4]arene cavitands, a diquinoxaline monomethylene-bridged cavitand and a monoquinoxaline dimethylene-bridged cavitand, linked by a tetraazaanthracene bridge. Successful synthesis of the desired heterocapsule will be determined by nuclear magnetic resonance and high-resolution mass spectrometry. We expect to obtain a heterocapsule that can reversibly open and close in response to different stimuli such as changes in temperature, pH, and solvent to encapsulate guest molecules. Studying the physical properties of our heterocapsule will grant us vital information that will give us insight on how to control the capsules' guest selectivity.

#### SAT-G77

##### STRUCTURE AND PROPERTIES OF THE LOW DIMENSIONAL-LAYERED MATERIAL $\text{PrCu}_x\text{Te}_2$

Roy N. McDougald Jr.<sup>1</sup>, Jess Evans<sup>2</sup>, Julia Chan<sup>1</sup>, Robin Macaluso<sup>2</sup>.

<sup>1</sup>The University of Texas at Dallas, Richardson, TX, <sup>2</sup>University of Northern Colorado, Greeley, CO.

The aim of this project is to understand the role of praseodymium-based low dimensional-layered materials on the magnetic and electrical properties. The ternary tellurides  $\text{PrCu}_x\text{Te}_2$  ( $x = 0.38$  and  $0.43$ ) have been synthesized in 2 steps: reaction of the elements with a soak at a temperature of 1,228 K, then reheated to 1,228 K in KI flux. The  $\text{PrCu}_x\text{Te}_2$  compounds are isostructural to  $\text{LaCu}_{0.40}\text{Te}_2$  and crystallize in the space group *Pbcm* (No. 62) of the orthorhombic crystal system, with cell dimensions of  $a = 7.6505(11)$  Å,  $b = 8.4449(11)$  Å,  $c = 6.2206(10)$  Å for  $\text{PrCu}_{0.38}\text{Te}_2$ , and  $a = 7.6480(14)$  Å,  $b = 8.4410(14)$  Å,  $c = 6.2320(15)$  Å for  $\text{PrCu}_{0.43}\text{Te}_2$ . The crystal structure consists of  $\text{PrTe}_8$  bicapped trigonal prisms, while each copper atom is surrounded by 4 tellurium atoms. The tellurium atoms form infinite chains along the *c*-axis, with Te-Te interactions of  $\sim 3.11$  Å. These Te-Te interactions are highly dependent on the concentration of copper, and the physical properties of our materials will be compared to other rare-earth analogues. We will present the synthesis, structural characterization, and preliminary properties of  $\text{PrCu}_{0.38}\text{Te}_2$  and  $\text{PrCu}_{0.43}\text{Te}_2$ .

#### SAT-G77

##### PROGRESS TOWARD THE TOTAL SYNTHESIS OF THE *LYCOPodium* ALKALOID (+)-FASTIGIATINE

Renzo Samame, Scott Rychnovsky.

University of California, Irvine, Irvine, CA.

Fastigiatine was isolated from the *Lycopodium fastigatum* in 1986 by Lock, et al. Its core structure contains a pentacyclic ring system with 5 contiguous stereocenters, 2 of which are vicinal quaternary centers. Recent studies by the Kobayashi group led to the isolation of 2 new structures, Himeradine A and Lyconadine D, which contained the fastigiatine-type scaffold. The

unique framework, as well as its biological activity, has motivated us to pursue the total synthesis of (+)-fastigiatine. Our synthetic approach toward fastigiatine will be presented.

#### **FRI-G75**

##### **METAL-MEDIATED ANCHORING OF [6,6]-PHENYL-C61-BUTYRATE TO GOLD NANOPARTICLES**

Julio Padilla, Tariqul Islam, Juan Noveron.

*The University of Texas at El Paso, El Paso, TX.*

Organic photovoltaic systems (OPVs) are solar cells that use organic compounds to convert light into electrical power. They have attracted considerable attention because of their potential to develop into low-cost, low-weight, and flexible solar cells that can be manufactured using high-throughput, thin-film deposition technologies such as roll-to-roll processing, spray coating, spin casting, and inkjet printing. Current OPVs are bulk-heterojunctions with ~10% efficiency. The Shockley-Queisser limit indicates that OPVs with multiple heterojunctions may have a theoretical efficiency of 83%. Typical OPVs consist of blends of donor (D) and acceptor (A) molecules where one of the materials absorbs photons, subsequently exciting electrons. These electrons and the holes they leave behind form electron-hole pairs called excitons. The excitons then diffuse throughout the D-A interface until they dissociate into electrochemical point charges that, in a closed circuit, create electrical power. The electronic properties of the D-A pair, particularly their highest occupied molecular orbit (HOMO) and lowest occupied molecular orbit (LUMO) energies, play a key role in OPVs, and thus, a large research thrust has been focused on designing compounds that can fine-tune these properties. However, since the diffusion length of the exciton is up to 22 nm, the supramolecular chemistry of the D-A components is expected to play a fundamental role, although it has received little attention. Our research focuses on the molecular and supramolecular structure-function relationship studies. Herein, we present the use of 5 nm gold nanoparticles to assemble [6,6]-phenyl-C61-butyrate on their surfaces using acid-base interactions and Cu(II)-mediated anchoring methods.

#### **SAT-G73**

##### **SYNTHESIS AND MAGNETIC RESONANCE ANALYSES OF MELPHALAN-TEMPOL FOR SITE-TARGETED DRUG DELIVERY**

Leonardo Castro, Yong Ba.

*California State University Los Angeles, Los Angeles, CA.*

A spin-labeled adduct of the therapeutic drug melphalan was synthesized using a 3-step synthetic route. Step 1 involves the protection of the amine group under basic conditions with Di-*tert*-butyl carbonate as the protecting group. Step 2 involves the addition of the spin label compound 4-hydroxy-2,2,6,6-tetramethylpiperidin-1-oxyl (TEMPOL) to the carboxylate group of melphalan via a Steglich esterification with the existence of the coupling agent *N,N'*-dicyclohexylcarbodiimide and a catalyst, 4-dimethylaminopyridine, under an inert atmosphere of nitrogen gas. The final step comprises the restoration of the amine group by using a strong acid to remove the protecting group and obtaining the final product after purification of the melphalan-TEMPOL adduct. To ensure the spin-label compound was successfully coupled to melphalan, structural analyses of the intermediates and final product have been carried out

using  $^1\text{H}$  NMR and EPR (electron paramagnetic resonance) for detecting free radical activity of the single electron spin of the nitroxyl group of TEMPOL. The main objectives of this project are to improve the bioavailability, retention time, and permeability of melphalan during drug delivery with the assistance of nanoparticle drug delivery techniques and to develop MRI techniques using the melphalan-TEMPOL adduct enclosed polymeric nanoparticles.

#### **FRI-G76**

##### **NMR EXCHANGE RATE MEASUREMENTS OF HYDROXYL PROTONS IN HEPARIN**

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*University of California Riverside, Riverside, CA.*

Heparin is a linear, anionic polysaccharide composed of repeating uronic acid-glucosamine disaccharides. Microheterogeneity is introduced during biosynthesis as various patterns of sulfation and uronic acid epimerization. Heparin is used clinically as an antithrombotic drug acting through the binding of a specific pentasaccharide sequence to the protease inhibitor antithrombin III (ATIII). It also mediates a variety of other biological processes through interactions with more than 300 proteins. Due to its microheterogeneity and polydispersity, the detailed structural characterization of heparin typically proceeds via partial depolymerization followed by chromatographic fractionation of the resulting oligosaccharides based on size and charge prior to characterization by NMR and mass spectrometry. In some microstructural motifs, heparin's exchangeable hydroxyl (OH) and sulfamate ( $\text{NHSO}_3^-$ ) protons may participate in intramolecular hydrogen bonds, stabilizing the localized secondary structure in a conformation favorable for protein-binding. Using  $^1\text{H}$  NMR temperature coefficients, chemical shift differences, line shape analysis, and solvent exchange rate measurements using EXSY, we have identified several hydrogen bonds involving the  $\text{NHSO}_3^-$  and OH groups of the synthetic pentasaccharide Arixtra. Arixtra contains several key structural elements of the native ATIII-binding pentasaccharide, including the GlcNS3S6S(III) 3-*O*-sulfo group. Affinity of Arixtra for ATIII decreases 1,000-fold without this 3-*O*-sulfate group. We have examined isolated oligosaccharides structurally similar to Arixtra, but without the important 3-*O*-sulfate group. These oligosaccharides show different hydrogen bonding patterns. The hydrogen bond involving the GlcNS3S6S(III)  $\text{NHSO}_3^-$  and IdoA2S(IV) hydroxyl protons are lost. Instead, the GlcNS OH3 protons appear to participate in stronger hydrogen bonds, demonstrating a shift in secondary structure.

#### **FRI-G77**

##### **KINASE INHIBITOR OPTIMIZATION FOR *TRYPANOSOMA BRUCEI* DRUG DISCOVERY**

Liseth Silva, Michael Pollastri.

*Northeastern University, Boston, MA.*

Neglected tropical diseases affect over one billion people worldwide. These diseases are neglected because they affect areas with poor financial conditions and do not attract research investment from for-profit institutions as they cannot recover research and developmental costs. Human African trypanosomiasis (HAT) is a neglected disease caused by the parasite *Trypanosoma brucei*. Current treatments for this disease are painful, toxic, and impractical, and

therefore new drug approaches are needed. Kinases have been found to be important targets involved in cellular signaling in infectious parasites such as *T. brucei*, which has attracted attention to these parasitic kinases as drug targets. The purpose of this research is to optimize one class of kinase inhibitor for activity against parasites and improve their physicochemical properties to enable further development as drugs. We are using state of the art hit-to-lead medicinal chemistry optimization techniques to better understand the structure-activity relationship of the hit compounds in terms of antiparasitic potency, host cell toxicity, selectivity over human kinases, and physicochemical properties. Analogs were designed to improve the potency and physicochemical properties of the hit compounds. Computed physicochemical properties indicate these analogs will be central nervous system penetrant and have improved solubility over the hit compounds. Several compounds were synthesized and tested against *T. brucei* cells to determine potency. Efforts are currently under way to synthesize and test additional analogs. Complete synthesis of these analogs will allow us to address their potency against *T. brucei* parasites' physicochemical properties and explore their structure-activity relationships.

### **FRI-G73**

#### **SUPERPARAMAGNETIC IRON OXIDE NANOPARTICLE INCLUSION IN POLYMERIC MICELLES FOR TARGETED DRUG DELIVERY**

Maria Flores, Yong Ba.

*California State University Los Angeles, Los Angeles, CA.*

Two major issues that currently face anticancer medication are poor solubility in water and lack of target specificity. This poses a problem because hydrophobic drugs are unable to reach hydrophilic target sites, and their lack of specificity causes unwanted side effects. In order to have an effective therapeutic delivery system, a magnetically targeted drug delivery system (MT-DDS) is under development. A typical MT-DDS encapsulates magnetite nanoparticles along with the anticancer drug inside the hydrophobic cores of polymeric micelles. Magnetite nanoparticles are used because of their superparamagnetic properties, small size, and low toxicity. Another advantage is their contrast effect on magnetic resonance imaging. Monodisperse  $2.4 \pm 1.3$  nm magnetite nanoparticles were successfully synthesized through thermal decomposition of iron acetylacetonate in a high boiling point organic solvent in the presence of a reducing agent and surfactants. The magnetic properties of the nanoparticles were investigated, and the particles were then encapsulated within polymeric micelles using a single emulsion method. Current investigations involve determining the NMR relaxation times for the magnetite nanoparticles and the cytotoxicity of the magnetic nanocarrier. Ultimately, we hope to develop a useful tool for co-encapsulating hydrophobic drugs and superparamagnetic magnetite nanoparticles in the polymeric micelles for anticancer therapeutic applications.

**SAT-G74****DISSOCIATION OF CHLOROBENZENE ON A DOUBLE DIMER CLUSTER MODEL OF THE Si(100) SURFACE**

Eric Butson, Nicholas Materer.

*Oklahoma State University, Stillwater, OK.*

In this paper, we discuss the hypothesis that the chlorobenzene dissociation mechanism involves a change in the spin state of the Si(100) surface, and the final structure is one in which benzene is attached to 1 Si atom, while chlorine is attached to the other Si atom of the same dimer. This hypothesis addresses controversies found in experimental studies on the adsorption and dissociation of chlorobenzene. The dissociation of chlorobenzene was studied using computational methods. Gaussian 09 was used to calculate stable structures, a Fortran program was used to search for minimum energy crossing points (MECP), and GAMESS (US) was used to calculate spin orbit coupling (SOC) constants. Using Landau-Zener theory, the SOC constants at the MECP give a spin crossing probability of  $1.9 \times 10^{-3}$  for the adsorption structure and  $2.3 \times 10^{-3}$  for the dissociated structure. Applying non-adiabatic transition state theory one obtains rate constants of  $2.7 \times 10^5 \text{ s}^{-1}$  and  $3.4 \times 10^9 \text{ s}^{-1}$  for the adsorption and dissociated structures, respectively. Given these relatively fast rate constants, we suggest a mechanism for the dissociation of chlorobenzene on the Si(100) surface that involves a change in the spin state. Although the probability lowers the rate of spin crossing, this step is not the rate limiting step in the formation of the proposed final structure. It is, in fact, the movement of the abstracted chlorine that is slow. It is possible to attain the lowest energy structure; however, any of the structures with one C-Si bond and one Cl-Si bond are favored over the molecularly adsorbed structure.

**SAT-G76****USING QUANTUM MECHANICAL COMPUTATIONS TO UNDERSTAND THE STABILITY AND SPECTROSCOPIC PROPERTIES OF METAL HYDROXO CLUSTERS**

Lindsay Wills<sup>1</sup>, Anna Oliveri<sup>2</sup>, Milton Jackson<sup>2</sup>, Darren Johnson<sup>1</sup>, Paul Cheong<sup>1</sup>.

<sup>1</sup>*Oregon State University, Corvallis, OR*, <sup>2</sup>*University of Oregon, Eugene, OR*.

Metal hydroxo clusters exist in a vast array of structural forms under aqueous conditions, and some of these clusters have recently been used as precursors in sustainable techniques for making metal oxide thin films. There is no universal understanding for the formation of specific clusters over others, and discovery of new clusters is still rare and serendipitous. Therefore, methods to understand the stability of different clusters and uniquely identify clusters in solution are important to making high quality films. Quantum mechanical computations have been used to assist in understanding the thermodynamic and spectroscopic properties of metal hydroxo clusters. A group additivity method has been developed that can predict the stability of any metal hydroxo cluster using simple algebra with a mean unsigned error of 5.0 kcal/mol (2.5 %) and standard deviation of 8.5 kcal/mol (3.6 %), compared to quantum mechanical energies. Additionally, computations have been used to analyze the peaks in the vibrational and NMR spectra of these clusters. Identifying these clusters through vibrational and NMR spectroscopy is difficult due to the lack of knowledge regarding the signature peaks for each cluster. The



vibrational modes and chemical shifts of several metal hydroxo clusters were computed, and spectra were generated based on the computed results and experimental spectra. These calculations show a new way for computations to further knowledge gained from experiments and to assist in material design and characterization.

#### **SAT-G72**

##### **MOLECULAR ORIENTATION OF GLASSES PREPARED BY PHYSICAL VAPOR DEPOSITION: EVIDENCE FOR LIQUID CRYSTALLINE ORDER**

Jaritzza Gomez, Mark Ediger.

*University of Wisconsin-Madison, Madison, WI.*

Organic glasses can be prepared by physical vapor deposition by condensing molecules on a substrate. Glasses with useful properties result from deposition at slow rates, 0.2 nm/s, and substrate temperatures near and below the glass transition temperature ( $T_g$ ). At temperatures  $\sim 0.85 T_g$ , molecules with higher mobility on the outermost layer of the glass have the opportunity to sample more favorable configurations. Glasses prepared in this manner have much higher kinetic stability and show an increase in density relative to glasses prepared in the traditional method of cooling from a liquid. Most recently, our group has shown that glasses prepared in this manner are anisotropic; the molecular orientation is coupled to the temperature of the substrate. Use of spectroscopic ellipsometry allows us to characterize the optical properties of glasses, which are dependent in molecular orientation. The ability to orient molecules in a desired configuration has long driven the interest behind the use of liquid crystals in many technological applications. Recent results in our work show that vapor deposited glasses of perylenemonoimide molecule, PMI-s-C8, can have a high degree of ordering in the plane normal to the substrate, similar to liquid crystal glasses. Our goal is an understanding of the molecular orientation of vapor-deposited glasses of PMI-s-C8 and other molecules with liquid crystalline order.

#### **FRI-G72**

##### **RECOGNITION OF SUGAR BIOMARKERS VIA A FLUORESCENT PROBE BASED ON BORONIC ACID APPENDED BIPYRIDINIUM SALTS**

Angel Resendez<sup>1</sup>, Dominic-Lucc Webb<sup>2</sup>, Bakthan Singaram<sup>1</sup>.

<sup>1</sup>*University of California Santa Cruz, Santa Cruz, CA,* <sup>2</sup>*Uppsala University, Uppsala, Uppland, SE.*

Gastrointestinal barrier dysfunction is now recognized as an early event in the pathogenesis of several problematic diseases, such as inflammatory bowel disease (IBD), Parkinson's disease, Crohn's disease, celiac disease, and type-1 and type-2 diabetes mellitus. Gastrointestinal permeability can be assessed noninvasively by analyzing saccharide biomarkers in urine such as sucrose, lactulose, mannitol, and the synthetic sweetener sucralose. Current methods for analyzing these biomarkers require expensive and time consuming instrumentation such as high performance liquid chromatography/mass spectrometry (LC/MS). An alternative approach has been taken by using a 2-component system that comprises a boronic acid substituted bipyridinium salt as the receptor and a fluorescent reporter dye in which the system operates at physiological pH. A comparative study was conducted between 2 types of boronic acid

receptors (bis and mono substituted viologens) to determine their binding capabilities for the sugar biomarkers of interest. Lactulose gave the highest fluorescence recovery with a limit of detection and quantification of 80 and 500  $\mu\text{M}$  respectively with bis substituted boronic acid viologen. In addition to analyzing the sugar biomarkers, an analysis of various sugar alcohols was also performed to determine the discriminatory properties of the 2 receptors. This developed 2-component system demonstrates a useful tool for measuring sugars in urine with excellent stability, cost, and throughput benefits.

## **GEOLOGY**

### **FRI-G78**

#### **INFLUENCE OF BACTERIA IN COMPOST ON GROUNDWATER QUALITY**

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Composting, which has been viewed as an environmentally beneficial activity for years, is now creating negative impacts in the environment and to humans. We studied manganese contamination in wells located down-gradient from a composting facility and the role of groundwater chemistry in transport of bacteria through the sandy aquifer. Over-exposure to manganese for long periods has been associated with human neurological problems such as trouble walking and muscle weakness. The compost facility located in Great Gardens, Long Island, New York is technically a yard waste transfer station. The yard waste is stored at the northwest corner of the site and is transferred in small batches to farms for composting. The water quality in the wells began to decline a few years after the facility began operation and led to a series of investigations conducted between 2009 and 2011 by the Suffolk County Department of Health Services (SCDHS), the New York State Department of Environmental Conservation (DEC), and the New York State Department of Health (DOH). Groundwater samples at various depths were obtained on-site as well as up-gradient and down-gradient of the facility. Surface water run-off samples were collected at additional composting facilities that do not have groundwater wells. In addition to water samples, compost and soil from Great Gardens and other facilities were analyzed and excess levels of manganese were found. The data also suggests that the compost plumes containing bacteria are causing manganese to become elevated in groundwater.

## PHYSICS (EXCEPT BIOPHYSICS)

### SAT-G79

#### SEARCHING FOR CORRELATIONS BETWEEN DISLOCATIONS AND TRAP STATES IN GALLIUM NITRIDE

Kevin Galiano, Drew Cardwell, Darryl Gleason, Pran Paul, Aaron Arehart, Steven Ringel, Jonathan Pelz.

*The Ohio State University, Columbus, OH.*

Gallium nitride, GaN, is a wide-bandgap semiconductor suitable for a variety of applications, including high temperature and high power electronics. Currently there is no good substrate for GaN. Often a substrate with a very different lattice constant is used for growth, and the different crystal structures between the substrate and the grown GaN film cause a large density of extended linear defects, known as dislocations. Electronic traps are defects where electrons can be captured, creating localized charge centers that alter device behavior. Electronic traps limit device performance and can lead to device degradation. It has been postulated that some traps are due to dislocation defects. Our goal is to characterize trap states and determine if they are localized at dislocations in GaN. Dislocations can alter the topography of GaN in characteristic ways depending on dislocation type and growth method. We have collected preliminary topography measurements using an atomic force microscope and have observed some features of individual dislocations. We are in the process of using an adaptation of scanning Kelvin-probe microscopy that we have developed, which we have named nano deep level transient spectroscopy, to look for trap states in GaN with nanometer-scale resolution. When a trap emits an electron, it causes a local charge transient, which is detected as a surface potential transient. An observation of specific traps located at dislocations would help us understand the origin of these traps in GaN and help lead to strategies to reduce their detrimental effects on device performance.

### FRI-G80

#### DESCRIBING THE INTERNAL STRUCTURE OF A BLACK HOLE

Shaun Hampton, Zaq Carson, Samir Mathur, David Turton, Jonathan Pelz, Patrick Osmer.

*The Ohio State University, Columbus, OH.*

Quantum mechanics is a theory that describes the behavior of matter at extremely small length scales. The gravitational force depends on the mass of the object, and for small objects, gravity is extremely weak compared to the other forces in nature (electrical, strong, and weak forces). However, when large masses are compressed into very small volumes, as in black holes, quantum mechanics and gravitation must be considered together in theories generally known as *quantum gravity*. One approach to quantum gravity is *string theory*, which is a theory predicting that all matter is composed of tiny vibrating strings. String theory also predicts that we live in a universe that contains extra dimensions. Remarkably, string theory can be used to figure out what is actually taking place within a black hole to help understand what the internal structure may be. We can describe a black hole in string theory by looking at a conformal field theory. In this description we have the twist interaction which takes 2 strings and twists them

together to form a longer string. We have applied this interaction and calculated the final state of the string. We examined 2 conditions. The first being where 2 initial strings contained no vibration along either of their transverse directions. The other in which 1 of the 2 initial strings contained a vibration along its transverse direction. These results provide a more complete description of a black hole's internal structure. Through investigating the twist interaction we hope to develop a complete theory of black holes in string theory.

#### **FRI-G79**

##### **INFLUENCE OF COPPER ON THE MAGNETIC AND MAGNETOCALORIC PROPERTIES OF $\text{Ni}_{50}\text{Mn}_{34}\text{In}_{14}\text{B}$ ALLOYS**

Abdiel Quetz<sup>1</sup>, Sudip Pandey<sup>1</sup>, Anil Aryal<sup>1</sup>, Igor Dubenko<sup>1</sup>, Tapas Samanta<sup>2</sup>, Shane Stadler<sup>2</sup>, Naushad Ali<sup>1</sup>.

<sup>1</sup>*Southern Illinois University Carbondale, Carbondale, IL*, <sup>2</sup>*Louisiana State University, Baton Rouge, LA*.

The magnetocaloric and thermomagnetic properties of the  $\text{Ni}_{50}\text{Mn}_{34-x}\text{Cu}_x\text{In}_{14}\text{B}$  ( $x = 0, 0.75, 1.25, 2.00$ ) system have been studied by room temperature X-ray diffraction, differential scanning calorimetry (DSC), and magnetization measurements. Partial substitution of Cu for Mn in  $\text{Ni}_{50}\text{Mn}_{34-x}\text{Cu}_x\text{In}_{14}\text{B}$  results in a shift of  $T_M$  to lower temperature while  $T_C$  remains unchanged at around 320 K. A second order transition was observed from a paramagnetic austenitic (PA) to a ferromagnetic austenitic (FA) phase at  $T_C = 320$  K, and first order magnetostructural transition (MST) was observed from a ferromagnetic austenitic (FA) to low magnetization martensitic phase at  $T_M = 220$  (for  $x = 1.25$ ). The values of the latent heat ( $L = 9.4$  J/g) and corresponding total entropy changes ( $S_T = 29.7$  J/kg K) have been evaluated using DSC measurements. The magnetic entropy change value is comparable to those of well-known giant magnetocaloric materials, such as  $\text{Gd}_5\text{Si}_2\text{Ge}_2$ ,  $\text{MnFeP}_{0.45}\text{As}_{0.55}$ , and  $\text{Ni}_{50}\text{Mn}_{37}\text{Sn}_{13}$ . A concentration-dependent phase diagram of transition temperatures (magnetic, structural, and magnetostructural) has been generated using magnetic, XRD, and DSC data. The role of magnetic and structural changes on transition temperatures is discussed. (This work was supported by the Office of Basic Energy Sciences, Materials Science and Engineering Division of the U.S. Department of Energy; USDOE-DE-FG02-06ER46291 and DE-FG02-13ER46946)

#### **SAT-G78**

##### **AN IMAGING SCATTEROMETER FOR CHARACTERIZING SURFACE AND BULK SCATTER**

Joshua Hacker, Joshua Smith.

*California State University Fullerton, Fullerton, CA*.

The Advanced Laser Interferometer Gravitational-wave Observatory (aLIGO) requires optics with specific scatter characteristics in order to detect gravitational waves. With this in mind, an angle-resolved imaging scatterometer has been developed to characterize scatter from diverse optics in order to determine their suitability for use in aLIGO. The scatterometer laser operates at 1,064 nm, to match the lasers used in aLIGO, with a fixed angle of incidence onto a sample optic. The laser and optic are placed on a rotating stage and the scatter is recorded by a ccd camera over a discrete range of viewing angles. Like photodiode-based angle-resolved

scatterometers, this setup is used to measure a sample's bidirectional reflectance distribution function (BRDF) and estimate the total integrated scatter (TIS). The primary advantage added by the ccd imaging is the ability to distinguish the character and spatial distribution of the scatter, allowing discrimination of point defects from micro-roughness, bulk scatter from surface scatter, and identify scatter associated with the setup, not the sample. In this article, we discuss the design, advantages, and limitations of the imaging scatterometer, giving examples of how it is used to characterize aLIGO optics and how it might be used for other applications.

# Postdoctoral Poster Abstracts

## BIO/AGR/ENV LIFE SCIENCES

### CELL/MOLECULAR BIOLOGY

#### SAT-G1

##### **SYNTHESIS OF SMALL MOLECULE FLUORESCENT PROBES FOR INTRACELLULAR TARGETING**

Steven Ontiveros, Rishi Sapkota, Charles Shuster, Jeffrey Arterburn.

*New Mexico State University, Las Cruces, NM.*

Understanding the pathological state requires an ability to visualize cellular dynamics and physiological processes in living cells and tissues. Genetically-encoded fluorophores such as green fluorescent protein have revolutionized cell biology, but these tools are limited to models amenable to exogenous gene expression. Similarly, there exists a diverse variety of chemical fluorophores, but the membrane permeability of these molecules is limited by their large size and polarity. We have recently developed a novel class of triazaborolopyridinium-based (HPY) fluorophores that hold promise as live cell imaging probes and, in an effort to demonstrate that these fluorophores may be functionalized to identify specific cellular structures, we developed small molecule fluorescent probes targeting acidic organelles. Our probe, HPY(530), is comprised of a fluorene group with an absorption maximum of 530 nm and no overall charge. Simple, unfunctionalized HPY(530) dyes in HeLa cells were observed to be cell permeable, and displayed no specific targeting. However, amine-functionalized HPY derivatives displayed a punctate staining pattern that co-localized with the lysosomal marker GFP-LAMP1 and resembled the commercially available LysoTracker. HPY(530)-Butylamine localization was abrogated in cells by inhibiting V-ATPase proton pumps with bafilomycin, suggesting that the HPY probe targets acidic compartments. Lastly, HPY(530)-Butylamine targeted vacuoles in yeast in a V-ATPase-dependent manner. Together, these studies provide strong evidence that this novel fluorophore may be used as a probe in living cells, and current efforts are focused on targeting novel cellular compartments that have been previously resistant to conventional probes.

### ECOLOGY/EVOLUTION

#### SAT-G3

##### **PHYLOGENOMIC RESOLUTION OF RELATIONSHIPS WITHIN BIVALVIA (MOLLUSCA)**

Vanessa Gonzalez.

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Bivalves represent the second largest living class of molluscs, following gastropods, and their internal phylogenetic relationships have been debated for decades. Although recent investigations have revealed general agreement on the phylogenetic placement of the major bivalve lineages, support for several critical basal nodes is lacking, and strong incongruence has

been shown between mitochondrial and nuclear gene-based phylogenies. Phylogenomic approaches have recently been employed to obtain robust resolution of molluscan relationships, but conflict in morphological and molecular datasets persists within some major molluscan lineages, particularly Bivalvia. Here we provide the first phylogenomic analysis of Bivalvia aimed at resolving deep divergences within this group to have a better framework for understanding this diverse and fossil-rich group of animals. All 6 major lineages of bivalves (Archiheterodonta, Anomalodesmata, Inaequidonta, Palaeoheterodonta, Protobranchia, and Pteriomorphia) were sampled resulting in 31 newly sequenced Illumina-based bivalve transcriptomes in addition to 6 transcriptomes from representatives of other molluscan lineages. This constitutes the most comprehensive phylogenomic dataset to date for inferring deep relationships within Bivalvia. Subsequent analyses obtained robust resolution of bivalve major lineages, largely corroborating classical taxonomic relationships based mostly on paleontological and neontological morphological data. This includes the monophyly of Autobranchia, Protobranchia, Pteriomorphia, Heteroconchia, Palaeoheterodonta, Heterodonta, Archiheterodonta, Euheterodonta, and Inaequidonta.

## **MATHEMATICS & STATISTICS**

### **APPLIED MATHEMATICS**

#### **SAT-G5**

#### **RICCATI-ERMAKOV SYSTEMS AND EXPLICIT SOLUTIONS FOR INHOMOGENEOUS PARAXIAL WAVE EQUATIONS: OSCILLATING AND SPIRAL LASER BEAMS**

Erwin Suazo.

*Arizona State University, Tempe, AR.*

In quantum optics, it is an extraordinary and useful fact that one can deduce the Schrödinger equation from Maxwell's equations using paraxial approximation. In this context, this derivation is usually called the paraxial wave equation. Thanks to this derivation, one can model laser beam propagation on nonhomogeneous media (e.g., lenses and ionosphere). However, explicit solutions are rare since it requires solving partial differential equations with non-constant coefficients, and numerical methods are most commonly used. By using recent hidden symmetries discovered for the Schrödinger equation, we present how one can find explicit solutions of the inhomogeneous paraxial wave equation in a linear and quadratic approximation, thus showing the existence of oscillating laser beams in parabolic waveguides (e.g., fiber optics) and spiral light beams in varying media. Our solutions are conditioned on solving nonlinear systems that we have called Riccati-Ermakov systems, and we show several examples of solutions of this kind of system. Our solutions will be useful for testing the standard numerical methods used.

## OTHER MATHEMATICS

### SAT-G6

#### GEOMETRIZATION OF N-EXTENDED 1-DIMENSIONAL SUPERSYMMETRY ALGEBRAS

Stefan Mendez Diez<sup>1</sup>, Charles Doran<sup>2</sup>.

<sup>1</sup>*Utah State University, Logan, UT,* <sup>2</sup>*University of Alberta, Edmonton, Alberta, CA.*

The problem of classifying off-shell representations of the N-extended 1-dimensional super Poincaré algebra is closely related to the study of a class of decorated graphs known as Adinkras. We will discuss how these combinatorial objects possess a form of emergent supergeometry; Adinkras are equivalent to very special super Riemann surfaces with divisors. The method of proof critically involves Grothendieck's theory of "dessins d'enfants," the work of Cimasoni-Reshetikhin expressing spin structures on Riemann surfaces via perfect matchings for embedded graphs, and an observation of Donagi-Witten about ramified coverings of super Riemann surfaces.

## PHYSICAL SCIENCES

### PHYSICS (EXCEPT BIOPHYSICS)

### SAT-G9

#### INCORPORATING INTERACTIVE SIMULATIONS INTO THE INTRODUCTORY CALCULUS-BASED PHYSICS SEQUENCE

Ximena Cid.

*University of Washington, Seattle, WA.*

Introductory physics courses can be considered gateway courses for many STEM majors. It is also a very challenging sequence for many students because of the abstract nature of some of the topics covered. In addition to conceptual difficulties, some diagrams introduce additional difficulties separate from the conceptual context. This work explores whether incorporating interactive simulations impacts student learning by reducing difficulties caused by various common representations. We have introduced simulations created in the GlowScript programming language and will assess student responses on pre and post tests in the tutorial component of the introductory, calculus-based sequence at the University of Washington.



# Graduate Oral Abstracts

## BIO/AGR/ENV LIFE SCIENCES

## BIOCHEMISTRY/BIOPHYSICS

### Room 301AB

#### SMALL MOLECULE EFFECTORS OF THE HYPOXIA SENSING ENZYME FIH

Cornelius Taabazuing, Michael Knapp.

*University of Massachusetts Amherst, Amherst, MA.*

Hypoxia inducible factor (HIF) is a transcription activator that controls O<sub>2</sub> homeostasis in mammals. Factor inhibiting HIF (FIH), is a Fe(II)/ $\alpha$ KG-dependent dioxygenase that regulates HIF transcriptional activity via post-translational hydroxylation. Signaling molecules such as NO, CO, and H<sub>2</sub>S have been reported to affect HIF transcriptional activity *in vivo*; however, the molecular mechanism remains unclear. As hypoxia is implicated in the progression of cancer and myocardial ischemia, understanding how endogenous gas molecules can attenuate HIF activity may provide novel avenues for therapeutic development. NO and H<sub>2</sub>S affect HIF regulated physiological processes; therefore, we hypothesized they exert their effects by binding to FIH in place of O<sub>2</sub>. We report our use of kinetics, EPR (electron paramagnetic resonance), and UV-Vis spectroscopy to investigate the effects of CO, NO and H<sub>2</sub>S treatment on FIH activity. Our data suggests that FIH selectively binds NO and H<sub>2</sub>S, discriminating against other ligands such as CO and N<sub>3</sub>. We show that H<sub>2</sub>S inhibits FIH activity in a pH and dose dependent manner with maximal inhibition (IC<sub>50</sub> = 34  $\mu$ M) occurring at physiological pH (7.40), suggesting that the anion (HS<sup>-</sup>) is the inhibiting species. We also demonstrate that NO inhibits FIH activity (IC<sub>50</sub> = 176  $\pm$  5  $\mu$ M at pH 7.40) by binding in place of O<sub>2</sub> to the active site Fe(II). Using NO as an O<sub>2</sub> mimic, we demonstrate that substrate binding increases the affinity for O<sub>2</sub> and stimulates activation. Inhibition of FIH provides a rationale for the observed physiological responses to NO and H<sub>2</sub>S seen *in vivo*.

### Room 301AB

#### LIPIDOMIC ANALYSIS OF EICOSANOID SIGNALING DURING CHORIOALLANTOIC MEMBRANE DEVELOPMENT IN AMERICAN ALLIGATORS (*ALLIGATOR MISSISSIPPIENSIS*)

Theresa Cantu<sup>1</sup>, John Bowdenes<sup>2</sup>, Louis Guillette<sup>1</sup>.

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Eicosanoids are important signaling molecules commonly associated with inflammation and immune response. To date, few methods have explored the presence and role of eicosanoids with respect to embryonic development. Traditionally, inflammation is studied in disease etiology; however inflammatory processes occur during normal development and the role of these compounds is poorly understood. We hypothesize that pro-inflammatory lipids play a significant role during the earlier stages of alligator chorioallantoic membrane (CAM)

development, and that anti-inflammatory signals increase before hatch-out. We have developed an LC-ESI-MS/MS method capable of quantifying 40 eicosanoids in biological tissues. Here, we examine the chorioallantoic membrane (CAM) of the American alligator. Eggs were collected from Lake Woodruff National Wildlife Refuge and incubated in the laboratory at several temperatures. CAM tissue was collected at different stages of development, flash frozen, cryo-homogenized, spiked with internal standards, and extracted. The resultant extract was analyzed on an Agilent 1100 LC system equipped with a C<sub>18</sub> column (4.6 x 250 mm, 5 mm i.d.). Measurement and quantification of each eicosanoid species uses standard calibration curves and the concentrations are expressed as pmol eicosanoid per mg of protein. Initial results identified the amount of tissue needed for extraction of these compounds and detected 32 of 40 compounds in CAM tissue. Future work will ascertain changes in these compounds during embryonic development and provide insight on the role of eicosanoids in the developing chorioallantoic membrane of the American alligator. This is the first study to investigate eicosanoids analytically in the CAM tissue of any wildlife species.

#### **Room 301AB**

#### **IDENTIFICATION AND CHARACTERIZATION OF AROGENATE DEHYDROGENASES (ADHS) INVOLVED IN TYROSINE BIOSYNTHESIS IN TABLE BEET (*BETA VULGARIS*)**

Samuel Lopez Nieves, Hiroshi Maeda.

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The aromatic amino acid tyrosine (Tyr) is a precursor of important secondary metabolites in plants (i.e., alkaloids, betalains, vitamins, etc.). As animals are unable to synthesize Tyr, we must uptake Tyr from external sources such as plants. However, most of our knowledge of Tyr biosynthesis comes from microbial studies, and limited research has been conducted for the Tyr pathway in plants. Previous studies reported that Tyr can be produced via 2 different routes: the 4-hydroxyphenylpyruvate (4-HPP) and arogenate pathways, in which the decarboxylation reaction is catalyzed by prephenate dehydrogenase (PDH), and arogenate dehydrogenase (ADH), respectively. In this study we investigated possible ADH and PDH enzymes involved in Tyr biosynthesis using table beet (*Beta vulgaris*) as a model system, which produces high levels of nitrogen-containing Tyr-derived pigments called betalains. We have detected ADH activity in the root and leaf crude extracts of table beet. Using the recently published sugar beet genome and PCR-based cloning, we identified 2 genes homologous to previously-reported *Arabidopsis* ADH genes in table beet. The purified recombinant enzymes showed only ADH but not PDH activity *in vitro*. These results suggest that Tyr is mainly produced via the arogenate pathway in *Beta vulgaris*. Currently, we are conducting kinetics analysis of the ADH enzymes. Genetic suppression of the identified ADHs in table beet can further allow us to investigate how plants produce and regulate biosynthesis of Tyr and Tyr-derived plant natural products.

## BIOLOGY (GENERAL)

### Room 303AB

#### SHAPE MATTERS: COROLLA CURVATURE IMPROVES NECTAR DISCOVERY IN THE HAWKMOTH *MANDUCA SEXTA*

Eric Octavio Campos, Thomas Daniel, Toby Bradshaw.  
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Nectarivorous pollinators use a variety of floral cues while foraging. Flower morphology is recognized as a potentially important contributor to a pollinator's ability to find and exploit the nectar source. However, it can be difficult to test hypotheses about the importance of whole-flower shape in pollinator foraging ability using either natural variation in floral form or traditional artificial flower construction techniques. We measured the effects of variation in whole-flower shape on pollinator foraging ability using the hawkmoth *Manduca sexta* and 3D-printed artificial flowers whose shapes were mathematically specified with 4 shape parameters. In dimorphic arrays containing curved trumpet-shaped flowers and flat-disk flowers, hawkmoths visited trumpet-shaped and flat-disk flowers with equal frequency but were able to find the nectar source in significantly more trumpet-shaped flowers regardless of nectary aperture size. Interestingly, trumpet-shaped flowers needed to deviate only slightly from the flat-disk morphotype in order to significantly increase hawkmoth foraging ability. Our study shows that whole-flower 3D shapes, particularly corolla curvature, have the potential to act as a mechanical nectar guides for *M. sexta*, further implicating direct flower-proboscis contact as an important contributor to success during flower handling in hawkmoths. Our approach of combining mathematical modeling with 3D-printing to construct precise and repeatable artificial flowers is novel and paves the way for previously impractical experiments regarding the importance of floral morphology in mediating plant-pollinator interactions.

## BOTANY

### Room 303AB

#### HOW HARVESTING IMPACTS WHITE SAGE (*SALVIA APIANA*) AS A CULTURAL RESOURCE IN SOUTHERN CALIFORNIA

Cassidy Adlof<sup>1</sup>, Paula Schiffman<sup>1</sup>, Kimberly Kirner.  
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*Salvia apiana* (white sage) is a culturally significant plant that is endemic to southern California and upper Baja California. The plant is harvested by Native Americans for cleansing ceremonies and the practice has expanded to Druidic, Wiccan, and other nature-centered groups. This study will address concerns expressed by members of the Native American community that different harvesting practices are harmful to the plant. To examine the biological effects on the plants, we performed combinations of harvest treatments on wild *Salvia apiana*. Treatments included gathering technique (by hand, cutting, and leaf only), amount (0%, 5%, 25%, and 50%), and season (spring and summer). Responses to treatments depended on the site. At cooler sites (mean summer temperature below 35 °C), higher amounts of harvest resulted in a decline in

plant size, while lower amounts resulted in growth or no change in plant size. Plants that had 25% of leaves harvested, using leaf only (spring or summer) or branches snapped by hand (summer), had more flowers than the control. At warmer sites (mean summer temperature greater than 35 °C), higher harvest amounts resulted in no change in plant size, while lower amounts declined in size. Plants that had 50% of leaves harvested; using a cutting tool (spring or summer), leaf only (spring), and snapped by hand (summer); tended to have more flowers than the control. Increased flowering and decreased growth are common responses to increased stress. Overall, harvesters must be aware of environmental conditions if they wish to collect with as little impact on the plant as possible.

## **CANCER BIOLOGY**

### **Room 301AB**

#### **PROTEOMIC STUDY OF PROSTATE CANCER EXTRACELLULAR VESICLES FOR IDENTIFICATION OF POTENTIAL DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS**

Gloria Polanco, Emma Arigi, Marc Cox, Igor Almeida.

*The University of Texas at El Paso, El Paso, TX.*

Extracellular vesicles (EVs) containing bioactive cargo such as proteins are used as a means of communication between cells. EVs have been described as a potential source of biomarkers for several diseases, including cancer. In addition, EVs have been thought to play a role in processes important for cancer progression. In prostate cancer (PCa), the second deadliest malignancy in men, there is a need for both therapeutic targets and diagnostic markers. The present study seeks to identify EV protein cargo derived from PCa 22RV1 and LNCaP cell models, as well as normal human prostate epithelial (NHPE) RWPE-1 cell model. Two EV populations were enriched from cell supernatant by differential ultracentrifugation for 2 and 16 hours (EV2 and EV16, respectively). Enrichment was confirmed by transmission electron microscopy imaging and nanoparticle tracking analysis. EV preparations were subjected to trypsin digestion, and 1D LC-MS/MS analysis of the resulting peptides was conducted. Bioinformatic analysis was performed using Sorcerer-SEQUEST and Scaffold softwares. Preliminary results suggest a qualitative difference in EV proteins derived from PCa and NHPE cell models; with a total of 296 and 456 proteins identified in either or both PCa cell-derived EV2 and EV16, respectively. PCa unique proteins of interest include carcinoma-associated antigen Ep-CAM and androgen receptor regulators FKBP52 and  $\beta$ -catenin. A quantitative differential proteomic analysis to observe the levels of protein expression in EVs derived from these cell models is currently underway. We expect that the outcome of this research will yield potential therapeutic target and diagnostic marker candidates.

**Room 301AB****DYNAMIC PERTURBATION OF NF- $\kappa$ B SIGNALING BY MERKEL CELL POLYOMAVIRUS SMALL T ANTIGEN**

Christian Berrios<sup>1</sup>, Megha Padi<sup>2</sup>, John Quackenbush<sup>2</sup>, James A. DeCaprio<sup>2</sup>.

<sup>1</sup>*Graduate School of Arts and Sciences, Harvard University, Boston, MA*, <sup>2</sup>*Dana-Farber Cancer Institute, Boston, MA*.

Merkel cell polyomavirus (MCV) is the etiological agent of the rare skin cancer Merkel cell carcinoma (MCC). In most MCC tumors, both MCV small T antigen (ST) and a truncated form of large T antigen (LT) are expressed. Classical studies using the related polyomavirus simian virus 40 (SV40) demonstrated that SV40 ST plays a critical role in cellular transformation by inhibiting protein phosphatase 2A (PP2A) and perturbing multiple signaling pathways. In contrast, MCV ST was recently shown to transform rat fibroblasts independent of PP2A binding, suggesting that novel mechanisms of transformation are employed by MCV ST. A large-scale, systematic investigation of transcriptome effects of viral oncoproteins in normal human IMR90 fibroblasts revealed that MCV ST specifically increased NF- $\kappa$ B-dependent gene expression. Timecourse expression analysis using RNA-seq of IMR90 cells with inducible expression of MCV ST revealed heightened levels of inflammatory response-related genes. In addition, a dramatic increase in SLC16A1 expression, which encodes the monocarboxylate transporter 1 (MCT1), was seen in MCV ST-expressing cells immediately after ST induction. MCT1 regulates lactate transport into cells, is upregulated in several cancer types, and is regulated by NF- $\kappa$ B. In concordance with MCT1 expression, MCV ST-expressing cells had a several-fold increase in intracellular [lactate] over control cells. Entering lactate can trigger NF- $\kappa$ B activation, driving cell migration and tumorigenesis, suggesting a potential positive feedback loop between lactate, MCT-1, and NF- $\kappa$ B that could contribute to the high levels of NF- $\kappa$ B seen in MCC tumors. This may represent a potential therapeutic opportunity, given the availability of MCT-1-specific inhibitors.

**CELL/MOLECULAR BIOLOGY****Room 304 BC****TRANSCRIPTOME ANALYSIS BY RNA-SEQ OF *SHEWANELLA* SP. ANA-3 GROWN ON ARSENATE AND OTHER TERMINAL ELECTRON ACCEPTORS**

Ruth Tilus Watson, Chad Saltikov.

*University of California, Santa Cruz, Santa Cruz, CA*.

Under low oxygen tensions, some savvy microbes can use non-conventional substrates such as radionuclides and even toxic heavy metals as terminal electron acceptors in cellular respiration. This metabolic activity can be exploited for use in bioremediation efforts; however, the underlying biological processes involved in toxin reduction are not fully understood. *Shewanella* sp. ANA-3 was developed as a model for studying respiratory arsenic reduction. In ANA-3, the arsenic reductase enzymes are present only under anaerobic conditions; however, the regulatory elements that govern this selective production have not previously been identified. In this study, we used comparative whole transcriptome sequencing (RNA-seq) to identify the unique regulatory signature of ANA-3 under arsenic vs. non-arsenic respiring conditions. We

identified several potential regulators that are expressed specifically in arsenic respiring cells. Of these, several genes in the sulfur assimilation pathway and stress response pathways were highly expressed which allude to their possible role in reducing arsenic while avoiding its toxic effects. The functional importance of several of these regulatory elements was then demonstrated through mutational analysis and kinetic growth experiments. These data demonstrate that arsenic respiration is under complex transcriptional control. These differential expression patterns under arsenic respiring conditions allowed us to identify several regulatory genes that are important for respiratory arsenic reduction. We continue to use the RNA-seq data to further elucidate the metabolic pathway of metal reduction in ANA-3.

#### **Room 304BC**

##### **FUNCTIONAL STUDY OF CONSERVED MEIER-GORLIN SYNDROME MUTATIONS IN *SACCHAROMYCES CEREVISIAE***

Joseph Sanchez, Bonita Brewer, M.K. Raghuraman.  
*University of Washington, Seattle, WA.*

Meier-Gorlin syndrome (MGS) is a rare form of primordial dwarfism, which causes short stature, small ears, and missing kneecaps. Recently, MGS has been associated with mutations in the pre-replication complexes (*orc1*, *orc4*, *orc6*, *cdc6*, and *cdt1*), which are important for origin initiation in DNA replication; however, it is unclear how perturbing origin initiation leads to the phenotypes observed in MGS. The current hypothesis states that people with MGS have a reduced size because of reduced cell number as a result from impaired cell division. We are using yeast to perform functional studies examining a conserved MGS mutation in *orc4* (*orc4*<sup>MGS</sup>) and discovered several interesting phenotypes, one of which is a drastically reduced ribosomal DNA (rDNA) locus. In addition to characterizing how *orc4*<sup>MGS</sup> affects origin initiation, we propose to investigate the relationship between origin initiation and the rDNA locus. Furthermore, since cells require such large numbers of ribosomes, we aim to determine if reducing the template for ribosomal RNA transcription impairs ribosome biogenesis. In addition to discovering how MGS mutations affect origin initiation, this study will provide a better understanding of how DNA replication machinery may be regulated by the rDNA locus and how reducing the number of repeats in the rDNA locus affects ribosome biogenesis.

#### **Room 304A**

##### **IDENTIFICATION OF PROTEINS INVOLVED IN THE FORMATION OF CROSS-LINKED ACTIN NETWORKS IN HUMAN TRABECULAR MESHWORK CELLS**

Jaclyn Bermudez, Abbot Clark, Weiming Mao.  
*University of North Texas Health Science Center, Fort Worth, TX.*

Glaucoma is a leading cause of blindness worldwide, and the primary risk factor of glaucoma is increased intraocular pressure (IOP). In glaucoma patients, outflow resistance through the trabecular meshwork (TM) is abnormally elevated. Comparison between normal and glaucomatous TM cells and tissues revealed excessive formation of cross-linked actin networks (CLANs). CLANs are web-like polygonal structures found within TM cells and tissues. CLANs alter TM cell functions and may increase cell rigidity, thereby contributing to elevated aqueous

outflow resistance as well as IOP. However, the proteins involved in CLAN formation in TM cells are not fully characterized. Therefore, we used a proteomic approach to identify the proteins that are involved in CLAN formation. Primary human TM cell cultures were treated with vehicle control or glaucoma-associated factors to induce CLAN formation. Cytoskeletal proteins were then collected and separated by 2D fluorescence difference gel electrophoresis (2D-DIGE). Proteins with increased expression levels in treated samples compared to control were subjected to mass spectrometry (MS) analysis. Differential expression of proteins identified by MS was confirmed by western immunoblotting (WB) and immunocytochemistry (IHC) analysis. A number of proteins were identified as being enriched in CLAN forming TM cells by MS analysis. Using WB and IHC, caldesmon, calponin, myosin light chain, and tropomyosin were found to be up regulated with treatment and each co-localized with CLANs. The potential role of these proteins in CLAN formation will be further investigated. These proteins may provide new insights into the pathogenesis of glaucoma.

#### **Room 304A**

#### **IMMUNOADJUVANT INTERLEUKIN 33 INDUCES ANTIGEN-SPECIFIC TUMOR AND VIRAL IMMUNITY**

Daniel Villarreal<sup>1</sup>, Megan Wise<sup>1</sup>, Jewell Walters<sup>1</sup>, Jian Yan<sup>2</sup>, Matthew Morrow<sup>2</sup>, David Weiner<sup>1</sup>.

<sup>1</sup>University of Pennsylvania, Philadelphia, PA, <sup>2</sup>Inovio Pharmaceuticals, Plymouth Meeting, PA.

Recent studies are beginning to show that IL-33 cytokine activities exceed those of the Th2 immunity, and can promote Th1 immune responses. However, the potential ability of IL-33 to act as vaccine adjuvant to influence the CD4 Th1 and CD8 T cell immune responses has not been well defined. Here we examine IL-33 for its immunoadjuvant effects in an HPV-associated cancer immune therapy model in which cell-mediated immunity is critical for protection. To this end, we developed a highly optimized DNA-vector encoding IL-33 and evaluated its adjuvant properties in combination with a DNA fusion HPV 16 E6/E7 construct *in vivo*. We showed that IL-33 was capable of enhancing potent antigen (Ag)-specific effector and memory T cell immunity *in vivo* in a DNA vaccine setting. Additionally, IL-33 augmented vaccine-induced Ag-specific polyfunctional CD4<sup>+</sup> and CD8<sup>+</sup> T-cell responses, with a large proportion of CD8<sup>+</sup> T cells undergoing cytolytic plurifunctional degranulation. Therapeutic studies indicated that established TC-1-bearing mice underwent rapid and complete regression after therapeutic vaccination with IL-33 in conjunction with an HPV DNA vaccine. Furthermore, we show that IL-33 can significantly expand the magnitude of Ag-specific CD8<sup>+</sup> T-cell responses and elicit effector-memory CD8<sup>+</sup> T cells. Given these significant findings, we also explored IL-33 adjuvant effects in conjunction with an HIV DNA vaccine and demonstrated that IL-33 also can increase the antigen-specific HIV T-cell immune responses. Overall, these results lay the groundwork for IL-33 as an immunoadjuvant candidate in future vaccination in the context of both antitumor and antiviral immunotherapy.

#### Room 304A

##### **A COUPLED *IN VITRO-*IN VIVO** APPROACH TO DISSECT APC-DIA-MEDIATED ACTIN ASSEMBLY**

Olivia Molinar<sup>1</sup>, Richa Jaiswal<sup>2</sup>, Vincent Stepanik<sup>3</sup>, Aneliya Rankova<sup>2</sup>, Bruce Goode<sup>2</sup>, Brooke M. McCartney<sup>1</sup>.

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Regulation of Wnt signaling, microtubule stability, and actin assembly are all important processes that are controlled by the colon cancer tumor suppressor Adenomatous polyposis coli (APC). While APC's role in Wnt signaling and microtubule stability is well-studied, APC's actin-associated functions are poorly understood. Two highly conserved homologs of APC, APC1 and APC2, are present in humans and exhibit some redundant functions. Human APC (hAPC) bundles and nucleates actin filaments and collaborates with the formin Diaphanous (Dia) to assemble F-actin *in vitro*. However, the physiological relevance of APC's actin assembly activity is unknown. *Drosophila* also express 2 APC proteins, and our lab utilizes the formation of actin furrows in the syncytial embryo as a model for actin assembly. We have shown that APC2 and Dia are required for actin furrow extension, but the role of APC1 is not well understood. We first showed through *in vitro* pyrene actin assembly assays and TIRF microscopy that fly APC1 shares a common mechanism of actin assembly with hAPC. In contrast, fly APC2 does not promote actin assembly alone and inhibits the actin assembly activity of Dia. Loss of APC1 in the early embryo leads to actin furrow extension defects, strongly suggesting that APC1 is necessary for actin assembly *in vivo*. Our lab will continue to dissect the APC1-APC2-Dia interaction by using a coupled *in vivo-in vitro* approach to better understand the mechanisms of APC and Dia proteins in actin assembly.

#### Room 304A

##### **THE NERVOUS SYSTEM MODULATES CD8<sup>+</sup> T-CELL FUNCTION THROUGH THE $\beta$ 2-ADRENERGIC RECEPTOR**

Leonardo Estrada, Didem Agac, J. David Farrar.

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There is growing evidence to suggest that various aspects of immune function are controlled by neural networks. Both cholinergic and adrenergic receptors are expressed by various major immune cell types. Specifically, expression of the  $\beta$ 2-adrenergic receptor (ADRB2) has been characterized in different cells of the immune system; however, our lab has demonstrated for the first time a differential expression of this receptor in subsets of effector and memory CD8<sup>+</sup> T cells. We found that the ADRB2 is upregulated in human effector memory CD8<sup>+</sup> T cells compared to central memory/naïve counterparts. Further, human CD8<sup>+</sup> T cells that are acutely activated in the presence of the ADRB2 natural ligand norepinephrine (NE) secrete significantly less IFN- $\gamma$  and TNF- $\alpha$ . Similarly, the cytolytic capacity of these cells is reduced when NE is present. This downregulation by NE was reversed in the presence of an ADRB2-specific antagonist, but not a pan  $\alpha$ -adrenergic or  $\beta$ 1-adrenergic receptor-specific antagonist. Additionally, mouse CD8<sup>+</sup> T cells behaved similarly to human cells to these antagonists, suggesting species conservation of this neural-immune network. Moreover, ADRB2-KO CD8<sup>+</sup> T



cells were completely resistant to the effects of NE. Current experiments using an adoptive transfer model will elucidate how ADRB2 signaling modulates CD8<sup>+</sup> T cell function *in vivo*. These experiments will provide insight into how the nervous system controls CD8<sup>+</sup> T cell function during the course of an infection.

#### **Room 304A**

##### **INVESTIGATING THE GENE REGULATORY NETWORK INVOLVED IN REGULATION OF TRUNK NEURAL CREST FORMATION**

Stefanie Monica<sup>1</sup>, Richard Harland<sup>1</sup>, Eric Liao<sup>2</sup>.

<sup>1</sup>*University of California, Berkeley, Berkeley, CA*, <sup>2</sup>*Center for Regenerative Medicine, Massachusetts General Hospital, Boston, MA*.

The neural crest (NC) is an unique population of multipotent cells in vertebrates, often referred to as the fourth germ layer because of their unique ability to migrate all over the developing embryo and contribute to multiple different tissue types. Cranial neural crest cells (NCCs) elaborate into the craniofacial skeleton and associated structures, while trunk NCCs give rise to the dorsal root ganglia, adrenal medulla, aortic nerve clusters, and melanocytes. The gene regulatory network (GRN) responsible for the formation of the cranial NCCs has been well studied in a number of species since its migration pattern is highly conserved across vertebrates. However, the GRN-regulating trunk NC is less well defined. We hypothesize that due to the differences in migratory pathways and derivatives that arise from trunk and cranial NCCs, the genes involved in their regulation are likely also distinct. In this work, we aim to elucidate the GRN-regulating trunk NC specification, migration, and differentiation. We use a *sox10:kaede* transgenic line in which the *sox10* promoter confers lineage restriction of the photoconvertible protein kaede to NCCs. This transgenic line enables us to identify *in vivo* and isolate *in vitro* precise trunk NC populations that will give rise to specific derivatives. As a first step to analyze the GRN regulating trunk NCC, we assayed the transcriptome profile of the trunk NCC progenitor populations by RNA-seq. This work will elucidate the molecular program that directs cranial vs. trunk NC development and address broader questions in cellular specification and differentiation.

#### **ECOLOGY/EVOLUTION**

#### **Room 305**

##### **SPATIAL MODELING OF A REALIZED NICHE: THE INVASION OF FENNEL INTO COASTAL HABITATS OF VIRGINIA'S EASTERN SHORE**

Kathryn MacCormick, Matthias Leu.

*College of William and Mary, Williamsburg, VA*.

Establishment is an important phase in the invasion process during which an exotic species escapes cultivation and successfully survives and reproduces in its new habitat, ultimately becoming naturalized and potentially invasive in its new range. One of the earliest cultivated plants, sweet fennel (*Foeniculum vulgare* Mill.) has gained a global distribution due to anthropogenically mediated dispersal; it alters vegetative structure and function by forming

dense stands and threatens invasion into coastal shrub and grassland habitats worldwide. Like many Mediterranean species adapted to disturbed habitats, fennel produces numerous small seeds that are capable of forming a persistent seedbank. The interaction of dispersal, anthropogenic disturbance, and competition for suitable micro-habitat sites in a species that is on the verge of regional invasion make Virginia's eastern shore an interesting system for studying the invasion process. By modeling the distribution of fennel vegetation and seedbank at the eastern shore of the Virginia National Wildlife Refuge, we are investigating the dispersal mechanisms, anthropogenic activities, and abiotic conditions that are contributing to fennel's success. We will conduct field surveys of fennel stem and seed densities with a stratified sampling design which will account for distance to anthropogenic features and refuge management methods. Using spatially applied statistical models and information theory, we will estimate the relative influence of multiple environmental and site variables to explain fennel occurrence. Preliminary observations suggest that proximity to roads and certain mowing methods may be important factors which could have management implications for future roadside mowing programs.

#### **Room 303AB**

#### **IS LORELEI, A PUTATIVE GPI-ANCHORED MEMBRANE PROTEIN INVOLVED IN POLLEN TUBE RECEPTION IN *ARABIDOPSIS THALIANA*, UNDERGOING SELECTION?**

Jennifer Noble, Mark Beilstein, Ravishankar Palanivelu.

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A pollen tube carrying the sperm cells overcomes several hurdles by navigating past multiple pistil cells before delivering the sperm cells to the female gametophyte, achieving double fertilization and initiating seed formation. One of the challenges the pollen tube encounters after entering the ovule is pollen tube reception, which includes arresting growth in the synergid cell and lysing to release sperm cells for double fertilization. In *Arabidopsis thaliana*, mutations in LORELEI (LRE), a putative glycosylphosphatidylinositol (GPI)-anchored membrane protein, disrupt pollen tube growth arrest in the synergid cells and consequently the pollen tube coils within the synergid cell. A similar behavior is also observed in *feronia* (*fer*) and *nortia* (*nta*) mutants. Furthermore, the coiling behavior is seen even when 2 closely related species are crossed to each other, suggesting that pollen tube reception is a pre-zygotic barrier in interspecific crosses. Therefore, we hypothesized that pollen tube reception genes are highly divergent and that they undergo positive selection. To test if LRE is undergoing selection, we calculated Tajima's D test of neutrality using 855 *A. thaliana* genomes. We determined that LRE and FER, but not NTA, are undergoing purifying selection. Next, we will test for positive selection in LRE using phylogenetic analysis by maximum likelihood (PAML) to identify regions of LRE that are highly divergent among different species of Brassicaceae. The data from this study will determine if genes involved in pollen tube reception are undergoing positive selection and help us understand species specificity in pollen tube reception.

### Room 305

#### FROM FOOD TO GARBAGE: THE REMODELING OF THE PLANT VACUOLE AND ITS ROLE IN CHLOROPLAST EVOLUTION

Amber Paasch<sup>1</sup>, Eunsoo Kim<sup>2</sup>.

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<sup>2</sup>American Museum of Natural History, New York, NY.

The chloroplast is one of the most important components of life on Earth. Its evolution more than 1.5 billion years ago caused a steep increase in atmospheric oxygen that led to the rise of multicellular aquatic and land organisms, and it continues to be the major producer of oxygen today. The chloroplast, previously a free-living cyanobacterium, was acquired through phagocytosis by a single-celled eukaryote, forming the first plant cell. Today, phagotrophy has been lost in almost all plants and green algae with the exception of the “early-divergent” green alga, *Cymbomonas tetramitiformis*. Structurally, the permanent nature of phagosome of *C. tetramitiformis* resembles a plant vacuole more than a traditional transiently formed phagosome found in animal cells and other protists such as ciliates and amoebozoans. This suggests that the plant vacuole may have prey-digesting origins. The goal of this study is to identify whether the plant vacuole originally functioned as an organelle used for phagocytosis. We have sequenced the nuclear and organellar genomes of *C. tetramitiformis* and used a large-scale comparative approach to map the evolution of the plant vacuole in distant organisms. The plant vacuole proteome was identified and compared in 22 taxa. Our data suggest that the plant vacuole was originally used to digest food in some single-celled eukaryotes and later remodeled to be a digester of cellular garbage in land plants. This study is the first to suggest that the organelle used to capture the chloroplast 1.5 billion years ago was a plant vacuole rather than a traditional phagosome.

### Room 305

#### FUNCTIONAL EVOLUTION OF A CONSERVED CIS-REGULATORY ELEMENT IN FINS AND LIMBS

Joyce Pieretti, Neil Shubin.

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The *cis*-regulatory architecture of key developmental genes is a major contributor to the evolution of complex traits. One approach to exploring this phenomenon involves comparative functional studies of gene regulation across distantly related species. *Sonic hedgehog* (*Shh*) plays an indispensable role in the development of vertebrate appendages where it is expressed in the zone of polarizing activity (ZPA). The *Shh* locus contains a complex assembly of regulatory elements, including the ZPA regulatory sequence (ZRS), an element controlling the abundance, location, and duration of gene expression in paired appendages. By testing regulatory domains from a variety of different species using zebrafish (*Danio rerio*) and mouse (*Mus musculus*) transgenesis, we sought to determine how *cis*, *trans*, or *cis-trans* coevolution shaped the *Shh* regulatory architecture observed in chordates and to draw conclusions regarding the origins of such elements. Gnathostome ZRS elements from all tested species drove reporter expression in the *Shh* domain of zebrafish fins and mouse limbs, which supported our hypothesis that the ZRS elements of all jawed vertebrates are functionally conserved and that the *trans* environment of

the hosts (zebrafish and mouse) is conserved. As the tetrapod limb is considered a vertebrate novelty that facilitated the water-to-land transition, these studies suggest that, despite the structural novelty of the limb, the underlying regulatory circuitry of *Shh*'s involvement in appendage patterning was pre-established.

#### **Room 306AB**

##### **FISHING FOR GENES: THE DISTRIBUTION OF NERVOUS NETWORK COMPONENTS ACROSS CNIDARIANS**

Adolfo Lara<sup>1</sup>, Estefania Rodriguez<sup>2</sup>.

<sup>1</sup>*Richard Gilder Graduate School, American Museum of Natural History, New York, NY,*

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Sea anemones, jellyfish, and their relatives are classified within the phylum Cnidaria and are a group of relatively simple animals characterized by having cnidocytes (stinging capsules) which are used in prey capture and defense. In addition, cnidarians are among the earliest diverging metazoan (multicellular animals) groups possessing an organized neural network, providing a unique window illuminating the origin of neural systems in all animals. To date, substantial nervous network studies exist for later diverging, more anatomically complex model organisms such as roundworms, fruit flies, and mice. Earlier diverging metazoans like anemones, however, require similarly comprehensive studies, as their less complex neural networks provide an opportunity to determine similarities and differences in structures, properties, and capabilities when compared to later-evolving metazoan neural networks. This project will identify such neurobiological architecture similarities and differences within cnidarians. Specifically, this project will test the following hypotheses: the neurotransmitters gamma-aminobutyric acid (GABA), glycine, epinephrine, and norepinephrine are specific only to Anthozoans (sea anemones and their relatives) and hydrozoans (hydroids) but not other classes of medusozoans (Scyphozoa, Cubozoa, and Staurozoa). Transcriptome data from 4 representatives of Anthozoa and Hydrozoa along with 2 representatives of the other cnidarian classes, Cubozoa (box jellyfish), Scyphozoa (true jellyfish), and Staurozoa (stalked jellyfish), were screened for presence of the previously mentioned neural genes. The presence, or lack thereof, and the distribution of the targeted neural genes within cnidarians will be discussed.

#### **Room 305**

##### **CONVERGENT EVOLUTION IN THE DEVELOPMENT OF VESTIGIAL EYES**

Ruben Tovar, Dana Garcia.

*Texas State University, San Marcos, TX.*

The south central Texas *Eurycea* clade exhibits a continuum of karst salamander phenotypes. The Texas blind salamander (*E. rathbuni*) is considered a stygobiont because it completes its life cycle in an aquatic subterranean habitat where it lives in perpetual darkness. Consequently, *E. rathbuni* exhibits highly reduced eyes. In contrast, the Barton Springs salamander (*E. sosorum*) is epigean and is endemic to surface habitats; it exhibits well developed eyes. To determine the sequence of events during development that leads to widely disparate ocular outcomes and to gain insights into the molecular mechanisms responsible, embryos at various stages of

development were obtained from two species (*E. sosorum* and *E. rathbuni*) and sectioned using a Shandon cryotome. Five developmental stages of *E. sosorum* and 6 developmental stages of *E. rathbuni* were identified, and sections taken from these embryos were labeled for Pax6 and Shh using immunohistochemistry. Images were obtained using a scanning confocal microscope. Expression of Pax6 and Shh proteins is observed in both morphotypes represented by *E. rathbuni* and *E. sosorum*. *Eurycea sosorum* maintained expression of *pax6* and *shh* through embryogenesis and into a juvenile stage. Decreased labeling of the Pax6 protein was observed during later stages of *E. rathbuni* development, while Shh protein labeling was increased in a select subset of cells surrounding the brain and eye. Interestingly, these results parallel *pax6* and *shh* expression in 2 morphotypes explored in *Astyanax mexicanus*, suggesting some degree of convergent evolution in the developmental mechanisms that lead to the development of vestigial eyes.

### Room 305

#### **COMPREHENSIVE DIET STUDY OF THE HIGHLY ENDANGERED ATTWATER'S PRAIRIE CHICKEN (*TYMPANUCHUS CUPIDO ATTWATERI*) WITH THE USE OF STABLE ISOTOPES**

Zaria Torres, Miguel Mora.

*Texas A&M University, College Station, TX.*

The population of the Attwater's prairie chicken (APC; *Tympanuchus cupido attwateri*) has significantly declined in the last century as a result of habitat degradation and fragmentation in the Western Gulf coastal prairies. This prairie grouse was listed as an endangered species in the mid-1960s, and today there are less than 200 individuals in the wild. Numerous research studies as well as management efforts have been implemented to preserve this endemic ground bird; however, there has been limited success. In this study, we examined the diet of the APCs using  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  stable isotopes. We conducted our study at the Attwater Prairie Chicken National Wildlife Refuge (APCNWR) near Eagle Lake, Texas, during 2012-2013. Throughout this period, we collected vegetation and insect samples known to be potential food items of the APCs. We also collected and examined feather samples from wild APCs on the refuge and museum feathers from historic specimens collected between 1890 and the 1960s. In addition, blood and fecal samples were also collected from 22 wild APCs. We are interested in determining if there are shifts in  $^{13}\text{C}$  and/or  $^{15}\text{N}$  values between museum feather samples compared to those of current APCs. Preliminary feather data shows a decrease in  $^{13}\text{C}$  values (-18 ‰ to -26 ‰) and an increase in  $^{15}\text{N}$  values (5 ‰ to 8 ‰), since release from captivity. Our goal is to determine if these shifts are a consequence of choice or availability of forage resources present at the APCNWR, and what this could mean for the conservation of this species.

## ENVIRONMENTAL SCIENCE/STUDIES

### Room 308AB

#### **DISTRIBUTION AND BIOAVAILABILITY OF TRACE METALS IN SHALLOW SEDIMENTS FROM GRAND LAKE, OK**

Shane Morrison<sup>1</sup>, Steve Nikolai<sup>2</sup>, Darrell Townsend<sup>2</sup>, Jason Belden<sup>1</sup>.

<sup>1</sup>Oklahoma State University, Stillwater, OK, <sup>2</sup>Grand River Dam Authority, Vinita, OK.

The abandoned Tri-State Mining District (TSMD) is a historic superfund site that covers 6,500 km<sup>2</sup> and 3 states (Kansas, Missouri, and Oklahoma) and is the source for trace metal loading in Grand Lake sediments. Despite elevated concentrations of cadmium, lead, and zinc, no evidence of sediment toxicity has been observed during previous investigations; however, these investigations were limited to just a few lake transects with mostly deep-water sediments. The lack of toxicity is likely due to specific water chemistry of the lake including high pH, high hardness, and frequent anoxic sediments. The current project aims to develop a more complete metal distribution map with emphasis on shallow water areas ( $\leq 6$  m depth) located in the northern reaches of Grand Lake where chances of sediment deposition from the TSMD is greatest. Distribution information is important because the shallow areas are subject to disturbance events (e.g., boat traffic, wave action, and dock construction) and have a higher chance of becoming dry during low-water periods. Changes in water chemistry and oxidation state of trace metals during these disturbance events could cause greater availability resulting in toxicity, bioaccumulation, and greater lake impacts. Therefore, total sediment concentrations, amphipod (*Hyaella azteca*) sediment toxicity tests, bioaccumulation in pond snails (*Helisoma trivolvis*), and accumulation in passive samplers will also be used to investigate the influence of highly oxygenated versus anoxic sediments. The results of this research will demonstrate the influence of changes in oxidation on trace metal releases from Grand Lake sediments, (bio)availability, and ultimately toxicity.

### Room 308AB

#### **DISEASE REDUCTION OF STRAWBERRIES VIA COVER CROPS AND ANAEROBIC SOIL DISINFESTATION, ALTERNATIVES TO FUMIGANTS**

Miriam Olivera, Carol Shennan.

University of California, Santa Cruz, Santa Cruz, CA.

Large-scale strawberry production is limited by disease. Knowledgeable intensive management can prevent disease, yet fast treatments such as fumigants are favored though they pose environmental health risks. Anaerobic soil disinfestation (ASD) is a fumigant alternative method whereby carbon from plant debris is incorporated into soil saturated with water and covered by plastic mulch for 3 weeks. Anaerobiosis results in reduction of disease. The price of externally derived carbon, like rice bran, may increase due to scarcity driven by California's ongoing drought and competing-use demands. Limitations may be remedied by growing rapidly maturing summer cover crops on site. They break the monoculture practices amenable to disease cycles. We hypothesize Sudan grass, wheat, no-cover crop, and +/- rice bran treatments will determine cover crop biomass production within 9 weeks through dry weight measure of

C:N ratios. Cover crops, in combination with rice bran, will reduce pathogen numbers after ASD and will be assessed through culture methods. The soil microbial communities before and after ASD will change. This will be assessed through partial community analysis using T-RFLP and Q-PCR. Diseases such as crown and root rot will occur on all treatments and will be assessed through visual inspection of randomly selected plants and roots after harvest. The economics of treatments will be the same for all cover crops and different for no-cover crop. We will assess this through treatment cost and strawberry marketable yield. ASD and cover crop rotation may provide direct economic solutions to regulatory loss of fumigants, provide effective application of sustainability concepts to industrial agricultural settings, and contribute dialogue on the role of microorganisms in disease suppression.

#### **Room 308AB**

##### **EFFECTS OF CADMIUM AND DIET ON FEEDING, GROWTH, BEHAVIOR, AND MACRONUTRIENT CONTENT IN *LYMNAEA STAGNALIS***

Evelyn Reátegui-Zirena, Christopher Salice, Bridgette Fidler.

*Texas Tech University, Lubbock, TX.*

Cadmium is toxic and ubiquitous in natural environments, but its sublethal effects on aquatic organisms are not well understood. The purpose of this study was to assess a number of sublethal responses related directly to bioenergetics. We evaluated feeding and growth rate and behavior and macronutrient content in the pond snail *Lymnaea stagnalis* exposed to cadmium and fed diets differing in nutritional content. Hatchlings were fed either lettuce or turtle pellets and exposed to 5, 10, and 20 ppb cadmium for 12 days. Length and weight were measured at the beginning and end of the test. The amount of food eaten and behavior (number of snails above waterline and on the food) were determined every 2 days. Total lipids, proteins, and carbohydrates were biochemically measured at test end. Growth coefficients based on length and weight were significantly higher for snails fed pellets ( $p < 0.001$ ). In addition, snails fed pellets and exposed to higher Cd had significantly smaller growth coefficients than those exposed to lower Cd ( $p < 0.05$ ). For feeding rate, there was an interaction between treatments and time for both diets, suggesting that the groups' rates were changing over time in different ways. Total carbohydrates and lipids were higher for snails fed pellets while the protein content was not significantly affected by Cd or diets. This study represents the first time a bioenergetics-based approach has been used to better detect and understand potential ecotoxicity of chemical stressors of freshwater gastropods.

#### **Room 308AB**

##### **INCREASED TEMPERATURES AND EXCESS NUTRIENTS MAY INCREASE GREENHOUSE GAS FLUXES FROM COASTAL SYSTEMS**

Melanie Garate, Serena Moseman-Valtierra.

*University of Rhode Island, Kingston, RI.*

Coastal ecosystems are known to be carbon sinks and thus are important in mitigating climate change. However, with excess inputs of anthropogenic nutrients, coastal systems may become sources of greenhouse gases (GHGs) rather than sinks. Invertebrates in coastal systems are also

potential sources of the GHG nitrous oxide (N<sub>2</sub>O), however, not much is known about their influences on fluxes or their responses to excess nutrients and increased temperatures. To test the hypothesis that excess nutrients and temperatures enhance GHG fluxes from coastal invertebrates, we examined 2 species, *Mytilus edulis* and *Mercenaria mercenaria*, in a 2-factor mesocosm study with 4 treatments: control, background nutrient levels and temperature; nutrient addition; increased temperature only; and nutrient addition and increased temperature. The *M. edulis* mesocosm study showed that N<sub>2</sub>O was significantly higher from treatments with elevated water temperatures ( $F_{3,9} = 3.77$ ,  $p = 0.05$ ) while N<sub>2</sub>O production from the *M. mercenaria* study showed significant response to elevated nutrients ( $F_{3,12} = 9.63$ ,  $p < 0.01$ ). These fluxes are an order of magnitude higher than previous studies. Additional experiments are now testing the reproducibility of these results and the biogeochemical impacts of tube building invertebrates on GHG fluxes. Understanding the roles of these invertebrates in ocean chemistry and their responses to anthropogenic disturbances will improve our ability to manage and mitigate global climate change.

#### **Room 308AB**

##### **FOOD SAFETY IMPACTS OF COMPOST TEAS IN ORGANIC AGRICULTURE**

Valerisa Joe<sup>1</sup>, Jean McLain<sup>2</sup>.

<sup>1</sup>University of Arizona, Tucson, AZ, <sup>2</sup>Water Resources Research Center, University of Arizona, Tucson, AZ.

Increasing organic farming throughout Arizona may provide multiple environmental benefits through reduced water usage and lower reliance on chemical fertilizers and pesticides. Despite such benefits, the use of compost teas as organic additives could have negative food safety impacts. Typically, compost leachate contains only soluble nutrients and few organisms, but the leachate is often anaerobic, which allows for the growth of certain pathogens, and the organic richness may favor growth of *Salmonella* and *E. coli*. Forty, 2-inch diameter pots were planted with spinach (*Spinacia oleracea*) seeds in a growth chamber under conditions of controlled light, temperature, and moisture. All pots received the same amount of soil supplemented with *Salmonella* at a rate of 10<sup>3</sup> organisms per gram of soil, and were treated with 1 of 4 levels of compost tea: none, 0.5 recommended level, 1.0 recommended level, or 2.0 recommended level. Every 7 days, one pot per treatment was sacrificed and soils were assayed for *Salmonella* concentrations using molecular and cultural methods. Soils were also analyzed for total carbon, and nitrogen and spinach seedling roots and shoots were also analyzed for the presence of viable *Salmonella*. We hypothesize that the likelihood of contaminants being retained on foliage will increase when compost tea is used as an added soil supplement. However, very limited information is available on soil conditions that may enhance pathogen proliferation related to the use of compost teas. This work will contribute to the sustainability and public health and safety of organic agriculture in Arizona.



## GENETICS

### Room 402AB

#### IDENTIFYING THE GENETIC MECHANISMS RESPONSIBLE FOR PIGMENTATION PATTERNING IN PIGEONS

Cassandra Garner, Zev Kronenberg, Michael Guernsey, Mark Yandell, Michael Shapiro.  
*University of Utah, Salt Lake City, UT.*

The role of plumage color patterning in mate choice and predator avoidance is well understood in many avian species. However, the genetic mechanisms underlying this evolutionarily important trait have received very little attention. To understand the genetic basis of plumage pattern variation, we are using the domestic rock pigeon *Columba livia*. Pigeons display 4 distinct wing plumage patterns resulting from differences in the amount and location of melanin deposited both within and among feathers. Classical genetic studies suggest that these patterns are generated by different alleles at a single locus; however, the molecular identity of this locus remains unknown. To find the patterning locus, we re-sequenced the genomes of 46 pigeons and identified a 500-kb region of the genome that shows high differentiation (peak  $F_{ST}$  = 0.92) between pigeons exhibiting different patterns. Interestingly, 2 of the 8 genes in this region are involved in metabolism of the melanin precursor, tyrosine. We are currently examining the coding sequence of all genes within this region to identify mutations. To address the possibility that differences in gene expression are responsible for variation in plumage pattern, we are studying the expression of all 8 candidate genes in regenerating feathers. Identification of the genetic mechanisms affecting the pigmentation pattern of wing plumage in pigeons will provide a better understanding of this evolutionarily important trait.

### Room 402AB

#### USING A GENOME-WIDE ASSOCIATION STUDY AND EXOME SEQUENCING DATA TO IDENTIFY THE GENETIC RISK FACTORS FOR FEBRILE SEIZURE FOLLOWING MEASLES VACCINATION

Carlos Rojo, Mark Seielstad.  
*University of California, San Francisco, San Francisco, CA.*

An individual's unique genetic makeup plays an important role in defining susceptibility to a variety of diseases and response to treatment. For example, some children who receive the common measles vaccine (MMRV) present with fever-induced convulsions. This reaction, termed febrile seizure, is known to be more common in children whose families display a history of such seizures, indicating a genetic predisposition. However, a detailed look at the genetic variation that may induce this reaction has yet to be performed. To accomplish this, we completed analysis of a genome-wide association study (GWAS) including 274 California residents, 133 of whom experienced febrile seizure post-MMRV vaccination and 141 matched controls. In total, over 165,026 single nucleotide polymorphic (SNP) sites were tested via the software PLINK for association with febrile seizure. In conjunction with this data, exome sequencing data was also analyzed using the Genome Analysis Toolkit. Furthermore, to demonstrate the genetic heterogeneity of the cohort, we performed multidimensional scaling (MDS) of the GWAS data via PLINK and compared the results to HapMap data from known

populations. Lastly, by combining the results of the MDS with study participants' self-reported ethnicities, we present the difference between study participants' self-reported ethnicity and their ethnicity or ancestry based on genetic markers. Thus, this study accomplishes 2 goals: it provides a detailed genetic analysis of febrile seizure post-MMRV vaccination, which could potentially be used to stratify febrile seizure risk for future patients; and it provides a glimpse into the expanding genetic heterogeneity of the population of California.

#### **Room 402AB**

##### **DIRECTED FUNCTIONAL CHARACTERIZATION OF A NEW MODEL YEAST SPECIES**

Monica Sanchez<sup>1</sup>, Frances Cheong<sup>1</sup>, Blake Hovde<sup>1</sup>, Amy Caudy<sup>2</sup>, Maitreya Dunham<sup>1</sup>.

<sup>1</sup>*University of Washington, Seattle, WA*, <sup>2</sup>*Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, ON, CA*.

Understanding gene function is a fundamental goal of genome biology. Although we have the ability to sequence genomes at a tremendous rate, assigning function to genomic sequence has been a significant bottleneck for gene annotation. Even within well-studied systems, functional annotation has plateaued, suggesting that new methods are required to better interrogate phenotypic information. Comparative, sequence-based studies can predict the function of orthologous genes in newly sequenced organisms through sequence homology. However, direct experimental testing of orthologous genes across closely related species is required to validate the predicted function. We will implement comparative functional analysis by high-throughput experimental testing of gene function in *Saccharomyces bayanus*, a species related to the model organism *Saccharomyces cerevisiae*. We have created an insertional mutagenesis library in *S. bayanus* to measure mutant phenotypes through quantitative fitness assays in a variety of conditions. This dataset has identified candidate essential genes and will be used to infer gene function in *S. bayanus*, providing experimental evidence for determining orthologous gene function comparisons between *S. bayanus* and *S. cerevisiae*. This approach can be modified for use in other organisms to inform gene function predictions. Expanding this analysis to closely related species of model organisms may also uncover phenotypes that will in turn help annotate the genome of model species. Furthermore, gene annotation in model organisms has proven to be useful for characterizing the function of human genes, and continuing to deepen our understanding of diverse model systems will further help de-convolute the complexity of the genotype-to-phenotype relationship.

#### **Room 304BC**

##### **KEEPING IT SIMILAR: INTERACTION OF HSP90 AND AGO1 IN BUFFERING PHENOTYPIC VARIATION IN *ARABIDOPSIS THALIANA***

Tzitziki Lemus Vergara, Jennifer Lachowiec, Christine Queitsch.

*University of Washington, Seattle, WA*.

Robustness to genetic and environmental perturbations is a fundamental property of living organisms. Previous work has demonstrated the importance of the molecular chaperone HSP90 in maintaining organismal robustness. HSP90 inhibition reveals cryptic genetic and epigenetic variation with significant phenotypic consequences in flies, fish, plants, and yeast. The

molecular mechanisms underlying the release of HSP90-dependent variation are not well understood. Recent studies found that microRNAs (miRNAs) are also important in maintaining robustness because of their function in modulating gene expression. In humans and flies, HSP90 is required for the formation of the miRNA-silencing complex. Moreover, in tobacco cell lines, HSP90 interacts physically with ARGONAUTE1 (*AGO1*), a key protein in the plant miRNA pathway and a component of the miRNA-silencing complex. We hypothesize that HSP90 and miRNAs interact in maintaining organismal robustness in the plant *A. thaliana*. Using established assays for HSP90 function, we demonstrate that HSP90 and AGO1 interact genetically in the buffering of phenotypic variation in early seedlings. Moreover, AGO1 polymorphisms correlate with sensitivity to HSP90 inhibition of divergent *A. thaliana* strains. Using expression analysis, we showed that the HSP90-AGO1 interaction in the buffering of variation is complex. In addition, we tested several morphological traits and observed that both HSP90 and AGO1 are epistatic to each other in a trait-specific manner. Currently, we are comparing AGO1's buffering potential and breadth to HSP90 by crossing *ago1* mutants into different *A. thaliana* accessions. We present evidence that the *ago1* mutant reveals different genetic variations than HSP90-deficient plants.

#### **Room 402AB**

#### **BACKGROUND SELECTION IN HUMANS RESULTS IN POPULATION SPECIFIC PATTERNS OF LOSS IN GENETIC DIVERSITY AND BIASES DEMOGRAPHIC INFERENCE**

Raul Torres Jr., Ryan Hernandez.

*University of California, San Francisco, San Francisco, CA.*

Different modes of natural selection in humans have been observed to remove genetic variation across specific regions of the genome that are physically linked to the locus under selection. These processes are known as genetic hitchhiking and background selection (BGS). In addition, population bottlenecks and expansions (i.e., demography) that human populations have experienced has impacted the strength of natural selection and genetic drift across time, thereby influencing patterns of variation genome-wide. However, the joint effects of demography and linked-selection have not been well described in humans. Classic models of BGS treat the local removal of diversity as a decrease in effective population size and we hypothesize that, in conjunction with demography, such effects will lead to different relative rates in the loss of genetic diversity across different continental populations. Measuring genetic diversity across the populations represented in the 1000 Genomes Project, we observe greater relative decreases in variation in regions under strong BGS in non-African vs. Africans (78.4% in CHS vs. 69.2% in YRI). (The 1000 Genomes Project categorizes populations based on the predominant component of ancestry; CHS denotes East Asia and YRI denotes Africa.) These observations are further supported with population genetic forward simulations. We also demonstrate that the fixation index ( $F_{st}$ ) between continental populations increases as a function of BGS strength, which is expected if rates of genetic drift are greater in such regions. Finally, the impact of BGS can lead to skews towards rare variants in the site-frequency spectrum, resulting in biases when performing demographic inference. We show that this can

lead to spurious signals of population expansion and influence the inferred timing of such events.

#### **Room 402AB**

##### **EXPLORING THE DYNAMIC INTERPLAY OF HUMAN MIRNA-TRANSCRIPTION FACTOR REGULATORY CYCLES**

Daniel Chee, John Stamatoyannopoulos.

*University of Washington, Seattle, WA.*

Micro RNAs (miRNAs) are short stretches of RNA that post-transcriptionally regulate gene expression. The “seed” region of miRNAs form Watson-Crick base pairings with the 3’ UTRs of specific mRNAs, leading to mRNA cleavage or, more commonly, translational inhibition. Although much work has been done to elucidate the biogenesis, targeting, and mechanisms for post-transcriptional repression of miRNAs, not much is known about the specific functions these RNAs serve on a cellular level. In this work we combine miRNA target predictions (TargetScan) with DNase I footprinting data to map the regulatory interactions between miRNA and roughly 550 transcription factors across 102 diverse cell types, to gain a better understanding of the regulatory functions of miRNAs. Specifically, we observe a significant number of feedback loops between miRNAs and transcription factors (TFs), occurring most frequently with TFs that form feedback loops with other TFs (including autoregulatory loops) and that have a high degree within each regulatory network. We found hundreds of feedback loops within a given cell type and identified a set of TFs, including SP1 and PLAG1, which are more prone to form these feedback mechanisms. These findings suggest that one function of miRNAs is to act as a cellular buffer, preventing out of control expression of self-regulating TFs (both direct and indirect) as well as TFs with large numbers of downstream targets. Furthermore, we seek to demonstrate that networks derived from DNase I sequencing data paired with computationally derived miRNA target predictions can elucidate the regulatory function of miRNAs.

#### **MARINE SCIENCES**

#### **Room 306AB**

##### **DISTRIBUTION OF POLYPHOSPHATE ACCUMULATING ORGANISMS IN THE COLUMBIA RIVER ESTUARY**

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Polyphosphate accumulating organisms (PAOs) are used in wastewater treatment for biological phosphorus removal. The importance of this process has led to intensive research on their metabolism and functional characteristics, however it is only recently that their role in the environment is becoming better understood. We have detected the presence of an important PAO, *Candidatus Accumulibacter phosphatis* (CAP) in association with particles in estuarine

turbidity maximum (ETM) events in the Columbia River estuary. Using culture-independent methods (PCR, cloning) we have identified DNA sequences that show the presence of CAP associated with variable dissolved oxygen environments where phosphorus is rapidly transformed, as determined from environment data collected from several years of ship-based sampling, *in situ* sensor measurements, and bottle-based growth experiments. These measurements suggest biological conversions of particle-bound phosphorus in the salinity transition zone resulting in release of inorganic phosphorus. We hypothesize that particle-based biogeochemistry within the ETM offers an important niche for PAOs metabolism and subsequent release of phosphorus in the salinity transition zone and therefore plays a significant role in phosphorus cycling in the estuary.

#### **Room 306AB**

##### **VARIATION IN ANTIOXIDANT ENZYME ACTIVITY PROFILES OVER SEASONAL AND REPRODUCTIVE SCALES IN HAWAIIAN CORALS**

James Murphy<sup>1</sup>, Robert Richmond<sup>2</sup>.

<sup>1</sup>University of Hawaii at Manoa, Honolulu, HI, <sup>2</sup>Kewalo Marine Laboratory, University of Hawaii at Manoa, Honolulu, HI.

Scleractinian corals play crucial roles in marine ecosystems by providing essential structure, food, and protection for coral reef habitats. Yet, recent investigations have identified an alarming increase in coral death as the result of stressors, which threatens the general health of tropical coastal environments. Of particular interest to our research are those stressors which either generate damaging reactive oxygen species (ROS) or inhibit detoxifying enzyme function in corals. However, in order to begin to gauge the impact of these stressors on corals, baseline stress levels of these enzymes must first be understood. In this study, 3 common Hawaiian corals, *Pocillopora damicornis*, *Porites compressa*, and *Montipora capitata*, were collected over a reproductive cycle and analyzed to understand fluctuations in activity levels of the antioxidant enzymes catalase (CAT), superoxide dismutase (SOD), and glutathione peroxidase (GSX). Though all corals did not exhibit any external signs of stress, antioxidant enzyme levels were found significantly elevated during reproductive peaks. These findings suggest reproduction as a major source of increased coral stress, which must be taken into consideration when examining the metabolic impacts of stressors on coral health.

#### **Room 306AB**

##### **THE INTERACTION OF CHINOOK SALMON (*ONCORHYNCHUS TSHAWYTSCHA*) WITH THE U, M, AND L GENOGROUPS OF INFECTIOUS HEMATOPOIETIC NECROSIS VIRUS**

Daniel Hernandez<sup>1</sup>, Gael Kurath<sup>2</sup>, Thomas Quinn<sup>1</sup>.

<sup>1</sup>School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, <sup>2</sup>United States Geological Survey, Western Fisheries Research Center, Seattle, WA.

Infectious hematopoietic necrosis virus (IHNV) is an acute viral pathogen that causes significant disease and mortality in wild and cultured salmonids. Genetic sequencing of hundreds of virus isolates has identified 3 genetic subgroups of IHNV designated U (upper), M (middle), and L (lower) for their relative geographic occurrence in western North America. Each genogroup of

IHNV contains many individual isolates, and genogroup-specific patterns of host specificity have been observed. In the Columbia River Basin (CRB), IHNV has been detected regularly in Chinook salmon since 1973 but primarily in the form of asymptomatic infection of adult fish with the U and M group viruses. A lack of disease in juvenile Chinook salmon in the CRB led to the belief that Chinook were refractory to disease caused by both the U and M genetic subgroups of IHNV, thus their potential role in the epidemiology of the virus throughout the CRB had gone unexplored. Our current investigation aims to describe the infection kinetics of the most commonly detected isolates of U and M IHNV in 4 populations of juvenile Chinook representative of the genetic and life history diversity present in the CRB. Using a viral plaque assay and an IHNV glycoprotein gene reverse transcription–quantitative polymerase chain reaction (RT-qPCR) assay, we have confirmed infection and quantified viral load from the tissues of fish experimentally challenged with U and M IHNV. Our approach and methodology have made it possible to begin discerning the role of Chinook salmon in the ecology of IHNV in the CRB.

## **MICROBIOLOGY**

### **Room 405**

#### **HOST-VIRUS INTERACTIONS BETWEEN THE HYPERTHERMOPHILIC CRENARCHAEON *SULFOLOBUS ISLANDICUS* AND *SULFOLOBUS* SPINDLE SHAPED VIRUS 9**

Maria A. Bautista, Changyi Zhang, Rachel J Whitaker.

*University of Illinois at Urbana-Champaign, Urbana, IL.*

Microbes and the viruses that infect them provide a framework to study coevolutionary interactions because evolution can be observed in real time in systems that are experimentally tractable. Our lab has established a model system using the archaeon *Sulfolobus islandicus* that enables us to study coevolutionary interactions in the context of the recently described CRISPR/Cas (clustered regularly interspaced short palindromic repeats) microbial adaptive immune system. Actively changing CRISPR/Cas systems have been observed in *Sulfolobus islandicus* isolates from Yellowstone National Park, United States, and Kamchatka, Russia through sequence-based analyses. However CRISPR immunity against a naturally occurring virus has not been shown experimentally in these isolates. To test for CRISPR immunity we challenged *S. islandicus* M.16.4, isolated from the Kamchatka Peninsula with *Sulfolobus* spindle-shaped virus 9 (SSV9) to which it has a perfectly matching spacer. Deletion mutants of CRISPR loci as well as *cas* (CRISPR associated genes) genes were constructed and challenged with SSV9. Viral infection was determined through plaque assays and quantitative PCR and host growth was monitored. Our results demonstrate that CRISPR immunity is active in *S. islandicus* M.16.4 and that one perfect spacer match is sufficient to confer immunity to SSV9. OD measurements and TEM imaging of SSV9 infected cultures show that, unlike previously characterized SSVs, SSV9 is highly virulent and suggests that although immunity eliminates the virus it does not prevent cells from experiencing the stress generated by SSV9 infection but rather mediates recovery from this “sick” state.

## Room 405

### SMALL MOLECULE MEDIATED DISPERSION OF *STREPTOCOCCUS MUTANS* BIOFILMS BY A NEW MECHANISM

Stephanie Garcia<sup>1</sup>, Meghan Blackledge<sup>2</sup>, Christian Melander<sup>2</sup>, Hui Wu<sup>1</sup>.

<sup>1</sup>University of Alabama at Birmingham, Birmingham, AL, <sup>2</sup>North Carolina State University, Raleigh, NC.

Dental caries is a costly disease characterized by the demineralization of the enamel and otherwise known as tooth decay. The etiologic causative agent of dental caries is *Streptococcus mutans*. *S. mutans* can use sugar to form hardy biofilms on the tooth surface and to rapidly produce lactic acid, which degrades enamel. In this study, we identify a novel small molecule capable of selectively dispersing *S. mutans* biofilms and elucidate its mode(s) of action. In order to develop a therapeutic agent that is species specific for *S. mutans*, we constructed a diverse library of small molecules based on the structural motifs of a natural product with antibiofilm and antibacterial properties. Small molecules were identified with a biofilm dispersion assay and characterized. We identified 3F1 as a novel small molecule that selectively disperses *S. mutans* biofilms. While 3F1 dispersed approximately half of *S. mutans* biofilms, it did not disperse biofilms formed by the commensal species *Streptococcus sanguinis* and *Streptococcus gordonii*. Addition of copper negated the effect of 3F1 and a copper chaperone (CopZ) mutant partially resisted dispersion by 3F1. Our data suggest 3F1 induces the dispersal of *S. mutans* biofilms by interacting with a unique copper-binding protein that plays a role in biofilm stabilization and maturation. Identification of the specific target of 3F1 is ongoing and will help determine the mechanism for 3F1 dispersal. The mechanism of 3F1 could lead to the discovery of a therapeutic target for the prevention or treatment of dental caries while maintaining the commensal populations.

## Room 405

### A ROLE FOR RHOMBOID PROTEASES IN *TRICHOMONAS VAGINALIS* PATHOGENESIS

Angelica Riestra<sup>1</sup>, Shiv Gandhi<sup>2</sup>, Clea Mantini<sup>1</sup>, Sinisa Urban<sup>3</sup>, Patricia Johnson, PhD<sup>1</sup>.

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*Trichomonas vaginalis* is an extracellular parasite that causes trichomoniasis, the most common non-viral, sexually-transmitted infection in the world. Little is known about the pathogenic mechanisms used by *T. vaginalis*. We hypothesize that *T. vaginalis* has intramembrane serine proteases called rhomboids that contribute to the parasite's virulence. We identified 4 putative active rhomboids and exogenously expressed 3 with N-terminal hemagglutinin tags to localize the proteins using indirect immunofluorescence assays. We found that 2 rhomboids localize near but not within the nucleus and 1 rhomboid (ROM1), localized on the cell surface and intracellular vesicle-like structures. Using heterologous cell cleavage assays we have demonstrated that ROM1 has protease activity. Furthermore, using cell viability assays we found that ROM1-overexpressing parasites are significantly more cytolytic to host cells compared to control parasites. Conversely, parasites overexpressing a mutant form of ROM1 in

which the catalytic residues were converted to alanines, display a reduction in cytolysis. To confirm the specificity of the observed phenotypes, we controlled the protein level of the catalytic mutant through its fusion to a destabilization domain (dd). Dd causes the fusion protein to be degraded in the absence of its ligand Shield. When Shield was added to stabilize the mutant protein, the significant decrease in cytolysis compared to vehicle-treated parasites was recapitulated. Lastly, we have used quantitative proteomics to identify substrates cleaved by the *T. vaginalis* rhomboids, and are currently validating their interactions. These studies will help elucidate the biological functions of rhomboid proteases in this widespread human pathogen.

#### Room 405

##### **GENETIC STUDIES OF PYRUVATE METABOLISM IN THE METHANOGENIC ARCHAEON *METHANOSARCINA BARKERI* FUSARO**

Madeline Lopez Munoz, William Metcalf.

*University of Illinois at Urbana-Champaign, Urbana, IL.*

*Methanosarcina* spp. are known to use H<sub>2</sub>/CO<sub>2</sub>, methylamines, methylsulfides, methanol, and acetate as energy sources, but complex organic compounds such as sugars and long chain fatty acids cannot be metabolized by methanogenesis. A *Methanosarcina barkeri* Fusaro strain capable of using pyruvate as a sole energy and carbon source was previously isolated. However, the genetic basis of pyruvate use was not determined. Whole genome sequencing of the mutant strain revealed 2 mutations. One mutation localized to the *Mbar\_A2165* locus, which encodes a potential transcriptional regulator. The second mutation localized to *Mbar\_A1588*, a gene that encodes the biotin protein ligase subunit of the pyruvate carboxylase operon. To assess the connection between these mutations, the pyruvate metabolizing phenotype (Pyr<sup>+</sup>) mutations were recreated in WT background. Transcriptome analysis of the mutant strain revealed an overexpression of genes encoding the enzyme pyruvate ferredoxin oxidoreductase (POR). POR catalyzes reversible reductive carboxylation of acetyl-CoA to pyruvate, making it a key enzyme for replenishing oxaloacetate in the cell. Here we report that a repressor similar to the heat-shock repressor *hrcA* controls *por* transcription. Recreation of the mutation in the regulator encoded by *Mbar\_A2165* results in an increase of *por* expression. In addition, an alternative method for replenishing oxaloacetate in the cells was revealed. Elucidating the genetic basis of pyruvate metabolism in the mutant strain allows a better understanding of substrate metabolism and gene regulation in methanogenic archaea

#### Room 405

##### **VIRUS ESCAPE: UNDERSTANDING THE ROLE OF SMALL MEMBRANE PROTEINS IN ENVELOPED VIRUS ASSEMBLY AND EXIT FROM HOST CELLS**

Jolene Ramsey, Suchetana Mukhopadhyay.

*Indiana University Bloomington, Bloomington, IN.*

To maximize successful assembly and transmission, viruses co-opt resources from their host in many clever ways. Some enveloped viruses exit host cells at the plasma membrane through normal host pathways. Alphaviruses, arthropod-borne enveloped animal viruses, release new



virus particles from a host cell's plasma membrane independent of known host mechanisms in a process called budding. To understand how alphaviruses escape host cells, we are investigating 6K, a small nonessential virus membrane protein which aids in budding. Deleting the 6K gene lowers overall infectious particle production and results in morphological defects. Despite its importance in proper formation of infectious particles, 6K localizes within the infected cell. We hypothesize that 6K functions inside the host cell by interacting with host proteins and lipids to promote the optimal environment for budding infectious particles into the extracellular medium. Direct involvement in budding is being tested using electron microscopy and immuno-gold staining, which can pinpoint 6K's localization relative to budding virus particles in the host cell plasma membrane. Co-immunoprecipitation and mass spectrometry are in use to identify 6K protein partners. Finally, directed mutagenesis is used to abolish post-translational modifications and specific lipid interactions. Preliminary results indicate that 6K's interactions with protein partners and membrane components affect localization and regulate activity. In conclusion, small membrane proteins play an important accessory function in the life cycle of enveloped animal viruses. The work described here seeks to define the mechanism by which the alphavirus 6K protein actively promotes assembly and exit from host cells at the molecular level.

## NEUROSCIENCE

### Room 304BC

#### NEURONAL MECHANISMS OF FOOD SEEKING

Dan Landayan, Fred Wolf, David Feldman.

*University of California, Merced, Merced, CA.*

The role of homeostatic hormones in the control of food intake is well established; however, the understanding of how cortical and subcortical reward systems like the dopaminergic reward pathways integrate with hormonal signals and other brain regions to regulate feeding is incomplete. To better understand the neuronal circuitry underlying the neurobiology of obesity and motivation, it is essential to address the pre-ingestive phase of motivated food seeking behavior when individuals are actively seeking reward. Our preliminary data provides evidence that dopaminergic wiring within the fly brain is necessary and sufficient to promote food-seeking behavior in well-fed flies. Here, we report a novel panel of neuronal elements in *Drosophila* that promote or inhibit pre-ingestive food seeking behaviors. In our behavioral circuit screen, we use sophisticated genetics to reversibly activate and inactivate discrete sets of neuronal ensembles in an unbiased fashion and have categorized the function of individual neurons or patterns that robustly promote or inhibit motivational food seeking behavior. In particular, from this screen, we have identified a novel neuronal pattern that promotes robust food seeking whether these neurons are activated or inactivated. Our future goal is to determine the functional relationship between motivational dopaminergic neurons and newly discovered candidate neurons to uncover new neural circuit pathways that contribute to hallmarks of obesity and eating disorders such as craving, motivation, learning, and impulse control.

## Room 304BC

### EFFECTS OF HISTONE DEACETYLASE INHIBITORS ON DEVELOPING NEURAL CIRCUITS

Eric James, Carolina Ramirez, Mashfiq Hasan, Arseny Khakhalin, Carlos Aizenman.

*Brown University, Providence, RI.*

Prenatal exposure to valproic acid (VPA), a commonly prescribed antiepileptic drug, greatly increases the risk for autism spectrum disorders (ASD). Animal models of VPA-induced neurodevelopmental disorders have provided a useful system in which to address the basic mechanisms underlying autism. Findings in rodent cortex and amphibian tectum revealed common effects of early developmental exposure to VPA such as reduced intrinsic neuronal excitability accompanied by increased spontaneous network activity and overly-connected local circuits. This anatomical hyperconnectivity is consistent with human fMRI and postmortem studies of people diagnosed with ASD. VPA is a very broad-acting drug with several mechanisms of action: GABA-transaminase inhibitor, T-type  $\text{Ca}^{2+}$  channel blocker, voltage-gated  $\text{Na}^{+}$  channel blocker, and histone deacetylase inhibitor (HDACi). Despite its various mechanisms of action, it remains unclear how prenatal exposure to VPA causes ASD. Suberoylanilide hydroxamic acid (SAHA) is a potent HDACi that interacts with many of the same HDACi targets of VPA without affecting ion channels or GABA. We exposed early stage *Xenopus* tadpole embryos to 100  $\mu\text{M}$  of SAHA to test the hypothesis that early exposure to VPA caused its neurodevelopmental effects via its mechanism as an HDACi. Using whole-cell patch clamp recording, we found that prenatal exposure to SAHA recapitulated both increased network activity and hyperconnectivity within the optic tectum; however, in contrast to VPA, it caused increased intrinsic neuronal excitability. These findings suggest that the HDACi mechanism of VPA accounts for part of the changes in neuronal functionality and connectivity associated with VPA-induced ASD.

## OTHER BIOLOGICAL SCIENCES

### Room 406AB

#### MICE DEFICIENT IN SFRP1 EXHIBIT INCREASED ADIPOSITY AND DYSREGULATED GLUCOSE METABOLISM

Lotfi Bassa<sup>1</sup>, Kelly Gauger<sup>2</sup>, Melissa Brown<sup>1</sup>, Elizabeth Henchey<sup>2</sup>, Sallie Schneider<sup>2</sup>.

<sup>1</sup>University of Massachusetts Amherst, Amherst, MA, <sup>2</sup>Pioneer Valley Life Sciences Institute, Baystate Health Medical Center, Springfield, MA.

The molecular mechanisms involved in the development of obesity and related complications remain unclear. Wnt signaling plays an important role in preadipocyte differentiation and adipogenesis. The expression of a Wnt antagonist, secreted frizzled related protein 1 (SFRP1), is increased in response to initial weight gain and then levels are reduced under conditions of extreme obesity in both humans and animals. Here we report that loss of *Sfrp1* exacerbates weight gain and glucose homeostasis in mice in response to diet induced obesity (DIO). *Sfrp1*<sup>-/-</sup> mice fed a high fat diet (HFD) exhibited an increase in body mass accompanied by increases in body fat percentage, visceral white adipose tissue (WAT) mass, and adipocyte size. Fasting glucose levels are elevated, glucose clearance is impaired, hepatic gluconeogenesis regulators are aberrantly upregulated, and glucose transporters are repressed in *Sfrp1*<sup>-/-</sup> mice fed an HFD.

Additionally, we observed increased steatosis in the livers of *Sfrp1*<sup>-/-</sup> mice. Our findings demonstrate that the expression of *Sfrp1* is a critical factor required for maintaining appropriate cellular signaling in response to the onset of obesity.

**Room 406AB**

**TGF- $\beta$  AND ITS SIGNALING PROTEIN SMAD3 DRIVE THE DE-DIFFERENTIATION OF SMOOTH MUSCLE CELLS**

Sarah Franco, Xudong Shi, Lian-Wang Guo, Daniel Drenzo, Toshio Takayama, Bowen Wang, Bo Liu, Craig Kent.

*University of Wisconsin-Madison, Madison, WI.*

Intimal hyperplasia (IH) is a complex process involving the phenotypic switch of vascular smooth muscle cells (SMC) from a differentiated state to a dedifferentiated state, and is the main contributor to restenosis, which is the re-narrowing of a blood vessel after vascular reconstructive procedures. Previously, we showed that TGF- $\beta$  and its signaling protein, Smad3, stimulate SMC proliferation and migration, resulting in enhanced development of IH. We hypothesize that activation of the TGF- $\beta$ /Smad3 signaling pathway drives SMC dedifferentiation by regulating the expression of multiple genes responsible for the SMC altered state. To determine the genes regulated by TGF- $\beta$ /Smad3, we performed Affymetrix gene expression arrays on rat aortic SMCs that were infected with adenovirus expressing either Smad3 or GFP (control), followed by treatment with TGF- $\beta$  for 24 h. Our results revealed that the expression of 200+ genes was significantly altered by TGF- $\beta$ /Smad3. On further analysis, we found that many of the genes upregulated were related to development. Quantitative RT-PCR confirmed upregulation of several developmental genes including *SOX18*, which is a gene involved in the regulation of embryonic development and determination of cell fate. To further analyze *SOX18*, we performed *in vivo* balloon angioplasty in rat carotid arteries, where TGF- $\beta$  and Smad3 levels were known to be elevated by injury, and sectioned arteries for immunohistochemistry. Results showed *SOX18* was substantially upregulated 7 d and 14 d post injury. Our data suggest that injury-induced upregulation of TGF- $\beta$ /Smad3 stimulates *SOX18* expression, which may contribute to SMC dedifferentiation and the development of IH providing new insights into TGF- $\beta$ /Smad3-mediated IH.

**PHARMACOLOGY**

**Room 406AB**

**ALLOSTERIC MODULATION OF THE HUMAN GABA-A RHO1 RECEPTOR BY ASIC NONPROTON LIGANDS**

Heather Snell, Eric B Gonzales.

*UNT Health Science Center, Fort Worth, TX.*

Gamma-amino butyric acid (GABA) is the major inhibitory neurotransmitter in the vertebrate brain and targets the ionotropic GABA-A receptors. The GABA-A rho receptor, a subclass of GABA-A receptors composed entirely of rho subunits, is mainly located on retinal bipolar cells. One difference between traditional GABA-A receptors and the GABA-A rho receptors is the

ability of the latter to form functional homomeric channels. Furthermore, the GABA-A rho1 receptor has a different pharmacological profile than the other GABA-A receptors such as insensitivity to bicuculine, benzodiazepines, and barbiturates. Guanidine compounds have also been shown to exhibit different modulatory effects on the heteromeric GABA-A and homomeric GABA-A rho1 receptors. These acid sensing ion channel (ASIC) compounds have the potential to alter the function of other membrane proteins. This compound family includes both the synthetic 2-guanidine-4-methoxyquinazoline (GMQ) and the diuretic amiloride, both of which have demonstrated activity on the heteromeric GABA-A receptors but have not been studied in the homomeric GABA-A rho1 receptors. In this study, we sought to elucidate the intrinsic activity of these compounds on the human GABA-A rho1 receptor. We showed that amiloride enhances GABA-mediated activity on the GABA-A rho1 receptors, similarly to other allosteric modulators. In contrast, GMQ antagonizes the GABA-A rho1 receptor in a noncompetitive manner similar to picrotoxin. Both compounds were reported to display competitive antagonism in heteromeric GABA-A receptors. Thus, our findings suggest that there are functional as well as therapeutic implications for the use of these guanidino compounds in targeting the GABA-A rho1 receptor-mediated activity.

#### **Room 406AB**

#### **EFFECTS OF ANTIOXIDANT SUPPLEMENTATION AND MODERATE EXERCISE ON MOTOR FUNCTION IN YOUNG AND OLD MICE**

Akram Sidhu, Philip Vann, Jessica Wong, Nathalie Sumien.

*UNT Health Science Center, Fort Worth, TX.*

Interventions such as exercise and antioxidant supplementation, when investigated independently, seem to improve motor function in both human and animal subjects. This study investigated the nature of the interaction between exercise and antioxidant supplementation on the motor performance in mice. Young (4 months) and old (20 months) male C57BL/6J mice were placed under the following treatments: sedentary/control diet (SedCon); sedentary/antioxidant-rich diet (vitamin E (128 IU/kg/d of bw) and vitamin C (189 mg/kg/d of bw) (SedEC); exercise/control diet (ExCon); and exercise/antioxidant-rich diet (ExEC). After 8 weeks of pre-treatment, the mice underwent a series of behavioral tests involving mazes, rotating rods, and bridges. Our preliminary data suggested that time spent in the closed arms of the maze increased in all treated mice compared to controls, and that increase seemed more evident in the young mice. The latency to fall from the rotating rod seemed to be increased in the ExEC young and old mice when compared to all other groups. The ExCon group had a higher latency to fall while the other treatment groups seemed to have lower latencies when compared to SedCon within the young group. In the old group, only the ExEC group had higher latencies than the SedCon group, while the others did not seem to differ. Latencies to fall from the bridge were increased in young groups where mice exercised (ExCon and ExEC), while they were decreased in SedEC and ExCon old mice compared to controls. Our preliminary data indicated that there seem to be some type of interaction between antioxidant supplementation and exercise that may increase their beneficial outcomes.

**Room 406AB****WHAT HAPPENS FIRST - HOW CALCIUM AND GUANIDINO COMPOUNDS INFLUENCE THE ACID-SENSING ION CHANNEL**

Rachel Smith<sup>1</sup>, Eric B Gonzales<sup>2</sup>.

<sup>1</sup>UNT Health Science Center, Fort Worth, TX, <sup>2</sup>Institute for Aging and Alzheimer's Disease Research, UNT Health Science Center, Fort Worth, TX.

Acid-sensing ion channels (ASICs) are sodium-selective ion channels activated by extracellular protons. Various studies indicate that ASICs are important components of physiological processes like action potential propagation as well as pathophysiological conditions like pain and ischemic stroke. Multiple subtypes exist that are widely distributed throughout human physiology, and these subtypes respond differently to concentrations of protons in the extracellular space. Crystal structures of the chicken ASIC1 (cASIC1) subtype showed that ASICs are trimeric channels composed of intracellular amino- and carboxyl-termini with 2 transmembrane domains per subunit. Additionally, the crystal structures revealed that combining 3 subunits creates a large extracellular domain, which is likely organized for interaction with ligands more complex than protons. Previously, we used whole-cell and outside-out patch clamp electrophysiology to show that the spider toxin psalmotoxin-1 (PcTx1) interacts with homomeric cASIC1, allowing other ligands containing a guanidino group like 2-guanidine-4-methylquinazoline (GMQ) and amiloride to further enhance sodium-mediated currents. We proposed that PcTx1 locks cASIC1 into a partially activated, intermediate channel state that exposes the central vestibule, also known as the nonproton ligand stimulatory site, for enhanced channel activation. Channel activation via a molecular wedge mechanism within the central vestibule likely applies to other ASIC subtypes as long as the channel is in a partially activated state. In the case of the peripheral ASIC subtype ASIC3, calcium removal may reveal this intermediate state. Using full-length ASIC1, ASIC3, and a chimera of the 2 previously described by Salinas and colleagues, we will study the interaction of GMQ, amiloride, and calcium using patch clamp electrophysiology.

**COMPUTER/INFORMATION SCIENCES****Room 506****COMPREHENSIVE CONFLICT RESOLUTION IN SECURE AUTHORIZATION IN HEALTH ORGANIZATIONS**

Hiva Samadian, Amirhossein Chinaei.

*University of Puerto Rico, Mayagüez Campus, Mayagüez, PR.*

Organizational assets and resources are administered to be accessed by some members and not to be accessed by others. The high sensitivity of assets (e.g., patients' health records and sensitive medical devices) in some organizations like health organizations causes the managers to pay special attention to deploying reliable authorization models. A reliable authorization model must be able to resolve the conflicts of different authorization policies. However, resolving authorization conflicts is quite a challenge in such models because of the existence of sophisticated inheritance hierarchies that might cause an exponential number of conflicts (in

terms of the number of subjects in the organizational hierarchy) and the diversity of ways to combine resolution policies. The need to have an approach that can handle as many resolution policies as possible and work in an appropriate time arises here. In this paper, a dynamic programming algorithm for resolving conflicts with all existing policies has been implemented and tested in the context of a health organization. The result of these experiments shows the algorithm works in a reasonable time in practical instances.

#### **Room 506**

##### **A RECOMMENDER SYSTEM FOR SCIENTIFIC LITERATURE**

Diego Aguirre, Olac Fuentes.

*The University of Texas at El Paso, El Paso, TX.*

A key challenge scientists face is finding and evaluating the utility of multiple pieces of information such as research papers. Identifying articles that not only relate to the researcher's field of study but also meet some other criteria, such as adequate quality and relevance, is a time-consuming and laborious task. Recommender systems have become suitable tools to tackle similar problems where large collections of data need to be filtered to identify the resources that are the most relevant for a given user. We present several extensions to traditional recommender system techniques to address the unique challenges posed by scientific literature. First, we propose to extend traditional feature extraction mechanisms for text entities by incorporating features that are representative of the quality of the text objects. Second, we introduce an extension to the notion of trust defined by O'Donovan and Smyth. We argue that incorporating the explicit references included in research papers and the citation indexes of the authors in the definition of trust and trust propagation can improve the quality of the recommendations. Finally, we present visualization mechanisms and evaluation techniques tailored to measure the performance of the system with respect to the unique demands of the problem.

#### **EDUCATION**

##### **OTHER EDUCATION**

#### **Room 409AB**

##### **ASSESSING THE IMPACT OF ELDERS ON STUDENT INTEREST IN STEM AT TRIBAL COLLEGES AND UNIVERSITIES (TCUS) AND MAINSTREAM UNIVERSITIES (MSUS)**

Sarah Alkholy<sup>1</sup>, Tanya Dahms<sup>2</sup>, Fidji Gendron<sup>3</sup>, Maria Pontes Ferreira<sup>1</sup>.

<sup>1</sup>Wayne State University, Detroit, MI, <sup>2</sup>University of Regina, Regina, SK, CA, <sup>3</sup>First Nations University of Canada, Regina, SK, CA.

Minorities are underrepresented in the STEM workforce and show high academic attrition rates in postsecondary STEM education. Academic performance improves when culturally relevant support is provided. We hypothesize that the presence of Elder educators in a STEM course will increase student interest in STEM. We plan to assess the cultural relevance and supportiveness of the STEM course, student learning outcomes, student interest in STEM, and the importance

of Elders in postsecondary STEM education. A pilot study was conducted in the spring of 2013 on an online STEM course (2 TCUS and 2 MSUs). Students took pre- and post-course surveys, and outcome measures of interest were assessed. The pedagogical quasi experiment will be conducted in the spring of 2014 with and without Elders. Group differences will be tested by ANOVA. Preliminary findings indicate that Canadian and non-White students believe that Elders are appropriate post-secondary STEM educators more than do U.S. students ( $p = .31$ ) and White ( $p = .45$ ) students. U.S. and White students indicate more interest in STEM fields than Canadian ( $p = .52$ ) and non-Whites ( $p = 0.80$ ). U.S. and non-White students show a trend to self-identify as scientists more than Canadian ( $p = .77$ ) and White ( $p = 0.31$ ) students. Although we lack significant pilot results, the intriguing trends lead us to re-conduct the experiment with a larger sample size (spring 2014). We will assess the impact of Elders as STEM educators in an online STEM course at TCUS and MSUs in the U.S. and Canada. Anticipated findings may improve teaching in STEM courses, especially for Native/Aboriginal students, by providing innovative ways to increase minority students' retention.

#### **Room 409AB**

#### **COMMUNITY-BASED ENGINEERING DESIGN PROBLEMS: ANALYZING LATINO STUDENTS' LINGUISTIC, CULTURAL, AND SOCIAL RESOURCES**

Joel Mejia, Amy Wilson.

*Utah State University, Logan, UT.*

This exploratory study is based on the assumption that creating a bridge between different formal resources (engineering design processes) and informal resources (funds of knowledge) is an important step toward encouraging Latino high school students to enter and remain in the field of engineering. Three Latino high school students were followed as they worked on a community-based engineering design problem. The students were recruited from a high school located in a semi-urban area and purposefully selected. All students received ESL services and spoke Spanish at home. The students selected a problem in their community and were asked to provide solutions to the problem using the engineering design process. This study takes an ethnographic approach to qualitative research in order to investigate the funds of knowledge of these students. In particular, this study seeks to analyze the funds of knowledge of Latino high school students through participant observation, student artifacts, group discussion, concurrent and retrospective protocols, and one-on-one interviews. The transcripts obtained from the audio and video files were analyzed using a modified version of constant comparative analysis and a list of a priori codes. The framework obtained from this study is intended to help provide a culturally responsive engineering education and enhance the educational experience of underrepresented minorities whose social and cultural practices have been traditionally undervalued in schools.

## TEACHER EDUCATION

### Room 409AB

#### **EMBODYING MÁSCARAS: A FRAMEWORK FOR MATHEMATICAL IDENTITIES**

Gabriela Vargas, Rochelle Gutierrez.

*University of Illinois at Urbana-Champaign, Champaign, IL.*

Current understandings of pre-service mathematics teachers' (PSMTs) identities revolve around their past experiences with mathematics as well as the influence of current teachers. These identity frameworks allow us to understand how PSMTs develop their mathematical identities, but we know very little about how they are enacted and performed in the classroom. By looking into decolonial theories, we see that identities are not only negotiated narratives but also a form of embodiment and performance. When we view identities as máscaras, we see how they are transformed and influenced by the narratives that one creates from within and those that are created by exterior elements. Máscaras that do not represent a person (internally or externally) can be mistaken as fake performances and embodiment of their identity. The goal of this theoretical presentation is to show how PSMTs develop máscaras that are influenced by their past math experiences, exposure to professional development, and by "trying on" what their cooperating teachers wear, highlighting the dynamic nature of identities. The manipulation of máscaras will allow us to bring into focus exterior elements that can affect how we embody identities in the classroom. Furthermore, we can understand how máscaras of PSMT's are seen by their students and the impact they can have on their learning of mathematics.

### Room 409AB

#### **PROSPECTIVE ELEMENTARY TEACHERS' CONCEPT MAP REPRESENTATIONS OF ASSESSING CHILDREN'S UNDERSTANDING OF FRACTIONS**

Lynette Guzman, Sandra Crespo.

*Michigan State University, East Lansing, MI.*

Teacher preparation programs play a role in supporting prospective teachers to develop professional skills that are specific to and required for teaching. Mathematics education researchers emphasize the importance of eliciting and building on children's mathematical thinking in mathematics instruction. Aguirre and colleagues define children's multiple mathematical knowledge bases (i.e., children's mathematical thinking and children's community, linguistic, and cultural funds of knowledge) as another important resource for mathematics teaching. This study investigates how prospective elementary teachers make connections among children's multiple mathematical knowledge bases in their thinking about assessing children's understanding of fractions. Participants included 20 prospective elementary teachers enrolled in a mathematics methods course at a large, public university in the United States. The researcher facilitated concept mapping tasks to examine the ways prospective teachers link concepts related to children's multiple mathematical knowledge bases and how these concepts and links change from beginning (pre-map) to end (post-map) of the elementary mathematics methods course. Concept map research analysis techniques were



used to examine 6 structural variables in the maps, and qualitative analysis was used for coding and identifying emergent themes across the connections and concepts in the maps. Pre-map analysis suggests that prospective teachers made few explicit connections to children's multiple mathematical knowledge bases in their concept maps; however, their knowledge of these ideas was evident through whole-class and small-group discussions. This presentation will focus on how prospective teachers incorporate knowledge of children's multiple mathematical knowledge bases in their post-maps and further implications for designing learning opportunities for prospective mathematics teachers.

**Room 409AB**

**NOT JUST FOR STUDENTS: AN AFTER-SCHOOL MATHEMATICS CLUB FOR PRE-SERVICE SECONDARY MATHEMATICS TEACHERS**

Juan Gerardo, Rochelle Gutierrez, Gabriela Vargas.

*University of Illinois at Urbana-Champaign, Champaign, IL.*

Community-based field experiences are opportunities for pre-service teachers to work with marginalized students. Further research is necessary to understand how volunteering at an after-school mathematics club contributes to the development of pre-service secondary mathematics teachers (PSMTs). Volunteering at an after-school mathematics club allows for PSMTs to practice mathematics teaching with marginalized students and may inform their stance for teaching secondary mathematics equitably (e.g., conception of students, pedagogy, and mathematics). Our theoretical framework is political *conocimiento*: mathematics teaching is a political act; seeking solidarity with marginalized students is necessary; lastly, it is important to leverage cultural, linguistic, and community knowledge of marginalized students. This is a qualitative study. Various data sources (e.g., interviews, field notes, etc.) will be analyzed for the kinds of practices that PSMTs enacted during the after-school club. Additional data may include examples from their classroom teaching. The coding will involve the degree to which these seem to align with political *conocimiento* framework and similarities and differences between their volunteering and mathematics teaching. PSMTs seem to have similar goals as volunteers (e.g., negotiating relationships, positioning them as experts, and doing and discussing mathematics with students). In the classroom settings, some practices seem to be similar but not to the same degree. Various constraints were salient (e.g., standards and standardized exams). Further research is necessary to better understand the affordances and efficacy of after-school mathematics club volunteering for PSMTs to develop political *conocimiento* and to the degree that it may influence teaching mathematics to marginalized students.

## TEACHING FIELDS

### Room 507

#### **CALCULUS STUDY PRACTICES OF LATINA/O STEM MAJORS AT A CALIFORNIA COMMUNITY COLLEGE**

Angelica Cortes, Tobin White.

*University of California, Davis, Davis, CA.*

Calculus is a gatekeeper course for many college students who aspire to attain a baccalaureate degree in one of the STEM fields. For community college STEM majors, not passing calculus during the first attempt delays their time to transfer and, in some cases, not passing the course in subsequent attempts deters them from their aspired major. Previous research has shown that studying in groups has increased minority student success in calculus at the university level. However, less is known about community college STEM students, especially about Latina/o students. Thus, throughout the course of one academic year, I have focused on the study practices of Latina/o STEM majors at one California community college using qualitative methods and a community cultural wealth framework. Preliminary findings from this dissertation research show that students studied alone, in groups, or a combination of both and utilized various forms of technology while they studied. All students who participated in groups and met at least twice per week were able to pass their first semester calculus course on their first try. Unlike previous findings in which study groups were comprised of students from the same ethnicity, Latina/o students included classmates from other ethnic groups during their study sessions and used centers such as the MESA Study Center on campus. However, the length of study sessions were greatly limited due to decreased funding. This suggests that calculus instructors need to facilitate student groupwork, and programs that provide support for STEM group study need increased funding.

## ENGINEERING

### BIOENGINEERING/BIOMEDICAL ENGINEERING

### Room 501A

#### **IMAGING TOF-SIMS TO IDENTIFY METABOLIC VARIATION IN HUMAN BREAST TUMOR TISSUES**

Blake Bluestein<sup>1</sup>, Fionnuala Morrish<sup>2</sup>, David Hockenbery<sup>2</sup>, Lara Gamble<sup>1</sup>.

<sup>1</sup>*University of Washington, Seattle, WA*, <sup>2</sup>*Fred Hutchinson Cancer Research Center, Seattle, WA*.

Tumor metabolism is crucial in cancer onset and progression, and its causes and effects are under intense scrutiny. Typical treatment for locally advanced breast cancer patients employs pre-surgical or neoadjuvant therapy. Since systemic treatment occurs with the tumor in place followed by definitive surgery, this treatment approach provides findings to treatment response, disease relapse, and patient survival. The focus of this project is defining the molecular and cellular mechanisms underlying this finding and informing better strategies for treating these patients. Critical to achieve this project's objective is the use of novel tumor analysis to elucidate pathways associated with tumor metabolic flexibility and chemoresistance.

An important component of this project is analysis of pre and post neoadjuvant frozen patient tissue specimens using time-of-flight secondary ion mass spectrometry (ToF-SIMS). ToF-SIMS provides mass spectral information with imaging capabilities within tissue samples. Using ToF-SIMS and principal component analysis (PCA), we study human tumor biopsy samples to understand the link between metabolism and potential drug resistance within tumors. Data have been acquired on an IONTof ToF-SIMS V using  $\text{Bi}_3^+$  in both high mass and high spatial resolution modes. Utilizing regions of interest (ROI) to select highly cellularized tumor regions within analysis areas resulted in a near distinctive chemical separation between pre and post tissues in the negative polarity. Chemical differences are observed between untreated and treated tissues relating to changes in fatty acids, monoacylglycerols, diacylglycerols, and cholesterol. These results aid in isolating tumor regions for further metabolic investigation to improve treatment efficacy.

#### **Room 501A**

#### **EGF AS A NEW THERAPEUTIC TARGET FOR MEDULLOBLASTOMA METASTASIS**

Jennifer Rico, Maribel Vazquez.

*The City College of New York, New York, NY.*

Medulloblastoma (MB) is one of the most solid pediatric brain tumors diagnosed among children in the United States. While surgery, radiation, and chemotherapy have significantly increased survival rates, these lead to devastating side effects. MB tumors are known to metastasize to the spinal column, and their migration is believed to be derived from cancer stem cells which are stimulated by different extracellular microenvironments. In order to identify new migration-targeted therapies for MB, we examined MB-derived cells toward controlled microenvironments of growth factors previously believed insignificant for MB migration: epidermal growth factor (EGF), hepatocyte growth factor (HGF), platelet-derived growth factor (PDGF), and the chemokine (C-X-C motif) ligand 12 (CXCL12). We determined migration using Boyden chamber experiments by exposing MB cells to different nano-concentrations of EGF, HGF, PDGF-BB, and CXCL12. We next measured the relative receptor expression via immunostaining assay for EGF-R, c-Met, PDGFR-BB, and CXCR4. Lastly, we implemented the use of microchannels to understand the roles of concentration gradients on the migration of MB cells via EGF and CXCL12. Our results showed that a large number of MB cells migrated towards 100 ng/mL of EGF, and EGF-R displayed the highest receptor expression as compared to the other molecules. MB cells migrated further distances within 100 ng/mL of EGF compared to CXCL12. MB cells responded strongly to EGF in a dosage and gradient-dependent manner to suggest that EGF-R plays a more important role in chemotaxis than previously believed. Thus, EGF should be implemented as a new migration-targeted therapy for MB metastasis.

## **Room 501A**

### **LUNG CANCER: NEW INFORMATION FROM OLD DATA**

Katia Camacho-Caceres<sup>1</sup>, Mauricio Cabrera Rios<sup>1</sup>, Clara Isaza<sup>2</sup>, Juan Irizarry-Nieves<sup>1</sup>, Juan Acevedo Diaz<sup>1</sup>, Valerie Gonzalez<sup>1</sup>.

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In bioinformatics, it is possible to generate experimental data at a high pace. For example, microarrays can provide large amounts of data for genetic relative expression in illnesses of interest such as cancer. These data are stored and often abandoned when new experimental technologies arrive. This work reexamines lung cancer microarray data with a multiple criteria optimization-based strategy developed in our research group. This strategy does not require any adjustment of parameters by the user and is capable of converging consistently to important genes, potential biomarkers, even in the presence of multiple and incommensurate units across microarrays. Groups with distinct smoking habits (nonsmoker or current smoker) and gender are contrasted to elicit a set of highly differentially expressed genes, several of which are already associated with lung cancer and other types of cancer. The list of genes is provided with a discussion of their role in cancer as well as the possible research directions for each of them. It is also recognized that, at this point, experimental validation is necessary to confirm the role of genes for which not enough evidence is found in the literature. Fundamentally, these genes with little information represent the best opportunities for biological discovery from existing data.

## **Room 501**

### **IDENTIFYING THE SOURCE OF SKELETAL PROGENITOR CELLS IN FRACTURE HEALING**

Jenny Lei, Elise Morgan.

*Boston University, Boston, MA.*

The regenerative process of bone fracture healing provides an opportunity to study the sources of skeletal progenitor cells and the processes by which these cells differentiate into osteoblasts (bone-forming cells) or chondrocytes (cartilage-forming cells). The lessons learned can inform a multitude of approaches to encourage tissue healing and regeneration. This study aims to investigate fracture healing in mice in which cells expressing *Prx1* (a gene associated with skeletal progenitor cells) are tagged with expression of beta galactosidase, an enzyme whose presence can be detected with a simple staining method. A transverse femoral fracture is generated by an externally applied blunt trauma and is stabilized by an intramedullary pin. The bolus of tissue that is formed at the fracture site, known as the *callus*, is initially loose connective tissue populated with progenitor cells. Over time, these cells differentiate into osteoblasts and, to a lesser extent, chondrocytes, resulting in large amounts of bone formation and, ultimately, a healed bone. Calluses will be harvested at post-operative days 7, 14, and 21. Histological analyses will be performed to visualize the tagged cells and to examine the spatial distribution of tissues. Micro-computed tomography will be used to visualize the 3D structure of the callus. Our hypothesis is that the skeletal progenitor cells originate in the periosteum, the membrane covering the outer surface of the bone. This study will identify the contribution of

skeletal progenitor cells to healing and will set the stage for subsequent studies on how mechanical loading influences fracture healing.

#### **Room 501A**

##### **METHODOLOGY FOR REDESIGNING THE SPECIFICITY OF SECRETED PROTEASES**

Jennifer Guerrero, Michelle O'Malley, Patrick Daugherty.

*University of California, Santa Barbara, Santa Barbara, CA.*

Proteases constitute 2% of the human genome and regulate many biological processes including cell growth and migration, blood coagulation, and programmed cell death. A generally applicable, high-throughput strategy to engineer proteases to cleave a target substrate with high specificity and high catalytic efficiency would greatly expand the use of proteases for therapeutic applications. We have developed a cell-based assay for redesigning protease selectivity by screening protease mutant libraries for cleavage of a fluorogenic peptide substrate exhibiting Förster resonance energy transfer (FRET). As a model system, these novel methods were applied to the protease human kallikrein 7 (hK7) to identify variants that selectively cleave the central hydrophobic core of the amyloid beta (A $\beta$ ) peptide, involved in Alzheimer's disease pathology. Using *Saccharomyces cerevisiae*, an expression system was constructed to produce active hK7 and a FRET substrate probe intracellularly. Expression of correctly folded, active hK7 was detected in the yeast cell lysate using an hK7 FRET reporter substrate and confirmed by western blot. We optimized expression conditions to detect hK7 activity in yeast with a co-expressed A $\beta$ 8 (KLVF↓F↓AED) FRET substrate using flow cytometry. No activity was detected for yeast cells co-expressing an inactive hK7 mutant or the FRET substrate alone. We randomly mutated the *hK7* gene using error-prone PCR to generate a library with an average of 2 base substitutions per gene. Screening this library for cleavage of the A $\beta$ 8 FRET reporter using fluorescence activated cell sorting (FACS) yielded *hK7* mutants with improved expression and activity against the therapeutically relevant A $\beta$ 8 substrate.

#### **CHEMICAL ENGINEERING**

#### **Room 501BC**

##### **COLLOIDAL METHODS FOR THE SYNTHESIS OF AU-CONTAINING BIMETALLIC NANOPARTICLES FOR CO OXIDATION**

Alexandra Landry, Enrique Iglesia.

*University of California, Berkeley, Berkeley, CA.*

Au-alloyed bimetallic nanoparticles can lead to catalysts with improved turnover rates and selectivity, but many synthetic protocols, such as impregnation or precipitation, typically form particles non-uniform in size and composition. Colloidal methods, which can potentially avoid such non-uniformity, often require reagents that poison the catalyst surface. To address this issue, we describe a colloidal synthesis method that forms uniform bimetallic AuPt, AuRh, and AuPd nanoparticles (3 - 4 nm diameter) with a narrow size distribution that are made using materials that contain only C, H, O, and N. We show that such materials can be removed from particle surfaces by post-synthetic H<sub>2</sub> treatment at low temperatures without detectable

sintering. The mechanism for bimetallic formation was examined by *in-situ*, UV-visible spectroscopy using Au-derived plasmon bands and by transmission electron microscopy, and involves a galvanic displacement-reduction mechanism that is governed by the relative reduction potentials of the 2 metals of interest. Reconstruction of the synthesized nanoparticles is shown to occur under CO treatment at low temperatures, indicating that the structure obtained post-synthesis changes based on its environment. Developing rigorous conclusions about the size and composition effects of bimetallic clusters on reactivity is key for designing valued catalysts for environmentally relevant reactions such as CO oxidation in automobile catalytic converters. Mechanistic knowledge of how to produce uniform clusters, such as those made in this study, is crucial to make such conclusions.

#### **Room 501BC**

##### **DFT ANALYSIS ON STRUCTURE-PROPERTY RELATIONSHIPS OF METAL-SUBSTITUTED ZEOLITES**

Brian Montejo, Maria Curet.

*University of Puerto Rico, Mayaguez Campus, Mayaguez, PR.*

Metal-substituted zeolites, have been proven to be effective catalysts for various important reactions involving molecules derived from biomass. These catalysts are unique because they exhibit excellent selectivities at mild conditions. This study aims at obtaining a fundamental understanding of the relationship between structure and catalytic properties of metal-substituted zeolites. We use density functional theory calculations to analyze the substitution of different zeolite-beta metals, such as Sn-BEA and Ge-BEC. The catalytic surfaces were simulated using clusters of 53 to 80 atoms with the software Gaussian09. We have performed systematic calculations with B3LYP, B3PW91, and  $\omega$ B97XD exchange-correlation functionals and compared calculated properties, such as Raman spectra with experimental results available in the literature. The basis sets used were 6-31+g\* for O, Si, and H atoms and LANL2DZ for Sn and Ge atoms. We have characterized the systems with the LUMO energies, the hardness, and the NBO (natural bond orbital) charges. We have also studied the interaction of Sn-BEA, Ge-BEC, and the unsubstituted BEC with water in order to determine their hydrothermal stability. Our preliminary results demonstrate that the LUMO of the double substituted Sn-BEA is located on both Sn atoms, suggesting that the pairing of Sn atoms might be responsible for the excellent catalytic activity; the LUMO energy as well as the hardness obtained for these systems indicate that Sn-BEA is more acidic than Ge-BEC; and all the functionals used in this study accurately described the geometries, but B3LYP and B3PW91 failed to describe the LUMO energies.

#### **Room 501BC**

##### **TEMPLATE-FREE SYNTHESIS OF CONDUCTING POLYMER MICROSTRUCTURES FOR SUPERCAPACITOR ELECTRODES**

Kryssia Diaz Orellana, Mark E. Roberts.

*Clemson University, Clemson, SC.*

New energy storage technologies face many challenges, such as efficiency, charge storage capacity, and long-term cycle stability. Devices like supercapacitors have the potential to provide high energy storage capacity and fast charge-discharge rates to bridge the gap between

batteries and capacitors. Electroactive conductive polymers (ECPs) are promising materials for supercapacitor electrodes since they are conductive, possess moderate to high energy storage capacity, and can be synthesized using low cost and large scale methods. In this work, we investigate a simple approach to growing large quantities of ECP microtubes without the need for a solution or substrate based template. Due to its relatively high specific power and energy, polypyrrole is used to synthesize electrodes comprising microtube structures. Polypyrrole was electrochemically polymerized on stainless steel mesh substrates with varying wire diameters and spacing. The structure and electrochemical properties of microtube electrodes were studied to understand the growth mechanism and microtube formation and how the electrode structure affects the charge storage properties. Electrodes prepared on small mesh sizes (i.e., 200 x 200) exhibited a high density of microtubes with excellent electrochemical properties. We also demonstrated that this synthesis approach can be scaled up to large area substrates without any loss in electrode performance. Our results clearly demonstrate the effects of the substrate and current density on the template-free assembly and electrochemical performance of polypyrrole, as well as new ways to manipulate the physical structure of redox materials for supercapacitor electrodes. Importantly, this approach is amenable for large-scale synthesis of micro and nanostructured electrode systems.

## **ELECTRICAL/ELECTRONICS/COMMUNICATIONS ENGINEERING**

### **Room 408B**

#### **TAKING ADVANTAGE OF MULTIUSER DIVERSITY AND BEAMFORMING IN WIRELESS CELLULAR NETWORKS**

Jose Armando Oviedo, Hamid Sadjadpour.

*University of California, Santa Cruz, Santa Cruz, CA.*

Multiuser diversity is a wireless scheduling concept in which the data-rate capacity of a selected mobile device increases as the number of total mobile devices increases, even when very limited channel state information (CSI) is known. Beamforming is an approach for transmitting a signal using multiple antennas in order to maximize the signal-to-noise ratio (SNR) at the intended receiver. These 2 approaches both show great promise in improving capacity when mobile applications demand greater amounts of information while signal resources (power, bandwidth) are constrained. Current systems transmit a mobile device's data on a time-sharing, pre-scheduled basis in order to guarantee all users have the opportunity to receive information. We demonstrate that a pre-scheduled mobile device (primary) and an opportunistically scheduled mobile device (secondary) can simultaneously receive data by taking advantage of beamforming and multiuser diversity using a novel approach. By requiring full CSI of the primary mobile device, we show that if there is another mobile device exhibiting multiuser diversity, we can simultaneously transmit to both mobile devices without degrading the primary mobile device's SNR, while the secondary mobile device's SNR increases as the total number of mobile devices increases. The practicality of the approach is that only the strong channel transmit antenna index is required as feedback from the secondary mobile device. Using the CSI of the primary mobile device, the nullspace of this channel is used to project the signal for the secondary mobile device in the direction of the strong channel index. We then

derive a lower-bound for the signal-to-interference-plus-noise ratio and use this to find an approximation for the channel capacity.

## ENGINEERING SCIENCES/MECHANICS/PHYSICS

### Room 408B

#### THE EFFECTS OF SUBSTRATE PRE-STRETCH ON POST-WRINKLING BIFURCATIONS

Anesia Auguste<sup>1</sup>, Ryan Hayward<sup>1</sup>, Lihua Jin<sup>2</sup>, Zhigang Suo<sup>2</sup>.

<sup>1</sup>*University of Massachusetts Amherst, Amherst, MA*, <sup>2</sup>*School of Engineering and Applied Sciences, Kavli Institute for Bionano Science and Technology at Harvard University, Cambridge, MA*.

Surface instabilities include a variety of different modes such as wrinkles, folds, and creases. Such surface instabilities have been used in numerous contexts including changing the wetting, optical, and mechanical properties of different material surfaces for applications in flexible electronics, tissue engineering, and biosensors. Wrinkles in elastic bilayers are known to result from a balance between the bending energy of the stiff skin layer and the stretching energy of a softer substrate. Previous work has shown that when a thin, stiff film on a thick, soft substrate is highly compressed, post-wrinkling bifurcations occur due to non-linearity in the substrate elasticity, leading to the emergence of sub-harmonic modes and eventual formation of self-contacting folds or ridges. However, it is not clearly understood how pre-stretch of the substrate affects period doubling and other post-wrinkling bifurcations. We develop an experimental system where the strain state in each layer can be independently varied and study how pre-stretch in the substrate affects post-wrinkling bifurcations. We find that pre-stretched substrates not only substantially shift the critical strain for the onset of post-wrinkling bifurcations, but also qualitatively change the post-wrinkling states. Our findings highlight the critical importance of substrate pre-stretch in determining the nature of post-wrinkling bifurcation modes.

## ENVIRONMENTAL ENGINEERING

### Room 501BC

#### ISLAND SUST'AINABILITY: WATER BUDGET STUDY FOR MOKU-O-LOE (COCONUT ISLAND)

Lelemia Irvine, Oceana P. Francis.

*University of Hawai'i at Mānoa, Honolulu, HI.*

Island Sust'ainability is a conscious movement within the Hawai'ian Isles to find human, environmental, and cultural harmony. There are many islets off the coast of O'ahu, only 2 of which are inhabitable. Moku-o-Loe is the proper Hawaiian name for a 28-acre island off the coast of Kāne'ohe Bay, O'ahu that houses a premier marine biology institute. The institute envisions Moku-o-Loe to be an independent island and model of sust'ainability in water, waste, and energy. A water budget study pertaining to island potable and non-potable uses will be presented. An initial site visit found 26 buildings as potential sites for rainwater harvesting. Later site visits evaluated roof catchment area ( $\sim 62,096.28 \text{ ft}^2$  of available roof space) and



roofing materials for the potential for rainwater harvesting. This information combined with available island rainfall data and water supply/demand evaluations were used to estimate tank size and treatment needs. Recommendations and cost/benefit analysis will be presented on best available sustainable island engineering and management practices in rainwater harvesting and catchment systems to meet the institute's water needs. Moku-o-Loe hopes to serve as a model to mainland O'ahu in water resources sustainability and innovation.

#### **Room 501BC**

##### **NEAR-INFRARED SPECTROSCOPY OF SEDIMENTS IN THE GREAT SALT LAKE DESERT, UTAH: ANALOGS FOR LACUSTRINE ENVIRONMENTS ON EARLY MARS**

Kennda Lynch<sup>1</sup>, Briony Horgan<sup>2</sup>, Jennifer Hanley<sup>3</sup>, Kevin Rey<sup>4</sup>, Robin Schneider<sup>1</sup>, Andrew Jackson<sup>5</sup>, Scott Ritter<sup>4</sup>, John Spear<sup>1</sup>, Junko Munakata Marr<sup>1</sup>.

<sup>1</sup>Colorado School of Mines, Golden, CO, <sup>2</sup>Purdue University, West Lafayette, IN, <sup>3</sup>Planetary Science Directorate, Southwest Research Institute, Boulder, CO, <sup>4</sup>Brigham Young University, Provo, UT, <sup>5</sup>Texas Tech University, Lubbock, TX.

Martian paleolake basins are prime habitability targets for future rover missions. The majority of terrestrial paleolakes transition to modern day evaporite basins with clay, sulfate, and chloride compositions similar to the mineralogy identified by orbital observations in inferred Martian lacustrine systems. Terrestrial basins are considered excellent analogs for habitability studies as they are known to harbor a diverse array of microbial life, enhance the preservation of organic matter and fossils, and serve as reservoirs for authigenic carbonate deposition. Therefore, developing a comprehensive understanding of the characteristics of terrestrial basin systems will prove useful for future astrobiology-driven investigations of Martian paleolake basins. Mineral observations and identifications by near infrared spectrometers such as OMEGA or MRO CRISM are based on spectral libraries composed primarily of pure, individual minerals. By contrast, terrestrial lacustrine systems tend to generate mixed sediments with varying grain sizes and mineral compositions, thus creating a potential difference in spectral quality and identification capability. In this study, we compare mineralogical identification of lacustrine sediments from the Pilot Valley sub-basin of the Great Salt Lake Desert (a terrestrial paleolake basin) by visible-near-infrared spectroscopy (VNIR) to ground truth methods such as X-ray diffraction (XRD) and automated scanning electron microscopy (QEMSCAN). Resulting data shows agreement for the presence of major mineral groups between VNIR and ground truth methods. However, VNIR fails to identify some of the specific minerals present in abundance at Pilot Valley due to either spectral contrast or burial just beneath the surface where VNIR cannot penetrate.

## INDUSTRIAL/MANUFACTURING ENGINEERING

### Room 504

#### **MULTIPLE CRITERIA SIMULATION OPTIMIZATION: FURTHER REFINEMENTS**

Esmeralda Nino, Bryan Rosas, Mauricio Cabrera–Ríos.

*University of Puerto Rico, Mayagüez Campus, Mayagüez, PR.*

This work approaches the multiple criteria simulation optimization problem. Many real world problems can be modeled as multiple criteria optimization problems in different areas and fields such as economics, biology, and engineering. Such problems entail using an optimization strategy to manipulate the parameters of a simulation problem to arrive at the best possible configuration in the presence of several performance measures in conflict. The use of optimization is critical in manufacturing problems; every day it is necessary to make decisions, hopefully in an optimal manner, to satisfy different design specifications or process performance requirements. Optimization algorithms are normally developed to optimize a single criterion. However, in many applications 2 or more criteria are relevant. In the presence of conflicts between multiple performance measures, decision making falls in the realm of multiple criteria optimization. Efficient methods to deal with this decision making problem are highly desirable. Pareto efficiency conditions are used in an iterative framework based on experimental design and pairwise comparison. In particular, this work improves on the use of data envelopment analysis to determine the efficient frontier as well as the use of a single-pass algorithm previously proposed by our research group. The results show a rapid convergence to a more precise characterization of the Pareto-efficient solutions. The revised algorithm is illustrated by a series of cases in manufacturing systems simulation.

### Room 504

#### **COMPARATIVE STUDY OF LUNG CANCER SCREENING POLICIES AND COST IMPACTS**

Ashley Anhalt, Jeffrey Kharoufeh.

*University of Pittsburgh, Pittsburgh, PA.*

According to the American Lung Association (ALA), lung cancer is the second most common type of cancer and the leading cause of cancer death for both men and women in the United States. Despite clinical efforts and extensive research to prevent and manage lung cancer, the 5-year survival rate is only 15.6%. Currently, the ALA supports low-dose, spiral computerized tomography (CT) screening for high-risk patients. However, the ALA does not recommend regular screening for the general population because it is cost prohibitive and an optimal screening policy does not currently exist. This research examines different screening policies by analyzing data from the National Cancer Institute's (NCI) National Lung Screening Trial (NLST). These data are used to create a discrete-event simulation model of different screening policies in order to assess their comparative costs and likelihood of detecting lung cancer when it exists, particularly for high-risk individuals. Policies are compared by assessing their downstream workload and associated costs. Preliminary results indicate that altering the definition of a positive screening result can significantly affect downstream care decisions and, consequently, costs. This suggests that to determine the most cost-effective screening policy, additional

emphasis should be placed on stratifying patients based on their initial screening result. This analysis is ongoing and will be completed by October 2014.

#### **Room 504**

##### **WIND TURBINE BLADE OPTIMIZATION WITH MULTIPLE AIRFOIL GEOMETRIES AS A DESIGN VARIABLE**

Arturo Del Valle, Delia Valles-Rosales.

*New Mexico State University, Las Cruces, NM.*

A new design approach for a fixed-pitch, fixed-speed (FPFS) wind turbine is presented. Previous optimization methods have focused on variations of the blade's chord, twist, and angle of attack parameters with the majority of studies using a single airfoil geometry along the span of the blade. This work seeks to add a new approach with the addition of multiple airfoils as a design variable to further optimize the energy production of a wind turbine in a site-specific location. An initial design replicates the phase VI blade used in the NASA Ames Research Center experiment and uses the blade element momentum (BEM) theory to simulate the energy production and for validation of the model. The initial phase VI wind turbine consists of a blade with a radius of 5.03 m and uses the S809 airfoil across the entire span of the blade. The optimized design consists of 4 different airfoils described by composite Bezier curves and their flow analysis is made using Drela's XFOIL code. Additionally, the chord and the twist are modeled using Bezier curves with 4 control points each in order to reduce dimensionality of the problem and achieve a smooth curved design. Structural compatibility requirements between the airfoils are taken into account, and the annual energy production is maximized using a genetic algorithm and a gradient based method; preliminary results show an improvement of the annual energy production is expected in a design if the method is implemented.

#### **HEALTH**

##### **OTHER HEALTH/MEDICAL SCIENCES**

#### **Room 404AB**

##### **A COMPARISON OF WRIST AND HIP ACCELEROMETER OUTPUT AT DIFFERENT WALKING SPEEDS**

Albert Mendoza, Amanda Hickey, Allison Gruber, John Staudenmayer, Patty Freedson.

*University of Massachusetts Amherst, Amherst, MA.*

Physical activity has been objectively measured using hip-worn accelerometers for decades. Wrist-worn accelerometers are currently used in large-scale studies. Differences in hip and wrist dynamics during locomotion affect monitor output, which may impact how prediction models are built. We propose to compare ActiGraph™ wrist and hip accelerations (g's) at different locomotion speeds. Participants (N = 7) wore ActiGraph™ GT3X+ accelerometers on the dominant wrist and hip (sampling rate 80 Hz). They performed three, 5 minute trials at self-paced (SP), slow (SL), and fast (F) over-ground walking speeds. Mean and standard deviation of the vector magnitude (VM) were calculated from 2, 20-second data windows per condition.

Linear, mixed-effects models were used to compare the relationship between speed and vector magnitude (VM) for the hip and wrist monitor locations. Significant differences were found between the model slopes (speed vs. VM) of the hip  $m = 0.0695$  (95% CI: 0.019, 0.119) compared to the wrist  $m = 0.1986$  (95% CI: 0.148, 0.248)  $p < 0.001$ . Wrist VM is more responsive to changes in speed than hip VM, suggesting that a wrist-worn accelerometer may be more sensitive to locomotion intensity. These differences may impact how prediction models are built. The advantages of wrist monitor placement over hip monitor placement warrant further investigation. Currently, no unified notion of how to collect, analyze, or interpret wrist-worn accelerometer data exists. Future investigations need to resolve this issue. Anatomical positioning of accelerometers appears to influence the detection of whole body movement. Collectively, this may impact measurement error and model development.

#### **Room 404AB**

##### **THE EFFECTS OF SOLDIER EQUIPMENT LOAD ON HEAD POSITION AND VISUAL DISCRIMINATION TIMING**

Luis Rosado, Mike Busa, Jongil Lim, Darnell Simon, Richard Van Emmerik, Christopher Palmer.  
*University of Massachusetts Amherst, Amherst, MA.*

During walking or other dynamic postural transition tasks we need to be able to orient the body to obtain relevant visual information. The purpose of this study was to examine the effects of magnitude and distribution of soldier equipment loading of the torso and the head on visual information discrimination during a dynamic marksmanship task. Ten expert marksmen were recruited to jump from a 14 inch platform under 7 equipment load distributions and asked to visually discriminate an eye level directional image (left or right) for target engagement. Larger loads to the body resulted in a more downward head pitch orientation angle after touch down ( $p < .05$ ) and a longer time-to-discriminate the visual target ( $p < .05$ ). The most downward head pitch angle and the largest increase in time-to-discriminate were observed in the condition with the heaviest loading to both the torso and the head. A downward head pitch posture after landing would require a greater reorientation of the head to the visual directional image. Thus, after landing, the more demanding initial head-down posture induced by the heaviest loads negatively affects visual information discrimination, with additional loading of the head resulting in the longest times to discriminate the target engagement direction. Indeed, any delay in retrieving relevant visual information from the environment could be disadvantageous to a soldier's survivability. (Funding provided by: Army Natick Soldier Research Development and Engineering Center (NSRDEC)/Naval Health Research Center (NHRC) W911QY-12-C-0006.)

## PHARMACY

### Room 404AB

#### DEVELOPMENT OF A KIDNEY MICRO PHYSIOLOGICAL SYSTEM FOR MODELING DRUG TOXICITY

Elijah Weber<sup>1</sup>, Alenka Jaklic<sup>1</sup>, Edward Kelly<sup>1</sup>, Jonathan Himmelfarb<sup>2</sup>.

<sup>1</sup>University of Washington, Seattle, WA, <sup>2</sup>School of Medicine, University of Washington, Seattle, WA.

In the drug development process, preclinical animal models have been used to assess drug efficacy, safety, and toxicity. In some examples, the largest downfall to using animal models has been failure to recapitulate drug action or toxicity in man. The solution to this preclinical-clinical problem is the movement toward testable human organ systems, such as the kidney. We have been modeling the kidney *ex vivo* by using a 3-dimensional micro-physiological device that will serve as a platform in which human derived kidney cells can function. To be considered a reliable model, the micro physiological device must be able to achieve functional characteristics of the human kidney. Current work has shown that the micro physiological device can serve as a viable platform for human-derived kidney cells for up to 28 days. The device has also shown functional properties of the human kidney in regards to glucose reuptake, creatinine secretion, and xenobiotic secretion. Since the kidney is a major organ of elimination of both endogenous and exogenous toxic compounds, this micro physiological device shows great potential for modeling toxicity. Current work using known nephrotoxic compounds, such as gentamicin and cisplatin, investigates toxicity in our 3-dimensional environment. With further development of this kidney model, this micro physiological system has the potential to become a pre-clinical gold-standard in the assessment of the toxicity of future compounds.

## PUBLIC HEALTH (INCLUD. ENV. HEALTH/EPIDEMIOLOGY)

### Room 404AB

#### DEPRESSION SYMPTOMS AND VITAMIN B6 STATUS AMONG REPRODUCTIVE-AGED WOMEN IN THE NATIONAL HEALTH AND NUTRITION EXAMINATION SURVEY, 2005-2006

Joycelyn Faraj, Alayne Ronnenberg.

University of Massachusetts Amherst, Amherst, MA.

Women are 2-3 times more likely than men to experience depression. The metabolite of vitamin B<sub>6</sub>, pyridoxal-5'-phosphate (PLP) is a coenzyme in the tryptophan-serotonin pathway, and a lack of vitamin B<sub>6</sub> may cause depression. We conducted a secondary data analysis to evaluate the association between depression symptoms and serum PLP in non-pregnant females ages 15 to 49 years from the National Health and Nutrition Examination Survey (NHANES) 2005-2006. Depression scores were calculated based on the Patient Health Questionnaire-9 (PHQ-9), and categorized into no depression, mild, moderate, and moderate to severe depression (scores 0-4, 5-9, 10-14, and ≥15, respectively). To account for NHANES' complex survey sample, weighted measures were used for analysis of the 4,211 observations included. Twenty-six percent of women reported symptoms of depression, and a third had vitamin B<sub>6</sub> deficiency (< 30 nmol/L). Vitamin B<sub>6</sub>-deficient women had higher depression scores

(5.03 vs 2.89;  $p = 0.001$ ), higher body mass index (30.1 vs 26.7 kg/m<sup>2</sup>;  $p < 0.001$ ), elevated inflammation (c-reactive protein 0.71 vs 0.35 mg/dl;  $p < 0.001$ ), lower serum vitamin D (51.1 vs 64.3 nmol/L;  $p < 0.001$ ) and increased homocysteine (7.36 vs 6.73  $\mu$ mol/L;  $p = 0.03$ ) compared to women with normal B<sub>6</sub> status. There was a significant positive linear trend among vitamin B<sub>6</sub> deficiency and depression categories ( $p$ -trend  $< 0.001$ ). Women who were moderately-to-severely depressed had 7 times the odds of being B<sub>6</sub>-deficient compared to women without depression (OR: 6.43,  $p = 0.02$ ) after controlling for age, serum vitamin D, BMI, and inflammation. Shedding light on the potential role of vitamin B<sub>6</sub> in this association may help develop adequate prevention and treatment strategies for depression.

#### **Room 404AB**

##### **PULMONARY CLEARANCE AND QUANTIFICATION OF SINGLE-WALLED CARBON NANOTUBES (SWCNTS) IN MICE**

Justine Nicholas, Joseph Besisi, Xiao Zheng, Donald Bolser, Tara Sabo-Attwood.  
*University of Florida, Gainesville, FL.*

Despite wide-scale use, the biotoxicity associated with single-walled carbon nanotube (SWCNT) exposures is not well established. Several studies report that SWCNTs induce pulmonary inflammation and fibrosis, but few reports have addressed whether these particles are cleared. Airway clearance is important in assessing long-term disease associated with SWCNT exposures. Detection of SWCNTs in biological systems is challenging as common techniques lack spatial resolution and specificity to delineate SWCNTs in carbon-based organisms. Near infrared fluorescence (NIRF) has emerged as a valuable tool for detecting and quantifying SWCNTs by exploiting the innate ability of SWCNTs to fluoresce in the NIR range. We have built and validated an NIRF imaging system to track and quantify SWCNTs in whole organisms and tissues. We hypothesized that SWCNTs administered to rodents' respiratory tracts are not readily cleared, which leads to chronic inflammation. To test this hypothesis we exposed C57BL/6 mice intratracheally to a single dose of SWCNTs and clearance was tracked using NIRF at various time-points for 10 days. NIRF whole animal tracking, microscopic tissue analysis, and quantification of lung homogenates revealed low systemic clearance while markers of inflammation (cytokines, immune cell differentials) were elevated. Quantification using NIRF spectroscopy revealed values consistent with fluorescence patterns observed with NIRF imaging. Overall, these results highlight the utility of NIRF as a tool to assess clearance and distribution of SWCNTs *in vivo*. This work further lays the foundation for advancing our understanding of the impact SWCNTs have on the pulmonary system and providing information relevant for risk assessment strategies.

## MATHEMATICS & STATISTICS

### APPLIED MATHEMATICS

#### Room 505

##### L2 AND POINTWISE ERROR ESTIMATES FOR FEM ELLIPTIC PDE

Fernando Camacho, Alan Demlow.

*University of Kentucky, Lexington, KY.*

We present efficient *a posteriori* L2 and pointwise error estimates for surface finite element methods (SFEM) for solving the Laplace-Beltrami equation  $\Gamma u = -f$  over a  $C^3$  surface  $\Gamma$ . In our work we use and prove approximation properties for the Scott-Zhang interpolant that are valid for broken Sobolev norms, whereas the usual approximation results for Scott-Zhang type interpolants require globally defined Sobolev spaces. Our error estimates contain a classical Galerkin component and a geometric component depending on the surface  $\Gamma$ . Our studies indicate that the geometric component is of the same order as the Galerkin one and can dominate adaptive algorithms naturally defined using our estimates. This contrasts with the corresponding *a posteriori* energy estimates where the geometric component of the error decreases with a higher order than the Galerkin one. We present numerical experiments where the estimators have been used to implement an adaptive SFEM over surfaces with different curvatures. We refine our meshes using newest vertex bisection and observe the appearance of intermediate meshes  $\Gamma_h$  that contain elements that are not transverse to  $\Gamma$ . The existence of such local “kinks” in our mesh do not affect the convergence rates but cause spikes in the geometric error and estimator.

#### Room 505

##### ORTHOGONAL POLYNOMIALS TO DEPICT BIOLOGICAL SEQUENCES

Saba Nafees, Sean Rice.

*Texas Tech University, Lubbock, TX.*

Cystic fibrosis is a genetic disease that arises due to misfolding of the protein CFTR. Analyses of the mutation data can show the way the various mutations act to produce disease. We propose to use multivariate polynomial regression to accomplish this. We use orthogonal polynomials and dual bases for multivariate data. We will use the sequence data of CFTR and assess the mutations. The observed distribution of mutations defines a covariant basis and a contravariant basis. Projecting different responses into these and taking the covariance would yield their interrelation. We then build functions that capture the properties of the mutations of CFTR, so we can assess each mutation’s interaction with other mutation(s). This will provide insight into the mechanism of the misfolding problem. The orthogonal and dual spaces approach conserves intrinsic biological properties of any phenomenon being tested while simultaneously capturing its quantitative properties.

## **MATHEMATICS (GENERAL)**

**Room 505**

### **UNIVERSAL DEFORMATION RINGS AND SEMIDIHEDRAL GROUPS**

Roberto Soto, Frauke Bleher.

*The University of Iowa, Iowa City, IA.*

To gain a better understanding of a given mathematical object, such as a representation of a group, it is often useful to study the behavior of this object under small perturbations. The theory of such perturbations, also called deformations, is useful in both pure and applied mathematics, and it has led to the solution of many long-standing problems. One particular such problem in pure mathematics is given, for example, by Fermat's last theorem, which was proved (after over 300 years) by Wiles and Taylor using universal deformation rings of group representations. Our goal is to study universal deformation rings of representations of semidihedral groups. A semidihedral group is a non-abelian group whose order is a power of 2. More precisely, for every power of 2 that is at least 16, there are exactly 4 isomorphism classes of non-abelian groups whose order is that power. The semidihedral groups make up one of these classes. We will give a description of all representations of a given semidihedral group that are guaranteed to each have a universal deformation ring. This description follows from the work of Carlson and Thevenaz on endo-trivial representations. We will then discuss how we can determine the universal deformation rings of these representations. Our methods include the use of character theory and decomposition numbers.

## **OPERATIONS RESEARCH**

**Room 505**

### **THE MM PROXIMAL DISTANCE ALGORITHM FOR CONSTRAINED OPTIMIZATION**

Kevin Keys, Kenneth Lange.

*University of California, Los Angeles, Los Angeles, CA.*

The majorization-minimization (MM) principle is a framework for creating iterative optimization algorithms satisfying a monotonic descent property. The descent property lends MM algorithm's remarkable stability and introduces desirable properties such as parameter separation and smoothing into the minimization process. Instead of minimizing an objective function directly, an MM algorithm minimizes a surrogate that is tangent to the objective at every iteration. Thus, by minimizing the surrogate, an MM algorithm drives the objective downward. The current survey emphasizes the role of the MM principle in nonlinear programming. For convex objective functions subject to nonsmooth or nonconvex constraints, one can combine an exact penalty method with distance majorization to create versatile proximal distance algorithms that are effective in both discrete and continuous optimization. These proximal distance algorithms are highly modular and easy to implement. They rely on set projections and proximal mappings, both of which are very well understood techniques in optimization. We test MM proximal distance algorithms in linear programming, binary piecewise-linear programming, sparse regression, matrix completion, and sparse precision



matrix fitting. In statistical settings, our algorithm tends to recover true models more reliably than current software, and we sketch some future statistical applications where our MM algorithm holds promise.

## STATISTICS

### Room 505

#### **A FIXED-EFFECTS APPROACH FOR PRECISE AND ROBUST ESTIMATION IN META-ANALYSIS**

Clara Dominguez Islas, Kenneth Rice.

*University of Washington, Seattle, WA.*

Meta-analysis refers to the use of statistical methods to combine and summarize the results from various independent studies. Two main approaches are commonly used for meta-analysis: the fixed or common effect approach, which is based on the assumption that the different studies estimate identical effects, and the random effects approach, based on the assumption that the effects underlying the different studies have been sampled from a hypothetical population. The latter is commonly used when the study effects are suspected to be different (heterogeneous), but estimators within this approach have been found to be too sensitive using the particular estimation method. We provide a novel yet simple justification for a third approach, based on an assumption of fixed but unknown effects underlying the different studies. In this approach, we propose estimating parameters that summarize both the overall location and the heterogeneity of the study effects included in the analysis that are different to those typically estimated in classical approaches. By switching our target of inference, we show that it is possible to obtain estimates that are more precise and stable, even under heterogeneity of the study effects. We use a published meta analysis of zinc lozenges for treating symptoms of the common cold as an example to describe and illustrate the estimates of our proposed parameters, comparing them to other meta-analysis methods.

## PHYSICAL SCIENCES

### ASTRONOMY/ASTROPHYSICS

### Room 506

#### **AUTOMATIC DATA REDUCTION FROM THE DEDICATED MONITOR OF EXOTRANSITS (DEMONEX): APPLICATION TO TRANSITS OF XO-4B**

Steven Villanueva Jr.<sup>1</sup>, Scott Gaudi<sup>1</sup>, Jason Eastman<sup>2</sup>.

<sup>1</sup>*The Ohio State University, Columbus, OH,* <sup>2</sup>*Las Cumbres Observatory Global Telescope Network, Santa Barbara, CA.*

The dedicated monitor of exotransits (DEMONEX) was a 20-inch robotic and automated telescope whose main science goal was to monitor bright stars hosting transiting exoplanets to discover new planets and improve constraints on the properties of host stars and known planets. DEMONEX recorded 600 - 2,500 raw science and calibrated images per night when weather and target availability permitted. This automated process ran over a 3-year period and

produced a large database of 75,000+ images that would be prohibitive using conventional manual data reduction and analysis techniques. We discuss an automated pipeline for DEMONEX that performs standard corrections to convert raw science images into usable reduced images and then uses automated astrometric measurements to identify and produce time-stamped relative photometry of target and comparison stars in each image. Each time-stamped series of measurements is processed through the EXOFAST suite of programs to determine the properties of the planets and host stars. We present initial results from our test system, XO-4, containing 16 transits of the planet XO-4b combined with archival radial velocity measurements to estimate the parameters of the host stars and planets. Comparison to existing parameters in the literature will serve as confirmation of the effectiveness of our data reduction and analysis pipeline which will ultimately be used on the full DEMONEX data set containing ~40 systems with ~350 transits. Finally, our pipeline will be required to reduce and analyze future observations in real time from a new and improved DEMONEX system expected to begin operations in the fall of 2014.

## **CHEMISTRY (EXCEPT BIOCHEMISTRY)**

### **Room 407**

#### **ENANTIOSELECTIVE BRØNSTED ACID-CATALYZED HYDROBORATION OF LINEAR $\alpha,\beta$ -UNSATURATED KETONES**

Susana S. Lopez, Lucas W. Hernandez, Jon C. Antilla.  
*University of South Florida, Tampa, FL.*

Asymmetric organocatalysis has evolved in the last decade, expanding to include reaction transformations previously accomplished by the use of transition metal catalysts. Given the importance of compounds with stereogenic centers at the  $\alpha$  or  $\beta$  position to a carbonyl, developing a method to obtain such products with high enantio- and chemo-selectivity is synthetically beneficial. In the case of linear  $\alpha,\beta$ -unsaturated ketones, chemoselectivity is a crucial issue due to the reactive nature of both the carbonyl and C = C double bond. Although chemoselective catalytic organometallic hydrogenations are well-known, enantioselective hydrogenations of linear  $\alpha,\beta$ -unsaturated ketones are scarce. Organocatalyzed reactions of this nature are even fewer and less studied. Herein, we present an enantioselective Brønsted acid-catalyzed hydroboration methodology for linear  $\alpha,\beta$ -unsaturated ketones, giving the corresponding saturated ketone an excellent yield and moderate to excellent enantioselectivity.

### **Room 408A**

#### **LOW TEMPERATURE SOLVENT PROCESSING OF TIN SULFIDE (SNS) THIN FILMS FOR LIGHT HARVESTING APPLICATIONS**

Priscilla Antunez, Richard Brutchey, David Webber.  
*University of Southern California, Los Angeles, CA.*

The sun's potential to fulfill the increasing global energy demand in a secure, clean, and sustainable manner is hindered by the high fabrication cost of solar energy technologies. In order to address this issue, we have applied a low temperature solvent processing system for

the fabrication of tin monosulfide (SnS) thin films. Recently, SnS has been reported as a highly efficient photoelectrode material for visible light-driven water splitting. Aside from being comprised of earth abundant elements, SnS is a relatively stable and nontoxic semiconductor. In addition, the direct ( $E_{g, \text{dir}} = 1.32$  eV) and indirect ( $E_{g, \text{ind}} = 1.07$  eV) band gaps of SnS make it attractive for light harvesting applications. We present a method to dissolve bulk material to produce semiconducting thin films that can be easily processed via spin-coating and a mild annealing step. The solution processing method preserves the material's crystal phase and purity in addition to its optical band gap, demonstrated by comparing XRD, SEM-EDS, and UV-vis of the material before and after processing, whereas FT-IR shows the organic content in the films is eliminated after mild annealing. The material's potential for light harvesting applications will be discussed.

#### **Room 408A**

##### **EVOLUTION OF A COLLECTIVE RESONANCE IN PLASMONIC MOLECULES**

Alexandria Stanton, Prashant Jain.

*University of Illinois, Urbana-Champaign, Urbana, IL.*

Localized surface plasmon resonances (LSPRs) are collective oscillations of conduction-band carriers on the surface of a nanoparticle in response to an electromagnetic wave. LSPRs have captured the interest of the scientific community due to their strong interactions with light and subsequent applications in areas like sub-diffraction-limit imaging, chemical sensing, and photovoltaics. However, there is little understanding of how such a collective resonance evolves from single-carrier excitations, a fundamental physical question which will be addressed in this talk. We study this evolution of a collective resonance by controlled charging and discharging of ultrasmall, sub-1 nm radii clusters of the semiconductor copper selenide. The copper selenide cluster samples have a molecular-level homogeneity because they are synthesized by the cation exchange of magic-sized CdSe clusters. The reduced size of the copper selenide clusters allows the achievement of high plasmonic carrier densities by means of a handful of carriers. At the same time, the molecular homogeneity of the samples obviates heterogeneous broadening of plasmonic spectra due to variations in size and/or charge density from one cluster to another. The measurement of the homogeneous linewidths of the cluster plasmon resonance as a function of the number of charge carriers in a cluster ( $n = 1$  to  $n = 5$ ) indicates that a collective resonance of carriers gradually evolves from a regime where single carriers can be excited independent of one another.

#### **Room 408A**

##### **EVOLUTION OF METALLOENZYMES THROUGH MULTI-SCALE DYNAMICS MODELING**

Crystal Valdez, Anastassia Alexandrova.

*University of California, Los Angeles, Los Angeles, CA.*

To design artificial enzymes for the catalysis of reactions that interest humankind, we must understand the principles by which Nature makes her own evolutionary choices. There are several questions of metalloenzyme evolution that are perplexing: the choices Nature makes for catalytic metals, effects of metal replacement, and/or removal of non-catalytic metals in

natural enzymes. 1) We will explain why the seemingly innocent replacement of Mg(II) with Ca(II) in catechol-O-methyl transferase (COMT) kills the activity of the enzyme. 2) We will show why the replacement of Fe(II) with Ni(II) in the identical structure of acireductone dioxygenase (ARD) completely reroutes the catalytic mechanism, with the oxidation of the same substrate into different products. 3) We will elaborate on the puzzling fact that 2 amide hydrolases, urease and  $\beta$ -lactamase, use different metals to catalyze similar reactions proceeding through identical mechanisms. Also, we will introduce our new efficient dynamics method for modeling metalloproteins, QM/DMD, which made this research possible. QM/DMD permits for fast and extensive sampling of metalloproteins done in conjunction with a quality *ab initio* description of the metal containing active site. Following our studies on natural enzymes, we will show how this method can be used to redesign an existing metalloprotein scaffold to specifically bind a substrate using carboxypeptidase A (CPA) as a text case, creating new artificial enzymes.

#### Room 407

#### **MERGING AIR QUALITY MODELS WITH EXPERIMENTAL MEASUREMENTS OF OH RADICALS IN THE LOWER ATMOSPHERE: THE ROLE OF SINGLET MOLECULAR OXYGEN REVISITED**

Geovani Montoya, Julia Montoya, Dong Zhang, Matthias Selke, Krishna Foster.

*California State University Los Angeles, Los Angeles, CA.*

Hydroxyl radicals (OH) are predominantly responsible for the oxidation of the lower atmosphere; they undergo complex reactions with pollutants and greenhouse gases. The effects of increased OH concentrations in the atmosphere have been correlated with adverse health effects including respiratory diseases, namely asthma. Air quality models composed of gas phase chemistry are used to identify sources contributing to increased OH concentrations and have served as a basis for constructing air quality protocols. However, current models under-predict the concentrations of OH. In this study, reactions between singlet molecular oxygen,  $O_2 (^1\Delta_g)$ , and volatile organic compounds have been identified as a potential source of OH formation, not yet considered by air quality models. Pyrene is one organic compound that has been studied. It is classified as a polycyclic aromatic hydrocarbon (PAH) that is primarily emitted by combustion engines. It is known that  $O_2 (^1\Delta_g)$  can be produced through an energy transfer mechanism between sunlight absorbing organic compounds and ground state  $O_2 (^3\Sigma_g)$ . Time-resolved near infrared (NIR) detection was used to obtain quantum yields of  $O_2 (^1\Delta_g)$  production by irradiating pyrene with a Nd:YAG Laser (at 355 nm). It was found that pyrene is highly efficient in producing  $O_2 (^1\Delta_g)$  with quantum yields of  $0.90 \pm 0.02$ . These results suggest that primary pollutants like pyrene can be used to study the role of photosensitized  $O_2 (^1\Delta_g)$  in the formation of hydroxyl radicals and provide corrections to air quality models. Oxy-PAHs (e.g., B[a]P-1,6-dione) that are formed through oxidation of PAHs were also considered.

## Room 407

### NOVEL FUNCTIONALIZED CYSTEINE LIPID ANALOGUES (CLAS) AS LIGANDS IN DRUG CARRIERS FOR COMBINATION THERAPY

Magaly Salinas<sup>1</sup>, Idaira Hueso-Falcon<sup>2</sup>, Shaunak Pandya<sup>3</sup>, C. Mauli Agrawal<sup>1</sup>, George R. Negrete<sup>1</sup>.

<sup>1</sup>*The University of Texas at San Antonio, San Antonio, TX*, <sup>2</sup>*Instituto Universitario de Bio-  
Orgánica Antonio González, Universidad de La Laguna, Tenerife, ES.*

We are investigating the use of functionalized cysteine lipid analogues (CLAs)-drug carriers as chemical homing systems for delivery of therapeutics to cancer cells. A novel class of CLAs was developed from L-cysteine via cyclocondensation with *m*-nitrobenzaldehyde and acylation with acryloyl chloride yielding a trifunctionalized thiazolidine core with carboxylic acid, aryl nitro, and acryloyl substituents. The core is used to generate an array of compounds in a highly modular process by appending hydrophobic units, ligands for binding to target tissues, or conjugation of medications (i.e., doxorubicin) and fluorophores for binding and localization studies. The fatty component of the CLA is appended via conjugate addition of a thiol derivative to the acrylamide functionality of the core. The amino terminus of a linker is connected at the carboxylate end of the thiazolidine via carbodiimide coupling chemistry. Subsequently, a peptide ligand is coupled to the carboxylate end of the attached linker for tissue targeting. In a different model, drug-releasing CLAs will be synthesized by coupling a hydrazine to the carboxylate end of the attached linker for succeeding conjugation of doxorubicin via a hydrazone linkage. Tumor surfaces, which are usually acidic, will induce drug releases due to the pH-sensitive hydrazone linkage. With this synthetic technology, we will develop novel functionalized CLAs capable of serving as targeting and drug releasing ligands in drug carriers for combination therapies.

## Room 408A

### CARBENES STABILIZING UNUSUAL BORON AND ANTIMONY SPECIES

David Ruiz, Guy Bertrand.

*University of California, San Diego, La Jolla, CA.*

Ever since the discovery by our lab of a “bottleable” carbene in 1988, the field of stable carbene chemistry has grown tremendously. Quickly, stable carbenes proved to be more than just laboratory curiosities as they were recognized as excellent ligands for transition metal catalysis. More recently, it was realized that carbenes could also stabilize metals and main group elements in their 0 oxidation state, and even activate small molecules. This allows for intensive studies on postulated intermediates and a better understanding of fundamental chemistry. Interestingly, carbenes are unique, and each type has its own properties. We will show that, by using the carbenes we developed, unusual main group species can be isolated. First, the deprotonation of a borohydride leading to a carbene-stabilized boryl anion and its reactivity as a boron-centered nucleophile will be discussed. Then, the isolation of 3 unique antimony compounds synthesized from the same parent carbene-stibine compound will also be presented. The products include a novel antimony(III) radical and an antimony(0) diatomic molecule. These results illustrate that carbenes are powerful tools to stabilize reactive species.

**Room 407****TORQUOSELECTIVITIES OF ELECTROCYCLIC RING OPENING REACTIONS OF 2-AZETINES**

Steven Lopez, K. N. Houk.

*University of California, Los Angeles, Los Angeles, CA.*

Quantum mechanical calculations were carried out with the M06-2X density functional and have revealed the role of nitrogen-substituent effects on the torquoselectivities of electrocyclic ring-opening reactions of 2-azetines. The 2 diastereomeric transition structures differ in that the lone pair orbital on nitrogen rotates inward or outward. A wide scope of nitrogen substituents were tested, and the inward rotation of the lone pair on nitrogen is favored for all substituents. The favored conrotatory transition state is stabilized by the favorable interactions of the nitrogen lone pair with the vacant  $\pi^*$  LUMO orbital. Electron-withdrawing groups dramatically alter the ground state geometry by rehybridizing nitrogen from  $sp^3$  to  $sp^2$ . The Taft  $\sigma_R$  parameter of N-substituents correlates with the calculated activation barriers for the favored conrotatory transition states. However, there is no correlation of  $\sigma_R$  with the calculated activation barriers for the disfavored conrotatory transition states. Mechanistic implications will be discussed.

**Room 407****DIELS-ALDER PRODUCT CHARACTERIZATION AND KINETIC STUDIES ON 3,4',5 TRIMETHOXY-TRANS-STILBENE WITH SINGLET OXYGEN**

Abegail Tadle, Matthias Selke.

*California State University Los Angeles, Los Angeles, CA.*

Resveratrol (trans-5-(para-hydroxystyryl)-resorcinol) is a polyphenol commonly found in the skin of grapes, mulberries, and wine. The trihydroxylated stilbene has been reported to exhibit preventive effects toward photo-oxidative damage in epithelial cells; however, the mechanism as to how this occurs is not well explored. We have established that resveratrol has 2 known pathways of reaction with singlet oxygen ( $^1O_2$ ): [4+2] cycloaddition with the central double bond and the adjacent double bond from the phenol ring and [2+2] cycloaddition to form an unstable dioxethane. However, *in vivo*, the 4' hydroxyl group is glycosylated, and 4'-methylated derivatives have also been reported. We suggest that the reaction of  $^1O_2$  with trimethoxylated stilbene (3,4',5 trimethoxy-trans-stilbene) produces the usual [2+2] cycloaddition product and a [4+2] reaction pathway followed by a sequential [4+2] Diels Alder reaction to produce a bisendoperoxide product. Products and intermediates will be analyzed by high resolution mass spectrometry,  $^1H$ NMR,  $^{13}C$ NMR, COSY, and VT NMR if unstable species are formed. Kinetic experiments using time-resolved luminescence spectroscopy have shown that resveratrol and its methylated derivative are poor  $^1O_2$  scavengers with  $k_t$  values of  $1.6 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$  in  $CD_3CN$  and  $8.03 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$  in  $CD_3CN$ , respectively.

## PHYSICS (EXCEPT BIOPHYSICS)

### Room 506

#### LEVEL DENSITIES IN THE SHELL MODEL MONTE CARLO APPROACH

Marco Bonett-Matiz<sup>1</sup>, Yoram Alhassid<sup>1</sup>, Abhishek Mukherjee<sup>2</sup>.

<sup>1</sup>*Yale University, New Haven, CT*, <sup>2</sup>*European Center for Theoretical Studies in Nuclear Physics and Related Areas, Villazzano, Trento, IT.*

Calculating the properties of nuclei from the underlying interactions among its constituents is a challenging problem in nuclear theory. Direct diagonalization methods in the framework of the configuration-interaction shell model approach are prohibited in medium-mass and heavy nuclei because of the large dimension of the required model space. The shell model Monte Carlo (SMMC) approach enables calculations in model spaces that are many orders of magnitude larger than those that can be treated by conventional diagonalization methods. In particular, SMMC has been a powerful method for calculating the nuclear density of states, defined as the number of nuclear states per unit energy. Nuclear densities govern nuclear reaction rates, which in turn play an important role in determining the elemental abundances in stellar nucleosynthesis. The density usually calculated in SMMC is the *state* density, which includes the spin degeneracy  $2J+1$  of each level with spin  $J$ . However, experiments often measure the *level* density in which each level is counted once irrespective of its  $2J+1$  spin degeneracy. Recently, we introduced a method to calculate the level density directly within the SMMC approach. We will briefly discuss this method and present its application to a family of nickel isotopes. The calculated SMMC level densities are found to be in close agreement with experimental results.

### Room 506

#### FRACTIONAL QUANTUM HALL EFFECTS AT SMALL FILLING FRACTION, QUASIPARTICLES, AND THE (2,0)-THEORY

Nesty Torres-Chicon, Ori Ganor.

*University of California, Berkeley, Berkeley, CA.*

The fractional quantum Hall effect appears as part of the low-energy description of the Coulomb branch of the  $A_1$  (2,0)-theory formulated on  $(S^1 \times R^2)/Z_k$ , where the generator of  $Z_k$  acts as a combination of translation on  $S^1$  and rotation by  $2\pi/k$  on  $R^2$ . At low-energy, the theory is described in terms of a 4+1D super-Yang-Mills theory on a cone  $(R^2/Z_k)$  with additional 2+1D degrees of freedom at the tip of the cone. Fractionally charged quasi-particles have a natural description in terms of BPS strings of the (2,0) theory. We analyze the large  $k$  limit where a smooth cigar geometry provides an alternative description. In this framework, a  $W$ -boson can be viewed as a bound state of  $k$  quasi-particles. The  $W$ -boson is described by a soliton solution of BPS equations on a certain auxiliary curved space. We show that axisymmetric solutions of these equations correspond to singular maps from  $AdS_3$  to  $AdS_2$ , and we present some numerical solutions.

## PSYCHOLOGY & SOCIAL SCIENCES

### EDUCATIONAL PSYCHOLOGY

#### Room 507

#### **LATINA ADOLESCENT ECOLOGICAL RISK FACTORS: FROM HOME (PARENTAL PSYCHOLOGICAL CONTROL) TO SCHOOL (PEER VICTIMIZATION, ETHNIC DISCRIMINATION, AND RESPECTFUL AND FAIR SCHOOL CLIMATE)**

Bryan Montano-Maceda<sup>1</sup>, Scott Plunkett<sup>2</sup>.

<sup>1</sup>University of Michigan, Ann Arbor, MI, <sup>2</sup>California State University, Northridge, Northridge, CA.

Although many United States Latino/a youth are successful academically, this group has a higher high school dropout rate than their ethnic counterparts. Thus, it is important to identify antecedents of Latina/o academics, especially since Latina/os are the largest ethnic minority. Various contextual factors, for example, parental psychological control, peer victimization, ethnic discrimination, and respectful and fair school climate, were examined in relation to academic motivation and self-reported GPA of Latina/o students. Specifically, this study used self-report survey data from 1,067 Latina/o ninth to twelfth grade students in 3 states (California, North Carolina, Oklahoma; 13 - 19 years, 54.5% girls). Bivariate correlations indicated that parental psychological control, discrimination, and victimization were significantly and negatively related to academic motivation and GPA. School climate was significantly and positively related to GPA and academic motivation. Path analysis indicated academic motivation was significantly and positively related to GPA, parental psychological control was significantly and negatively related to academic motivation, and school climate was indirectly related to GPA through academic motivation. When students are more actively engaged, they may study more and spend more time in academic endeavors which increases grades. When students experience psychological control from parents, for example, guilt, shame, love withdrawal, their confidence in their own abilities may be diminished. When students perceive a fair and respectful school climate, they may be more likely to stay academically engaged. Teacher training programs and in-services should encourage respectful and fair school climates. Also, Latina/o parents could be discouraged from using psychologically controlling behaviors.

### EXPERIMENTAL PSYCHOLOGY

#### Room 507

#### **STOP! IN THE NAME OF CONTACT**

Deon Benton, David Rakison.

*Carnegie Mellon University, Pittsburgh, PA.*

Despite the large database of research on causal perception in the first year of life, relatively little is known about infants' understanding of the motion and causal properties of humans and inanimate objects. Thus, a primary aim of the experiments reported here was to replicate Spelke, Phillips, and Woodward (1995) and examine whether 7-, 11-, and 15-month-old infants



have expectations about whether humans and inanimate objects are caused to move, are self-propelled, and can cause action at a distance. Following the procedure of Spelke et al., infants were habituated to events in which either a computer-animated person or inanimate object moved behind a central screen, after which point, a second, half-occluded person or inanimate object exited stage right. Following habituation, infants were given collision and no-collision test events in which either the second person or inanimate object moved after being contacted by the first person or object (collision event) or after the first person or inanimate object failed to make contact with it (no-collision event). We hypothesize that if infants expect people to be self-propelled but not inanimate objects, they should look longer at the inanimate-object, no-collision event than at the same event that involves people. However, if infants do not have expectations about the motion properties of people and inanimate objects, then they should look equally at both test events. Data collection is ongoing. Understanding how infants represent the causal motion of different object kinds is important because it may underlie infants' later causal reasoning abilities.

## TRADITIONAL KNOWLEDGE

### Room 507

#### **HONOHONONUI COASTAL RESOURCE ASSESSMENT: AN INTEGRATIVE APPROACH TO COASTAL RESOURCE MANAGEMENT**

Hoku Pihana, Misaki Takabayashi, V.Kalani Quiocho.

*University of Hawaii at Hilo, Hilo, HI.*

Natural resource management strategies in Hawai'i must integrate indigenous Hawaiian and non-indigenous epistemologies in order to effectively and sustainably manage coastal resources. Our project focused on the traditional Hawaiian land division of Honohononui along the Keaukaha coastline in Hilo Hanakahi, Hawai'i Island. Our goal was to develop a project in collaboration with stakeholders and community members that met the needs of the Keaukaha community and investigated the ecology of the coastal marine environment, both of which would support a functional model for community-driven resource management. The study location focused on 5 sites within Honohononui: Hale o Lono, Kaupō, Laehala, Kaumealani, and Kamokuna. Hawaiian oral traditions such as *mo'ōlelo*, *'ōlelo no'eau*, and *oli* were used for the inception of our methodologies and understanding of these places. The initial data from each site consisted of water quality parameters, benthic substrate type, and the presence of native and non-native terrestrial and shallow water reef species. The preliminary findings of our study indicated that there is a large variability in water quality, species diversity, and human interactions among the sites. The next phase of our project is to develop monitoring techniques that enable the Keaukaha community to participate in effective coastal resource management efforts.