2019 SACNAS

The National Diversity in STEM Conference

STUDENT RESEARCH PRESENTATION

ABSTRACT BOOK

If you plan on printing this abstract book, please consider printing double-sided to conserve paper.

Thursday, October 31, 2019

10:00 AM – 12:00 PM

Thursday Graduate Posters

THU - G1 Exploring Electron Rich Cobalt Complex As a Potential Phip Catalyst.

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Safiyah Muhammad*, *University of Illinois at Urbana-Champaign* and Alison Fout, *University of Illinois at Urbana-Champaign*

Abstract: Earth-abundant transition metal complexes have recently gained much interest for their use as catalysts for the synthesis of fine chemical products. However, their widespread implementation currently trails less abundant and more toxic second- and third-row transition metal congeners. One reason for this is due to the intrinsic preference of late first-row metal complexes to undergo one-electron or radical chemical transformations. The incorporation of strong-field ligand systems, such as phosphines and N-heterocyclic carbenes, into first-row transition metal complexes has led to an increased number of catalytic two-electron processes. Following this approach, new ligand derivatives of previously examined cobalt bis(carbene) complexes have been synthesized and characterized. Namely, electronic modifications of the ligand system were achieved through the incorporation of an electron withdrawing trifluoromethyl group and an electron donating tert-butyl group. Metalation of the two ligands derivative, $^{Mes}CCC^{tBu}$ ($^{Mes}CCC^{tBu}$ = bis(mesityl-benzimidazol-2-ylidene)-4-tert-butylphenyl) and $^{Mes}CCC^{CF3}$ ($^{Mes}CCC^{CF3}$ = bis(mesityl-benzimidazol-2-ylidene)-4-trifluoromethyl), afforded the cobalt(III) complexes which were characterized. The carbonyl complexes, ($^{Mes}CCC^{R}$)Co(CO)$_2$ (R = ^{t}Bu or CF$_3$), were synthesized to examine the electronic effects the electron-withdrawing and -donating group exhibit on the metal center using IR spectroscopy. Furthermore, cobalt(I) analogues, ($^{Mes}CCC^{R}$)Co(N$_2$)PPh$_3$ and ($^{Mes}CCC^{R}$)Copy, were synthesized and examined for the catalytic hydrogenation of alkynes and alkenes. Preliminary results revealed that the electron withdrawing group gives rise to a less active hydrogenation catalyst. Lastly, mechanistic studies based on *para*-hydrogen induced polarization (PHIP) NMR spectroscopy revealed that the electronic modification of the ligand system does alter the process of *cis* hydrogenation followed by *trans* isomerization.

THU - G2 Effects of Charged Residues on the Stabilization Role of Antifreeze Proteins on Alcohol Dehydrogenase

Discipline: Chemistry
Subdiscipline: Other Chemistry

Yasmeen Solano*, *California State University, Los Angeles* and Xin Wen, *California State Univeristy, Los Angeles*

Abstract: Antifreeze proteins (AFPs) are found in many organisms that need to survive in subzero environments including bacteria, fish, plants, and insects. Previous studies have demonstrated the presence of transcripts of AFP genes in a summer desert beetle *Microdera punctipennis*, where its AFPs (MpAFPs) have a thermal protective function. In our previous study, we demonstrated the thermal stability and the thermal protective function of an AFP isoform from *Dendroides canadensis* (DAFP-1). Alcohol dehydrogenase (ADH) is a group of dehydrogenase enzymes that occur in many organisms and facilitate the interconversion between alcohols and aldehydes with the reduction of nicotinamide adenine dinucleotide (NAD$^+$) to NADH. When ADH is placed under thermal stress it easily loses its enzymatic activity. Studies found DAFP-1 to have a thermal protective role when interacting with ADH at varying temperatures. In this study we will look at how the positively charged arginine residues will influence this newly found thermal protective role by using R9/25/30/54A, a DAFP-1 mutant where positively charged arginine residues in DAFP-1 was replaced by alanine residues. We hypothesize that the positively charged arginine residues are important for interacting with ADH and thus a decrease in the protective role of R9/25/30/54A when compared to wild-type DAFP-1. These studies are important to further understand the thermal protective properties and mechanisms of AFPs that could lead to the screening of effective protectants for thermal labile proteins and the design of highly effective protectants.

THU - G3 Chemical Evolution in the Milky Way: Rotation-Based Ages for Apogee–Kepler Cool Dwarf Stars

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Zachary Claytor*, *Institute for Astronomy, University of Hawai'i* and Jennifer van Saders, *Institute for Astronomy, University of Hawai'i*

Abstract: Precise stellar ages are imperative in understanding the evolution of the Milky Way. Previous investigations of galactic evolution have relied on ages from isochrones, kinematics, or asteroseismology, but these ages are unreliable or imprecise for the most common, low-mass field stars. Rotation periods from *Kepler* and stellar parameters from the Apache Point Observatory Galactic Evolution Experiment (APOGEE) provide a rich dataset for use in obtaining ages using gyrochronology, or rotation-dating, which is most useful for low-mass field stars. Combining APOGEE spectroscopic temperatures and chemical abundances with *Kepler* rotation periods, we use models of stellar angular momentum evolution to determine ages for 796 stars in the APOGEE-*Kepler* Cool Dwarfs sample. We investigate the impacts on age inferences of including or neglecting detailed chemical abundance patterns as well as varying initial conditions. Under our model assumptions, the ages for our stars have a median relative precision of 8%, which is better than other age determination methods for similar dwarf star samples. Finally, we use our inferred ages to investigate trends of *α*-element enhancement with age, and consider their implication for galactic chemical evolution.

THU - G4 Tip of the Red Giant Branch Distances to Nearby Galaxies

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Gagandeep Anand*, *University of Hawaii- Manoa*; Brent Tully, *University of Hawaii- Manoa* and Luca Rizzi, *W. M. Keck Observatory*

Abstract: Our collaboration is interested in understanding the large-scale structure and dynamics of the local universe. Accurate distances are a requirement for the reconstruction of the individual motions of galaxies. One method that is becoming increasingly popular to determine distances to galaxies uses the brightest red giant branch stars in a galaxy as a standard candle. This tip of the red giant branch technique has matured to the point where we can reliably determine distances to within 5% for galaxies within 10 Megaparsecs (Mpc) with the Hubble Space Telescope. We report results from our ongoing work in which we use these distances to disentangle galaxies from the Hubble Flow and retrieve the underlying peculiar velocity field. Our work highlights the main structural features present in the Local Volume, along with their peculiar motions. In the near future, the James Webb Space Telescope will allow us to extend this work out to 40 Mpc. This greatly increases the number of galaxies for which we can obtain precise distances. This will also allow us to establish a direct linkage with distances obtained from surface brightness fluctuations, allowing us to determine the value of the Hubble constant with a completely independent technique from what is done at the present.

THU - G5 The Deep Underground Neutrino Experiment and the Protodune Detectors

Discipline: Physics & Astronomy
Subdiscipline: Physics

Casandra Morris*, *University of Houston* and Lisa Koerner, *University of Houston*

Abstract: Neutrinos are the most abundant matter particles in the universe; despite this they are one of the most mysterious. We know that there are 3 different types, or flavors, of neutrinos and that as each of these flavors travel they have the ability to change, or oscillate, into a different flavor. By exploring the phenomenon of neutrino oscillation there is the possibility of unlocking some of the secrets of the origin of matter, such as, why is there more matter as opposed to antimatter in the universe? The Deep Underground Neutrino Experiment (DUNE) plans to build a 40 kt liquid argon detector a mile underground and 1300 km away from our neutrino source. This gives enough distance for the neutrinos we create to oscillate, and the distance underground will provide enough cover to protect from the cosmic ray background. There are two prototypes of DUNE at CERN that are each 1/20 the size of DUNE, testing the technologies to be used in DUNE. One implements technologies for liquid argon only (ProtoDUNE SP) and the other for liquid and gaseous argon (ProtoDUNE DP). So far ProtoDUNE SP is the largest and most successful detector of its kind in the world. DUNE will not only be looking to more precisely measure the parameters that dictate how the neutrinos oscillate, but also search for proton decay and be on the lookout for core-collapse supernovae. In this talk I will discuss the physics goals of DUNE and the current status of the prototype detectors.

THU - G6 Stimuli Responsive Polyurethanes That Rapidly Degrade *Via* Intramolecular Cyclization

Discipline: Materials Research
Subdiscipline: Materials Research

Ephraim Morado*, *University of Illinois at Urbana Champaign* and Steven Zimmerman, *University of Illinois at Urbana-Champaign*

Abstract: Millions of tons of polyurethanes (PU) are produced every day for coatings, foams, and adhesives but due to the mass production of PU there is a buildup of PU waste in landfills and the aquatic environment. Disposal of PU waste involves incineration of PU, which requires a large energy input. Therefore, there is a need to develop milder methods to degrade PU. We present a simple hydroxy acetal unit that undergoes an intramolecular cyclization mechanism under anhydrous acidic conditions leading to a breakdown into smaller units. Incorporating this moiety as a monomer in a crosslinked PU network would allow the depolymerization of the polyacetal backbone and thus provide a new class of material with a distinct degradation mechanism. Herein, the hydroxy acetal unit is incorporated into bulk polymer and light triggered core shell microcapsules. A tetrahydroxy acetal is copolymerized with toluene diisocyanate to make foams that degrades efficiently under acidic conditions. Additionally, a diamino hydroxy acetal urethane monomer was synthesized for interfacial polymerization with trimesoyl chloride to obtain acid responsive microcapsules. We show that the hydroxy acetal monomer can degrade under mild conditions, which can possibly be utilized as a new PU material to aid in accumulation of PU waste.

THU - G8 Using Supervised Methods to Identify Heart-Healthy Dietary Patterns in the Multi-Ethnic Study of Atherosclerosis (MESA)

Discipline: Mathematics
Subdiscipline: Statistics

Natalie Gasca*, *University of Washington* and Robyn McClelland, *University of Washington*

Abstract: Most studies investigating nutrition-disease relationships have used dimension-reduction techniques that create diet patterns using only food information, such as principal component analysis (PCA). However, methods that additionally use disease information, such as partial least squares (PLS) and sparse PLS (SPLS), could construct more relevant summaries. In this study, we compare how these methods identify diet patterns related to BMI, as excess body weight is an important pathway between nutrition and heart disease. The Multi-Ethnic Study of Atherosclerosis cohort includes 6814 participants aged 45-84 at baseline (53% female). Their typical diet was assessed with a Food Frequency Questionnaire, which 6531 participants completed. BMI was pre-adjusted for age, gender, race/ethnicity, total energy consumption, and intentional exercise. PCA constructed 23 patterns from 120 foods and beverages, with a cross-validated root mean squared error (RMSE) of 4.93. PLS summarized the data with only two diet patterns (RMSE=4.91). SPLS also identified two patterns, but only required 11 variables to do so (RMSE=4.94). SPLS's first diet pattern described hamburger and diet soda intake, both positively associated with BMI. The second pattern summarized unfried potato and wine consumption, both negatively associated. The remaining foods in the SPLS model were positively (lettuce, steak, ham, and fries) or negatively (sweet potatoes, nuts, and sugar in coffee/tea) associated with BMI. We have illustrated that by using outcome data and variable selection, SPLS creates more interpretable diet patterns because it uses fewer patterns and foods without much loss of predictive ability for the outcome, as measured by RMSE.

THU - G9 Do False Positive Rates Increase When Police Wrongfully Assume a Suspect's Ethnic Background?

Discipline: Computer & Information Sciences
Subdiscipline: Other Computer and Information Sciences

Monique Ceberio*, *San Francisco State University* and Rori Rohlfs, *San Francisco State University*

Abstract: Forensic DNA profiling tools are becoming increasingly sensitive and can be used by authorities to identify crime suspects. Crime scene profiles (CSP) can be generated from picograms of DNA, which corresponds to only a few cells. This type of assay is called low template analysis (LTA). LTA can be ambiguous and difficult to interpret because samples are small and often contain DNA from multiple contributors. The error rates associated with LTA mixture analysis is unknown, yet the method is used regularly in forensic casework. To generate CSP, The FBI has selected 13 highly variable short tandem repeats (STRs) loci to constitute the core of the United States national database called the Combined DNA Index System (CODIS). The allele frequencies (AFs) of these core STRs loci can vary considerably from one population to another. This experiment aims to determine how false positive rates (FPRs) change when police wrongly assume a suspect's ethnic background and use the wrong AFs in forensic casework. I hypothesize that using the wrong AFs will increase FPRs in populations with low genetic diversity. We obtained AFs for various populations to determine the expected heterozygosity amongst populations. The statistical software, Forensim, was employed to generate genetic data encountered in forensic casework. The computer programming language "R" and Forensim were used to model forensic cases and determine FPR. The results of this experiment will help identify if populations with low genetic diversity are at risk of being incorrectly identified as crime suspects.

THU - G10 A High-Dose-Rate Brachytherapy Specific Automatic Treatment Planning and Quality Assurance System

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Yesenia Gonzalez*, *University of Texas Southwestern Medical Center*; Chenyang Shen, *University of Texas Southwestern Medical Center* and Xun Jia, *University of Texas Southwestern Medical Center*

Abstract: High-dose-rate brachytherapy (HDRBT) treatment planning for gynecological cancers is a time-consuming and error-prone process. Typically, this time-sensitive process is performed on the day of treatment where manual planning times can take up to 45 minutes. After manual planning, treatment plans undergo a quality assurance (QA) check prior to treatment delivery. In an effort to overcome the inefficiency of the manual planning and QA workflow, we have created the AutoBrachy system, an automated treatment planning and QA system for HDRBT. AutoBrachy is a web-based system that takes patient specific treatment information to create treatment plans and perform QA checks. Currently, we have developed automated treatment planning modules for cylinder, tandem-and-ovoid (T/O), and interstitial applicators. QA modules have been developed for cylinder and T/O applicators. A generalized workflow for treatment planning begins with applicator specific digitization performed using image processing techniques. Dwell positions are placed based on applicator digitization and source dwell times are determined via inverse optimization. All information is stored as RT-files. The final plan is able to be modified as needed prior to a QA check where geometric and dosimetric parameters are verified to meet clinical requirements. We found that the automatic digitization was successfully completed with error within 1 mm compared to manual digitization. The AutoBrachy system was able to create a treatment plan within 4 minutes for all applicator types and create a more comprehensive QA check than performed manually. Work is ongoing to create additional applicator-specific treatment planning and QA modules.

THU - G11 3D-Printed Graphene/Polymer Structures for Electron-Tunneling Based Devices

Discipline: Engineering
Subdiscipline: Engineering (general)

Deisy Arrington*, *University of Illinois at Chicago* and Vikas Berry, *University of Illinois at Chicago*

Abstract: 3D printing of electronic materials is expected to have important consequences towards the mission of 'on-demand' device fabrication. However, this requires an understanding of the electronic transport in such structures. Here we show controlled nozzle-extrusion based 3D printing of a nano-composite of graphene/polylactic acid enabling the fabrication of a tensile gauge functioning via the readjustment of the electron-tunneling barrier width between conductive graphene-centers. The electronic transport in the graphene/polymer 3D printed structure exhibited a transport-barrier of 0.15 meV and a tunneling width of 0.79 – 0.95 nm (Fowler Nordheim electron tunneling) with graphene centers having a carrier concentration of 2.66 *1012/cm3. Furthermore, a mechanical strain that increases the electron-tunneling width between graphene nanostructures (~10.5 nm) by only 0.16 Angstrom, reduces the electron flux by 1 e/s/nm2 (from 566 e/s to 537 e/s) through the polylactic acid junctions in the 3D-printed heterostructure. We envision that the proposed electron-tunneling model for conductive 3D-printed structures with thermal expansion and external strain, will lead to an evolution in design of next-generation of 'on-demand' printed electronic and electromechanical devices.

THU - G12 Evaluating Alternative Strategies to Reduce Greenhouse Gas Emissions

Discipline: Engineering
Subdiscipline: Other Engineering

Mark Temis Lozano*, *University of California, Davis* and Alissa Kendall, *University of California, Davis*

Abstract: California's landmark 2006 Climate Change Solutions Act (Assembly Bill 32) tasked many government entities with reducing greenhouse gas (GHG) emissions to 1990 levels by 2020, and 80% below 1990 levels by 2050. Identifying, quantifying, and then selecting among possible strategies to achieve GHG reductions is difficult, especially without a standardized approach for comparison. This study develops a GHG mitigation "supply curve" to support selection of the most cost-effective strategies by the California Department of Transportation (Caltrans) by undertaking the following process for each strategy: (1) quantify the net GHG emitted or avoided over a strategy's lifecycle, (2) consider the timing of changes in GHGs, (3) explore the process and difficulty of implementation, and (4) calculate the initial and lifecycle costs of the strategy. By combining time-adjusted lifecycle GHG reductions and costs, each strategy can be assigned an "emissions reductions per dollar" value by which the strategies can be ordered to determine which of them achieve the biggest "bang for the buck". This study applies the above methodology to various mitigation strategies that could be implemented by Caltrans, including alternative fuel technology for the Caltrans fleet and installing solar and wind energy technologies within the state highway network. The strategies are presented as a supply curve by placing them in terms of the magnitude of reduction potential and their cost (initial and lifecycle); a color-coding scheme is used to communicate confidence in the calculated values, which is affected by the reliability of cost and emissions change information available, and technology maturity.

THU - G14 Fire Activity in Central Amazonia and the Consequences of Smoke Transport for Air Quality and Climate across South America

Discipline: Geoscience
Subdiscipline: Earth Science

Eimy Bonilla*, *Harvard University*; Igor Ribeiro, *National Institute of Amazonian Research and University of Amazonas State*; Loretta Mickley, *Harvard University*; Daniel Cusworth, *NASA Jet Propulsion Laboratory*; Suzane de Sá, *McKinsey & Company*; Taylor Jones, *Harvard University* and Scot Martin, *Harvard University*

Abstract: The Amazon Basin lost 15% of its forest from 1976-2010, and much of that loss occurred by burning. Such rapid deforestation has implications for rainforest composition, biodiversity, human health, and climate. Forest fragmentation has led to drier vegetation and soil, making the region even more susceptible to ignition. We hypothesize that smoke particles from fires in the Amazon Basin are transported across South America, degrading air quality and perturbing regional climate. For example, deposition of soot particles on the Andes may have contributed to the melting of mountain glaciers. We will investigate these hypotheses with a combination of observations and models. Observations include in-situ data from the GoAmazon campaign, Brazil, the Huancayo Observatory, and the National University in Cuzco, Peru, and ice core measurements from the Bolivian Andes. We simulate transport and fate of soot particles using Stochastic Time-Inverted Lagrangian Transport model (STILT) and the global atmospheric chemical transport model GEOS-Chem. Preliminary results from STILT indicate that air quality at a measurement site near Manaus, Brazil, is highly sensitive to biomass burning emissions 1,300 km upwind. Results from GEOS-Chem show strong enhancement of black carbon (BC) particles from Amazonian fires across Brazil and into the Bolivian Andes. We find BC concentrations in the Andes at values ~2-5 times greater than those observed over the Arctic, where BC has also been hypothesized to contribute to snow/ice melting. These results suggest that biomass burning in the Amazon Basin could have profound implications for both air quality and for regional hydrology and climate.

THU - G15 Estimating Methane Fluxes from California Dairy Farms Using Inverse Dispersion Modelling and the Eddy Covariance Method

Discipline: Geoscience
Subdiscipline: Other Geoscience

Valerie Carranza*, *University of California, Riverside*; Akula Venkatram, *University of California, Riverside*; Ray Anderson, *United States Department of Agriculture-Agricultural Research Station, US Salinity Laboratory*; Ranga Rajan Thiruvenkatachari, *University of California, Riverside*; Faraz Ahangar, *University of California, Riverside* and Francesca Hopkins, *University of California, Riverside*

Abstract: Dairies contribute close to 50% of methane (CH_4) emissions in California according to the greenhouse gas (GHG) emissions inventory. State legislation is in place to reduce GHG emissions—including CH_4—to 40% below 1990 levels by 2030. However, there is disagreement between atmospheric observations and statewide inventories over the magnitude of CH_4 emissions from dairy manure management, resulting in substantial uncertainty over emissions. Therefore, it is difficult to evaluate the effectiveness of CH_4 emission reduction strategies, such as digesters that convert CH_4 into fuel. To address these challenges, we collected atmospheric CH_4 measurements at two California dairies with contrasting manure management practices in the San Joaquin Valley (SJV) and in Moreno Valley. Two types of measurements were made: 1) 10-minute stationary CH_4 mole fractions were collected at multiple locations around manure lagoons paired with micrometeorological measurements and 2) vertical fluxes of CH_4 using eddy covariance that used a stationary open-path gas analyzer downwind from manure lagoons. A state-of-the-art dispersion model was used to estimate methane emissions from these lagoons by fitting model estimates of mole fractions and vertical fluxes to corresponding measurements. We produce 95% confidence intervals for the emission estimates by bootstrapping the residuals between model estimates and observations. We present CH_4 fluxes from measurements taken in Fall 2018 and Spring and Summer of 2019. We also compare CH_4 fluxes before and after digester installation at the SJV. The results from this study will improve CH_4 emission estimates from dairy manure management and evaluate the efficacy of mitigation efforts.

THU - G16 Development and Evaluation of Thymoquinone Loaded Polymeric Films for the Treatment and Management of Wounds

Discipline: Health
Subdiscipline: Medicine

Anika Alam*, *Rutgers, The State University of New Jersey*; Suneel Kumar, *Rutgers, The State University of New Jersey*; Francois Berthiaume, *Rutgers, The State University of New Jersey* and Bozena Michniak-Kohn, *Rutgers, The State University of New Jersey*

Abstract: The purpose of this study was to synthesize and characterize a biocompatible novel topical polymeric film system that has the potential to deliver antibacterial/anti-inflammatory agent thymoquinone (TQ) directly to the skin target site and that may be useful for the treatment and management of skin wounds. The polyvinyl pyrrolidone (PVP) matrix-type films containing TQ were prepared by the solvent casting method using dibutyl phthalate as a plasticizer and Azone (laurocapram) as a penetration enhancer. The developed films were evaluated for thickness, drug content uniformity, weight variation, flatness, folding endurance, percentage of moisture content and uptake which were found to 1.17 ± 0.04 mm, 100 ± 6.4 %, 82.04 ± 1.9 mg, 100%, 68 ± 2.38, 14.12 ± 0.42 %, and 2.26 ± 0.47 % respectively. FESEM photograph of the film showed polymer networks inside the film and a homogeneous dispersion of drug inside the polymer networks. *In vitro* skin permeation studies on human cadaver skin produced a mean flux of 3.4 $\mu g/cm^2/h$. *In vitro* scratch assay results revealed that 100 ng of TQ had significant wound closure activity in human dermal fibroblast cells compared to both control (p = 0.0014) and positive control (p = 0.0004). Using human keratinocyte cell line, 100 ng TQ group showed 85% wound closure activity at day six which was significantly higher (p = 0.0001) than the control group. In summary, TQ is effective for wound healing scratch assays and TQ/PVP films developed in this study have potential for the treatment and management of wounds.

THU - G17 Opioid/Substance Use in California American Indian/Alaska Native (AI/AN) Youth: Findings from a Statewide Needs Assessment

Discipline: Health
Subdiscipline: Public Health

Victoria Telles*, *University of Southern California*; Ingrid Zeledon, *University of Southern California*; Cynthia Begay, *University of Southern California*; Bryce Henderson, *University of Southern California* and Claradina Soto, *Univeristy of Southern California*

Abstract: Compared to other US ethnic/racial groups, American Indian and Alaska Native (AI/AN) youth are at the greatest risk for substance use disorder (SUD), particularly opioid use. The age of onset for substance use initiation is much younger than in previous years for AI/AN youth, therefore, understanding of the trends and patterns of opioid/substance use is particularly important. Our aims for this needs assessment study are to understand the perspective of AI/AN youth in urban and Tribal communities in CA about protective and risk factors to opioid/substance use, trends and patterns of use, and culturally relevant programs and services that are available and accessible.

Fourteen focus groups (N=94) were conducted with AI/AN youth living in Tribal and urban AI/AN communities throughout California to assess community/social norms around opioid/substance use, youth access to substances, risk and resilience factors related to substance use, service system needs and barriers, and recommendations to reduce opioid/substance use in the community.

Participants indicated an early age onset of drug use and discussed trends in accessibility and availability of drugs. Common themes that emerged included peer pressure, family issues, trauma, co-occuring mental health disorders, and post-injury opioid dependence.

There are cultural youth programs available for both Tribal and urban AI/AN youth, but additional prevention programs are needed to address issues of drug use and co-occurring disorders. Recommendations are provided to further address improving the well-being of AI/AN youth.

THU - G18 Irradiation Impacts Body Composition and Propagates Metabolic Disease in Nonhuman Primates

Discipline: Health
Subdiscipline: Public Health

Alistaire Ruggiero*, *Wake Forest University School of Medicine*; Nicole Bacarella, *Wake Forest University School of Medicine*; Chrissy Sherrill, *Wake Forest University School of Medicine*; Beth Uberseder, *Wake Forest University School of Medicine*; Matt Davis, *Wake Forest University School of Medicine* and Kylie Kavanagh, *Wake Forest University School of Medicine*

Abstract: A documented late effect of irradiation (IRRAD) exposure is type 2 diabetes mellitus (T2DM). T2DM is characterized by peripheral tissue insulin resistance, thus irradiation exposure suggests important changes to tissues such as adipose. Our prior work in IRRAD nonhuman primate skeletal muscle suggested that diabetogenesis post irradiation accompanied altered extracellular matrix and tissue capillarization. Here, we investigate changes in body composition, adipose character and metabolism in response to irradiation. We hypothesized that total body irradiation initiates lipodystrophy and disordered energy homeostasis. We evaluated changes in body composition, glycemic control, insulin responsiveness and basal lipolysis of subcutaneous adipose tissue in 16 male rhesus macaques two years post irradiation, 10 IRRAD and 6 controls (CTL). Body composition results show IRRAD have lower fat mass, lower fat-to-lean mass ratio and demonstrate stunted growth. Our metabolism-related findings show that the IRRAD had increased percent glycation of hemoglobin A1c, indicating poor glucose metabolism. Four IRRAD monkeys had values that define them as T2DM. Adipose tissue was insulin resistant as evidenced by reduced phosphorylation of the insulin receptor substrate 1 when challenged with insulin and had increased basal lipolysis despite having comparable insulin exposures to CTL. Our controlled study is the first to illustrate that sub-lethal irradiation exposures directly propagate metabolic disease in the absence of obesity in primates. We propose that irradiation exposure induces fibrosis and capillary rarefaction in adipose, which results in structural and functional changes that interfere with insulin receptor activation, highlighting the importance of peripheral tissues in whole body glucose metabolism.

THU - G19 Investigating the Basis for Substrate Specificity of DNA Glycosylase Endonuclease VIII-like 3 (NEIL3)

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alyssa Rodriguez*, *Vanderbilt University* and Brandt Eichman, *Vanderbilt University*

Abstract: DNA damage within a cell can cause damaging effects on genome stability if not properly corrected. Exogenous factors such as UV-light and environmental toxins, and endogenous factors including reactive metabolites and oxidative stress cause DNA damage in the form of modified DNA nucleobases. Base excision repair (BER) is the primary pathway to fix these lesions, and begins with recognition and excision of the damaged nucleobase by DNA glycosylase enzymes. The DNA glycosylase endonuclease VIII-like 3 (NEIL3) removes oxidized bases from single-stranded (ss) DNA, and also unhooks interstrand cross-links (ICLs), which covalently tether opposing DNA strands and block transcription and replication. Here we show that the conserved glycosylase domain (GD) has specificity for lesions at specific branched structures present at stalled replication forks. In addition to the GD, NEIL3 contains two GRF-type zinc finger (GRF-ZF) motifs absent in other NEIL paralogs, although the role of the GRF-ZFs are unknown. We show using fluorescence anisotropy and electrophoretic mobility shift assays that the GRF-ZFs bind specifically to ssDNA with low nM affinity and inhibit base excision activity of the NEIL3-GD *in trans*. DNA binding residues identified from other GRF-ZFs, abrogates DNA binding. These results begin to shed light onto the domain functions and substrate specificity of NEIL3.

THU - G20 Trade-Offs with Under-Actuated and Fully-Actuated Animal Flight Control Systems

Discipline: Life Sciences
Subdiscipline: Biology (general)

Jorge Bustamante*, *University of Washington* and Thomas Daniel, *University of Washington*

Abstract: Animals use a multitude of actuators simultaneously to coordinate and control complex movement and manipulation tasks. These movements are often over-actuated (having more actuators than necessary to perform a given task), which can potentially yield better control. In some instances, traditional engineered systems are often fully-actuated (having as many actuators as degrees of freedom). Yet in other systems, number of actuators is less than the degrees of freedom associated with the system: such systems are under-actuated. In insect flight, weight is a premium and muscles are the dominate contributor. Thus, strategies that permit flight control with fewer actuators can lead to lower weight, helping address the classic size, weight, and power challenge of flight. To explore the control consequences of actuation architecture, I developed a computational model of the dynamics for flying insects. The model is inspired by insect flight control and includes biomechanical properties, aerodynamic forces, as well as muscle and wing forces leading to body deformations. I use this approach to assess the trade-offs of utilizing under-actuated systems when compared to fully-actuated systems. Simulation results indicate the under-actuated model yields instabilities with higher incidence than the fully-actuated model. This suggests that under-actuated systems, may require more sensing and processing to perform the same task. Concepts from this work can help understand constraints on flight and body size as well as help guide development of micro-air vehicles.

THU - G21 The α-Arrestin ARRDC3 Regulates GPCR Activation of the Hippo Pathway in Invasive Breast Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Aleena Arakaki*, *University of California, San Diego*; Wen-An Pan, *University of California, San Diego*; Helen Wedegaertner, *University of California, San Diego* and JoAnn Trejo, *University of California, San Diego*

Abstract: G protein-coupled receptors (GPCRs) regulate the Hippo pathway, a critical mediator of tumorigenesis and cancer progression which lacks effective inhibitors. Although GPCRs are upstream therapeutic targets for cancer and highly druggable, there are currently no FDA-approved drugs targeting GPCRs for cancer. Protease-activated receptor-1 (PAR1) is a GPCR that activates the Hippo pathway and promotes breast cancer progression. PAR1 is overexpressed in breast cancer patient tissue biopsies and in breast carcinoma cell lines, and correlates with increased metastasis and poor prognosis. PAR1 overexpression results from defective lysosomal trafficking and leads to persistent signaling. We recently showed that expression of arrestin domain containing protein-3 (ARRDC3), a tumor suppressor, is reduced or lost in highly aggressive triple-negative breast carcinoma and results in aberrant PAR1 trafficking. The dysregulation of PAR1 trafficking due to loss of ARRDC3 expression results in persistent signaling and promotes breast cancer invasion. However, the mechanism by which ARRDC3 regulates PAR1-stimulated Hippo signaling to promote breast cancer metastasis remains unknown. Here, we show that ARRDC3 regulates GPCR activation of the Hippo pathway in triple-negative breast cancer, where the transcriptional co-activators YAP and TAZ display distinct functions. ARRDC3 re-expression in invasive breast carcinoma cells attenuates PAR1-stimulated Hippo signaling and invasion that is mediated by TAZ but not YAP. Furthermore, siRNA-targeted depletion of TAZ, but not YAP inhibits PAR1-induced Hippo signaling and invasion. An understanding of the mechanisms by which the Hippo pathway is regulated by GPCRs may lead to new potential therapeutic targets for the treatment or prevention of metastatic breast cancer.

THU - G22 Investigating the Immunomodulatory Effects of Exosomes Derived from Cancer Stem Cells

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Shannon Clayton*, *California State University, Sacramento*; Joehleen Archard, *University of California, Davis* and Johnathon Anderson, *University of California Davis*

Abstract: Head and neck squamous cell carcinoma (HNSCC) is highly recurrent and facilitates a tumor microenvironment promoting tumor growth, drug resistance, angiogenesis, and immune evasion through the secretion of exosomes. HNSCC exosomes induce differentiation of Regulatory T cells (T_{regs}) to promote a pro-tumorigenic environment. Additionally, Cancer stem cells (CSC), the drivers of reoccurrence, have been demonstrated to induce T_{regs}. However, the mechanisms underlying how HNSCC evades the immune system is to be determined and investigations of exosomes have been on heterogenous tumor populations. We hypothesize that HNSCC's immunoregulatory properties are partly mediated by the induction of Tregs by exosomes secreted from CSCs. We investigated the immunoregulatory properties of HNSCC CSC cell lines by investigating the anti-inflammatory and Treg-induction properties of their derived exosomes. We generated CSC lines by subculturing distinct subpopulations of cells isolated from tumor tissue and verified CSC surface markers via flow cytometry. We isolated exosomes from the CSC lines and perform quantitative liquid chromatography-mass spectrometry, followed by bioinformatic analysis, to characterize the proteomic profile of the CSC-derived exosomes. We evaluated the immunoregulatory properties of CSC-derived exosomes by stimulating an inflammatory response and determined whether CSC-exosomes can induce Tregs. Through understanding the mechanisms by which CSC's evade the immune system, we can discover new druggable targets to develop novel immunotherapies to eliminate CSCs that lead to tumor reoccurrence. We have generated 6 HNSCC tumor CSC lines and demonstrated that they are >97% positive for CSC markers, CD44, CD90, and nestin.

THU - G23 Rb-Deficient Cells Are Sensitive to Epigenetic Regulation

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Luis Gregory Gutierrez-Zamalloa*, *Worcester Polytechnic Institute*; Margaret Pruitt, *Worcester Polytechnic Institute* and Amity Manning, *Worcester Polytechnic Institute*

Abstract: Loss or functional inactivation of the retinoblastoma protein (Rb) tumor suppressor promotes DNA damage and compromises mitotic chromosome segregation. Although epigenetic modifications are best studied for their impact in gene expression, they are also important in the organization of mitotic chromosomes. We hypothesized that Rb-deficient cells may be very sensitive to epigenetic regulators. Hence, we performed an imaging-based screen of 96 small molecules that target epigenetic marks and identified those that synergized with Rb to promote DNA damage and decreased cell viability. Using mitochondrial activity as a readout of cell viability, my work has confirmed that loss of Rb sensitizes cells to a variety of epigenetic regulators, leading to decreased cell viability. Ongoing work will further define the mitotic sensitivities of Rb deficient cells and test if they represent a feature of Rb deficient cancers that can be exploited therapeutically.

THU - G24 Identification of Protein Biomarkers of Relapse in a Relapsing-Remitting Mouse Model of Multiple Sclerosis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Carol Chase Huizar*, *University of Texas at San Antonio* and Thomas Forsthuber, *University of Texas at San Antonio*

Abstract: Multiple sclerosis (MS) is a debilitating and unpredictable inflammatory disease of the central nervous system (CNS) that affects over 1 million Americans. Approximately 85 percent of individuals newly diagnosed with MS have the relapsing-remitting form of the disease (RRMS) characterized by attacks of neurologic symptoms that are both unpredictable in occurrence and duration. The lack of markers that predict the occurrence of MS relapses hinders the ability for proactive therapeutic intervention. To address the urgent need for biomarkers of relapse we investigated proteome changes over the disease course of relapsing-remitting experimental autoimmune encephalomyelitis (RR-EAE) in SJL mice as a preclinical model of the disease using a high-throughput quantitative proteomic technique. In this study, we utilized this established proteomic technique as well as bioinformatics tools to prioritize key proteins that were expressed differentially at different stages of disease including remission and relapse. Principal component analysis of protein expression shows that the remission and relapse phases of disease cluster separately, indicating distinguishable variation between the two disease states. Importantly, statistical testing identified proteins with differential expression in the CNS at different stages of disease, several of which are CNS specific. We are seeking to detect corollary changes in these CNS-specific proteins in the serum, pointing to a minimally invasive means of monitoring disease progress and measuring drug efficacy. Our studies will provide proof-of-concept for identifying homologous human biomarkers to guide treatment in individual patients. Furthermore, our results may provide insights into mechanisms that contribute to disease pathology and offer additional therapeutic targets.

THU - G25 Replacing Endogenous Microglia with Exogenous Myeloid Cells Via Bone Marrow Transplantation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

L. Angel Ayala*, *San Francisco State University*; Yohei Shibuya, *Department of Pathology, Institute of Stem Cell Biology and Regenerative Medicine, Stanford University School of Medicine* and Marius Wernig, *Department of Pathology, Institute of Stem Cell Biology and Regenerative Medicine, Stanford University School of Medicine*

Abstract: One major challenge to treating neurological disorders is the blood-brain barrier (BBB) which separates the central nervous system (CNS) from circulating blood. Drug manufacturers have struggled to develop small molecules that can penetrate the BBB, which has lead to a lack of available treatments for neurological disorders. Microglia are CNS-resident myeloid cells that are a developmentally distinct population from circulating myeloid cells. Under normal conditions circulating myeloid cells do not enter the brain. However, when there is low abundance of microglia, circulating myeloid cells have been observed to cross the BBB and enter the CNS. Upon entering the CNS, circulating myeloid cells will differentiate into microglia-like cells. Bone marrow (BM) transplantation has been shown to allow for BM derived myeloid cells to populate the CNS and differentiate into microglia-like cells. However, it is inefficient and the protocol needs to be improved to demonstrate the viability of microglia replacement as a potential therapeutic for neurological disorders. In our study, we optimized a BMT protocol that established a speedy and robust population of BM derived myeloid cells in the CNS. In our optimized protocol we paired bone marrow transplantation with PLX5622 which is an inhibitor of colony-stimulating factor-1 receptor and this led to a high chimerism of donor derived cells in a (host) mouse brain. This optimized protocol offers a promising tool to treat neurological disorders by providing a method to deliver therapeutic genes to the CNS.

THU - G26 The Oxidoreductase FSP1 Acts in Parallel to GPX4 to Inhibit Ferroptosis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Joseph Hendricks*, *University of California, Berkeley*; Kirill Bersuker, *University of California, Berkeley*; Zhipeng Li, *University of California, Berkeley*; Melissa Roberts, *University of California, Berkeley* and James Olzmann, *University of California, Berkeley*

Abstract: Ferroptosis is an iron-dependent form of regulated cell death caused by the accumulation of lipid peroxides. Glutathione peroxidase 4 (GPX4) is a glutathione-dependent lipid hydroperoxidase that prevents ferroptosis by converting lipid hydroperoxides into non-toxic lipid alcohols. Induction of ferroptosis by inhibition of GPX4 has emerged as a therapeutic strategy to trigger cancer cell death, yet sensitivity to GPX4 inhibitors varies across cell lines, suggesting additional factors may regulate resistance to ferroptosis. To identify resistance mechanisms that function together with GPX4, we employed a synthetic lethal CRISPR/Cas9 screen to identify genes that confer resistance to the GPX4 inhibitor RSL3. We identified the oxidoreductase ferroptosis suppressor protein 1 (FSP1) as a potent ferroptosis suppressor in cancer cells. We find that high expression of FSP1 positively correlates with resistance to RSL3-induced ferroptosis. In addition, we show that overexpression of FSP1 in low expressing lung cancer cells is sufficient to provide resistance, and knockout of FSP1 sensitizes cancer cells to ferroptosis in cell culture. Finally, we demonstrate that mouse tumor xenografts that lack both FSP1 and GPX4 show reduced growth rates compared to tumors lacking GPX4 alone. Our cell-based assays and *in vivo* mouse models suggest FSP1 is a vital component of a lipophilic antioxidant system that acts in parallel to the canonical GPX4 pathway to prevent ferroptosis. These findings reveal a novel ferroptosis suppressing pathway that furthers our understanding of cancer cell resistance to ferroptosis and suggests that pharmacological inhibition of FSP1 may provide an effective strategy to sensitize cells to ferroptosis-inducing chemotherapeutics.

THU - G27 Regulation of the *C. Elegans* Molt By Conserved Nuclear Hormone Receptors, NHR-23 and NHR-85

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Londen Johnson*, *University of California, Santa Cruz* and Jordan Ward, *University of California, Santa Cruz*

Abstract: Conservation among nematode molting factors makes *Caenorhabditis elegans,* C. elegans, an important model for studying molting in the parasitic nematode, *Brugia* malayi. During development, nematodes undergo four periodic larval stages between which they molt shedding their existing exoskeleton, also known as a cuticle, and grow a new one. The majority of *C. elegans* molting genes are conserved in the *Brugia malayi* genome, including *nhr-23* and *nhr-85*, which suggests a conserved molting mechanism. Additionally, loss of *nhr-23* and *nhr-85* in *C. elegans* has been found to cause developmental arrest and lethality resulting from molting defects. Despite being essential for molting, little is known about the protein expression and interactions of NHR-23 and NHR-85 in *C. elegans*. To understand the regulatory roles of NHR-23 and NHR-85 we have determined their expression pattern throughout the *C. elegans* molt using fluorescent tags. Additionally, we have determined key points during the *C. elegans* molts where NHR-23 activity is essential. Currently we are identifying phenotypes resulting from the loss of NHR-85 using an Auxin Inducible Degradation system that allows for temporal and tissue specific protein degradation. Our findings will provide insight into the nematode molt, an essential developmental process, as well as the unknown roles of conserved transcriptional regulators. This research explores molting as model for development, expanding our knowledge on the regulatory gene networks which regulate essential developmental processes. Future work will be aimed at identifying potential drug candidates in *Brugia malayi*.

THU - G29 Applying Biophysical Approaches to Understand the Cellular Mechanics of Oocytes and Early Embryos

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Florencia Visconti*, *New Mexico State University*; Clara Ross, *New Mexico State University*; Debadrita Pal, *New Mexico State University*; Charles Shuster, *New Mexico State University* and John Henson, *Dickinson College*

Abstract: In motile cells, actin networks are organized such that branched actin networks (nucleated by Arp2/3) are found at the leading edge of the cell whereas linear (and contractile) actin networks are found in the rear. In large spherical cells, both branched and unbranched actin is enriched at the cell cortex, and in contrast to crawling cells, much less is known about how these differentially regulated networks contribute to overall cellular mechanics. We hypothesize that branched actin may act as a break on global myosin II contractility in oocytes and early embryonic blastomeres. Toward these ends, we are applying live cell imaging and MicroPipette Aspiration (MPA) in echinoderm oocytes and early embryos. Imaging of oocytes expressing GFP-Lifeact or a Rho biosensor revealed a transient elaboration of actin-based projections and a general enrichment of cortical actin immediately post-stimulation with hormone that subsided as the oocyte entered meiosis. Cortical tension (as measured by MPA) revealed that prior to hormone activation, cortical tension is high, but drops as the oocyte enters meiosis I. This is the inverse of what happens in zygotes, where cortical tension increases as the embryo progresses through mitosis. Phosphatidylinositol-3-Kinase (PI3K) activity is required for meiotic resumption, and interestingly, inhibition of PI3K blocked the normal decreases in both Rho activity and cortical tension. Current efforts are focused on understanding the possible negative feedback loop involving PI3K activity and whether branched actin networks play a role in regulating cortical mechanics during meiosis and mitosis.

THU - G30 The Aging Gene p38 MAPK Regulates Collagen IV in *Drosophila Melanogaster*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Briseida Oceguera Perez*, *Illinois State University*; Basheer Becerra, *Illinois State University*; Josh R. Hill, *Illinois State University* and Alysia Vrailas Mortimer, *Illinois State University*

Abstract: Aging is an expected and inevitable process that affects organisms almost universally. It is characterized as a loss of stress resistance, degeneration of tissues, and decline in motor function that happens gradually across the lifespan. As organisms age, they become susceptible to diseases (e.g. neurodegenerative and dystrophic conditions) that are not a normal aspect of aging. Discerning the difference between normal and aberrant aging states will give insight into the mechanisms behind the progressive dysfunction shared among living organisms. Previous work in our lab has shown that the aging gene p38 MAPK in *Drosophila melanogaster* plays a significant role in the aging process through its downstream effects on nuclear and cytoplasmic targets, specifically through the regulation of protein turnover and response to oxidative stress. Through a proteomics analysis of p38Kb mutants across different ages, we found that levels of the extracellular matrix protein collagen IV varied significantly with p38Kb manipulation. We will explore the nature of this relationship and determine if loss of p38Kb results in aggregation of collagen IV, a loss of muscle structure, or impairment of collagen IV trafficking across the plasma membrane. Additionally, we will determine if loss of collagen IV results in increased oxidative stress and a decrease in lifespan.

THU - G31 Ethanol Perturbs Normal Skeletal Patterning in Sea Urchin Embryo Development.

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Nahomie Rodriguez-Sastre*, *Boston University*; Nicholas Shapiro, *Boston University*; Monique Peyreau, *Boston University*; Andrea E. Correa, *Universidad de Puerto Rico-Aguadilla*; Kristin Dionne, *Boston University* and Cynthia Bradham, *Boston University*

Abstract: During skeletal development in sea urchin embryos, epithelial tissue communicates with and controls mesenchyme behaviors including cell migration, positioning, and diversification. The sea urchin larval skeleton provides a simple model to study pattern formation, where the primary mesenchyme cells (PMCs) receive cues from the adjacent ectoderm that dictate the spatial pattern the skeleton. Fetal Alcohol Syndrome (FAS) is caused by alcohol exposure during pregnancy. FAS leads to morphological and neural defects in vertebrates and mammals. We observe similar morphological defects in ethanol-exposed sea urchin embryos, including midline and rotational defects in skeletal patterning. These skeletal defects are reminiscent of the facial defects observed in children with FAS. In addition, PMCs in ethanol-exposed embryos fail to migrate properly which likely contributes to skeletal defects. We observe that the skeletal patterning defects induced by ethanol are mimicked by treatment with acetaldehyde, implying that ethanol mediates its toxic effects via oxidative stress, similar to its effects in mammals. Taken together, our data show that ethanol treatment is sufficient to perturb PMC migration and skeletal patterning in sea urchin embryos and indicate that ethanol functions via an oxidative mechanism. This suggests that sea urchins provide a novel model for FAS that offers morphological simplicity and ready access to systems-level measures.

THU - G32 Cold-Inducible RNA-Binding Protein May Regulate Gonadal Development in the Red-Eared Slider Turtle

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Rosario Marroquin-Flores*, *Illinois State University*; Nathan Mortimer, *Illinois State University*; Ryan Paitz, *Illinois State University* and Rachel Bowden, *Illinois State University*

Abstract: Heat shock proteins play a vital role in embryonic development. Cold-inducible RNA-binding protein (Cirp) is a heat shock protein with a potential regulatory role in the sex-determining pathway. The red-eared slider turtle (*Trachemys scripta elegans*) exhibits temperature-dependent sex determination (TSD), where incubation temperatures trigger gonadal differentiation. During the thermosensitive period, embryos respond to relatively cooler or warmer temperatures to initiate male or female development, respectively. In *T. s. elegans*, Cirp is upregulated prior to estrogen-inducing transcripts at female-producing temperatures. RNA-binding proteins can coordinate splicing events of their target transcripts, and thus, have the capacity to regulate gene expression. We hypothesize that Cirp plays a regulatory role in gonadogenesis by impacting the expression of sex-determining genes. To test this, *T. s. elegans* eggs will be incubated under fluctuating temperature treatments to mimic an incubating nest and will either be held under conditions to produce males, or will be given a 5-day simulated heatwave to induce female development. Gonads from embryos experiencing both treatments will be dissected for quantitative PCR (qPCR) and RNAseq to measure Cirp expression under male- and female-producing incubation conditions and to determine potential Cirp targets by analysis of RNA transcript reads. Preliminary qPCR results suggest that Cirp is upregulated within the first five days of a shift to female-producing temperatures. Our approach will help us understand how Cirp responds to fluctuating temperature treatments and if Cirp targets sex-determining genes in *T. s. elegans.*

THU - G33 A New Statistic D^+ to Detect Local Gene Flow

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Lesly Lopez*, *University of California, Merced*; Diego Ortega-Del Vecchyo, *National Autonomous University of Mexico*; Emily Jane McTavish, *University of California, Merced* and Emilia Huerta-Sánchez, *Brown University*

Abstract: Introgression is a common phenomenon that can reveal the shared evolutionary history between species across taxa. Existing statistical methods such as Patterson's D statistic can detect introgression by measuring shared excess mutations between populations. The D statistic is effective genome wide but gives spurious inferences of local introgression when applied to small regions in the genome. In these small regions D can take extreme values and can also be undefined because there is a low probability of finding shared derived alleles between pairs of populations. We propose a new statistic $D+$ that can identify introgressed loci. Introgressed haplotypes are inherited in chunks that contain both ancestral and derived alleles. We increased the number of informative sites per region by incorporating both shared derived and ancestral alleles to calculate $D+$. To test the robustness of $D+$ we ran coalescent simulations following the Out of Africa model with Neanderthal introgression into the non-African population. We calculated the power of D and $D+$ using the simulated genetic variants and found that $D+$ has more power than D to identify introgressed loci.

THU - G34 Trabecular Bone in the Ankle of a Rapid-Growing Avian Bipedal Model in Response to Locomotor Inactivity

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

America Guerra*, *Pennsylvania State University*; Nicholas Stephens, *Pennsylvania State University*; Suzanne Cox, *Pennsylvania State University*; Matthew Salzano, *Pennsylvania State University*; Stephen Piazza, *Pennsylvania State University*; Jonas Rubenson, *Pennsylvania State University* and Timothy Ryan, *Pennsylvania State University*

Abstract: Under the framework of bone functional adaptation, bone structure is predicted to reflect the loads experienced during an animal's lifetime. This framework is often used in paleoanthropology to reconstruct behavior in the fossil record. However, the precise relationship between skeletal loading and bone structure remains unclear. Here, we provide a controlled experimental study for how load stimulus alters bone structure.

We predict that trabecular structure will directly reflect differences in locomotor (in)activity. To test this, juvenile guinea fowl (*Numidia meleagris)* were exercised over a period of 24 weeks and separated into three groups: an exercise "free range" group (n=8), a sedentary group (n=8), and a sedentary group with additional induced paralysis of the gastrocnemius via botulinum toxin injection (n=8). The exercised group was in a large pen that allowed for running and high-power perch jumps while the sedentary groups were in small pens that restricted movement to solely standing or walking. The birds were then sacrificed, the tarsometatarsal joint was microCT scanned, and trabecular architecture of the entire joint was characterized. Bone volume fraction (BV/TV), degree of anisotropy (DA), trabecular spacing (Tb.Sp), trabecular number (Tb.N), and trabecular thickness (Tb.Th) was quantified in all three groups to determine differences in trabecular structure due to locomotor behavior. Preliminary results suggest a modest effect of activity with the free-range group displaying more robust bone than the more sedentary groups. This experiment serves as a proxy for understanding bone functional adaptation in other bipedal animals, such as extant and extinct hominins.

THU - G35 The Impact of Modern Human Specific Sites on Human Phenotypes

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Christopher Robles*, *University of California, Los Angeles* and Sriram Sankararaman, *University of California, Los Angeles*

Abstract: Uncovering genetic changes that make anatomically modern humans "unique" is critical for a comprehensive understanding of human evolution. By analyzing genome sequences from our closest evolutionary relatives, Neanderthals and Denisovans, we can functionally characterize these genetic changes. Towards this end, we identified 321,821 mutations that are nearly fixed for the derived allele in African individuals from the 1000 Genomes project (>90% derived allele frequency) but are absent in at least some of the deeply sequenced Altai Neanderthal or Denisovan genomes. To understand the phenotypic impact of these fixed derived mutations (FDMs), we leverage the observation that interbreeding with Neanderthals likely re-introduced the ancestral allele at a number of these sites. We estimate that ~33% of FDMs are polymorphic in European populations so that their phenotypic impact can be analyzed by genotyping these mutations in large cohorts with phenotypic information.

We analyzed ~114,000 FDMs across 107 phenotypes that include anthropometric, blood, bone density, and disease related traits measured in ~475,000 individuals of European ancestry in the UK Biobank dataset. We discovered 3266 independent associations of FDMs in all 107 of our phenotypes with p-values that pass a threshold accounting for both FDM number and phenotypes tested. Controlling for frequencies and linkage disequilibrium patterns at these variants, we find the contribution of FDMs to phenotypic variation is significantly depleted for several traits including those related to body mass and bone density. These results direct us towards genetic and phenotypic changes important for contemporary human biology since diverging from archaic humans.

THU - G36 Molecular Karyotyping of Chromosomal Inversion 2Rb in *Anopheles Gambiae* and *Anopheles Coluzzii.*

Discipline: Life Sciences
Subdiscipline: Genetics

Raquel Montañez González*, *University of Notre Dame*; R. Rebecca Love, *University of Notre Dame*; Verena Pichler, *Sapienza University of Rome*; Maria Calzetta, *Sapienza University of Rome*; Marco Pombi, *Sapienza University of Rome*; Beniamino Caputo, *Sapienza University of Rome*; Alessandra Dellatorre, *Sapienza University of Rome* and Nora J. Besansky, *University of Notre Dame*

Abstract: The Afrotropical mosquitoes *Anopheles gambiae* and *An. coluzzii* are the deadliest vectors of human malaria. Types of structural chromosomal mutations known as chromosomal inversions are very common in these species, and they appear to have a direct consequence on mosquito behavior and physiology. Current methods of microscopical karyotyping are time consuming, prone to human error, and feasible only for female mosquitoes at one particular developmental stage—and only if they are properly preserved. Failure to account for inversion status is a barrier to further knowledge of important vector traits (e.g. biting and resting behavior, seasonality, aridity tolerance and *Plasmodium* infection rates), which can be influenced by inversions. To overcome this limitation, we exploited genome sequences of cytogenetically karyotyped specimens to identify tag SNPs (Single Nucleotide Polymorphisms) highly predictive of inversion status. Using these SNPs, three low cost PCR-RFLP (Polymerase Chain Reaction-Restriction Fragment Length Polymorphism) diagnostic assays were developed and then validated on cytogenetically karyotyped population samples field collected from eight different African countries. One assay showed a high concordance rate of 95% between PCR-RFLP and cytogenetic approaches in both *An. gambiae* (N=437) and *An. coluzzii* (N=133), and the other two assays agreed well (93%-97%) on either one or the other species only. The combination of the two most specific assays provides a useful diagnostic for inversion 2Rb in *An. gambiae* and *An. coluzzii* with a concordance rate of >96% with the 'gold standard' cytogenetic karyotyping method and opens the way to extensive assessment of the adaptive role of this inversion.

THU - G37 Features of Histone H2A Variant HIS-35 Incorporation before and after Fertilization

Discipline: Life Sciences
Subdiscipline: Genetics

Wesley Huang*, *San Francisco State University*; Criszel Corpuz, *San Francisco State University*; Meghnan Shorrock, *San Francisco State University* and Diana Chu, *San Francisco State University*

Abstract: Genetic material inheritance requires proper germ cell and embryo development. These processes are regulated by chromatin remodelers such as histone variant. Histone variants are proteins that rearrange DNA structure to allow for tissue specific gene regulation. The remodeling of germ cell chromatin upon fertilization is crucial to form the zygotic epigenome. In *C. elegans*, 3 histone H2A variants were identified, HTZ-1 HTAS-1, and HIS-35. Studies revealed parent derived HTZ-1 is removed from the maternal and paternal genome after fertilization. However, sperm-specific HTAS-1 retains in the paternal genome. These results suggest parent derived H2A variants may epigenetically establish the zygotic genome. However, little is known about how HIS-35 participate in this process. Preliminary *his-35*mutant studies revealed a 35% reduction in progeny compared to wildtype. Immunostaining also showed HIS-35 incorporation in germline and fertilized embryos, suggesting roles on fertility and embryogenesis. I hypothesize that HIS-35 assist in germ cell development and remodeling of embryo chromatin. We tracked HIS-35 incorporation throughout germline progression. Result showed that HIS-35 colocalizes with histone marks of active transcription but not with repressive mark. This indicates HIS-35's involvement in upregulating germline specific genes needed for germ cell development. We also tracked maternally derived (matHIS-35) and paternally derived HIS-35 (patHIS-35) during embryogenesis. Upon fertilization, matHIS-35 retains in maternal genome and incorporates into paternal genome. In contrast, patHIS-35 is removed from paternal genome and is not detected until late stage embryo suggesting parent specific remodeling events. This study demonstrates distinct epigenetic roles between parent derived histone variants.

THU - G38 Dynamics of Gene Expression in Single Root Cells of *Arabidopsis thaliana*

Discipline: Life Sciences
Subdiscipline: Genetics

Ken Jean-Baptiste*, *University of Washington School of Medicine*; Jose McFaline-Figueroa, *University of Washington School of Medicine*; Cristina Madeira Alexandre, *University of Washington School of Medicine*; Michael Dorrity, *University of Washington School of Medicine*; Lauren Saunders, *University of Washington School of Medicine*; Kerry Bubb, *University of Washington School of Medicine*; Cole Trapnell, *University of Washington School of Medicine*; Stanley Fields, *University of Washington School of Medicine*; Christine Queitsch, *University of Washington School of Medicine* and Josh Cuperus, *University of Washington School of Medicine*

Abstract: Single-cell RNA-seq can yield high-resolution cell-type-specific expression signatures that reveal new cell types and the developmental trajectories of cell lineages. Here, we apply this approach to A. thaliana root cells to capture gene expression in 3,121 root cells. We used Monocle 3, ordering single-cell transcriptomes in an unsupervised manner reconstructing single-cell developmental trajectories. We identify hundreds of genes with cell-type-specific expression, with pseudotime analysis of several cell lineages revealing both known and novel genes that are expressed along a developmental trajectory. We identify transcription factor motifs that are enriched across development, together with the corresponding candidate transcription factors that likely drive the observed expression patterns. We assess and interpret changes in total RNA expression along developmental trajectories and show that trajectory branch points mark developmental decisions. Finally, by applying heat stress to whole seedlings, we address the longstanding question of possible heterogeneity among cell types in the response to an abiotic stress. Although the response of canonical heat shock genes dominates expression across cell types, subtle but significant differences in other genes can be detected among cell types. Taken together, our results demonstrate that single-cell transcriptomics holds promise for studying plant development and plant physiology with unprecedented resolution.

THU - G39 ***Vibrio Cholerae*** **Interaction with the Commensal Fungus** ***Candida Albicans***

Discipline: Life Sciences
Subdiscipline: Microbiology

Mylea A. Echazarreta*, *South Texas Center for Emerging Infectious Diseases, University of Texas at San Antonio*; Daniel Montelongo-Jauregui, *South Texas Center for Emerging Infectious Diseases, University of Texas at San Antonio*; Stephen P. Saville, *South Texas Center for Emerging Infectious Diseases, University of Texas at San Antonio*; Jose L. Lopez-Ribot, *South Texas Center for Emerging Infectious Diseases, University of Texas at San Antonio* and Karl E. Klose, *South Texas Center for Emerging Infectious Diseases, University of Texas at San Antonio*

Abstract: *Vibrio cholerae* is the etiological agent of the enteric disease cholera, which can be fatal. In the aquatic environment, *V. cholerae* colonizes chitinous surfaces, which activates Type VI Secretion (T6S) and induces natural competence. Chitin is also present in the cell wall of fungi, and commensal fungi of the human GI tract are likely to interact with *V. cholerae* during infection. *Candida albicans* is an opportunistic fungal pathogen that is commonly found as a commensal in the human GI tract. Invasive *C. albicans* infections can be fatal, but require *Candida* to transition from a yeast to hyphae form, which is also required for biofilm formation. We have found that *V. cholerae* forms mixed biofilms with *C. albicans in vitro* and reduces *C. albicans* biomass. Imaging flow cytometry and electron microscopy have revealed a high affinity interaction between *V. cholerae* and *C. albicans*. Reduction of *C. albicans* biomass is apparently due to the ability of *V. cholerae* to inhibit *C. albicans* filamentation. *V. cholerae* can inhibit filamentation of *C. albicans* lacking *NRG1* or overexpressing *BRG1*, indicating that filamentation is blocked downstream of *BRG1* signaling. Mutations in chitin sensing (*tfoX*) and quorum sensing (*hapR*) regulators results in defects in *V. cholerae* inhibition of *C. albicans* biofilms. Our results suggest that *V. cholerae* at high cell density responds to the presence of chitin in the *C. albicans* cell wall and inhibits filamentation. Characterization of *V. cholerae-C. albicans* interactions will illuminate the influence of fungi within the GI tract on susceptibility to cholera.

THU - G40 **Restoration of Biofilm Formation in the Legume Symbiont** ***Sinorhizobium Meliloti*** **and Enhancement of Infection Efficiency**

Discipline: Life Sciences
Subdiscipline: Microbiology

Joseph Sapienza-Martinez*, *San Francisco State University* and Joseph Chen, *San Francisco State University, San Francisco*

Abstract: Bacteria possess the ability to colonize surfaces in multicellular aggregations known as biofilms. In agriculture, biofilms may prove advantageous to nitrogen-fixing rhizobia by enhancing infection efficiency during symbiosis with leguminous plant hosts. *Sinorhizobium meliloti* serves as our model for characterizing genes critical for biofilm formation and other phenotypic changes that influence host colonization. Previously, in *S. meliloti* laboratory strain Rm1021 we identified a nonsense mutation in the *podJ* gene, whose ortholog in *Calobacter crescentus* encodes a polarity factor required for the development of extracellular organelles, including the flagellum and adhesive holdfast. Correcting the mutation resulted in a strain (*podJ*$^+$) capable of producing a polar adhesin and forming robust biofilm. The *podJ*$^+$ strain appears to possess a competitive advantage over the parental Rm1021 strain when infecting *Medicago truncatula*. To identify additional factors that contribute to PodJ-dependent biofilm formation, we carried out a transposon mutagenesis screen. We found numerous genes that, when individually interrupted, hindered biofilm formation on abiotic surface: they include those involved in flagellar motility, exopolysaccharide synthesis, and signal transduction. Complementation analysis confirmed that the transposon insertions are solely responsible for the defects in biofilm formation. We are conducting further characterization of the mutants to determine how the various factors may influence different aspects of biofilm development. Future investigation will provide insight into the complex genetic circuitry that controls biofilm formation during symbiosis. Such insight may facilitate more widespread use of biological nitrogen fixation in crop production and reduce reliance on synthetic fertilizers that have negative ecological impacts.

THU - 133 **Glycosylation of Polycyclic Aromatic Hydrocarbons (PAHs) By UDP-Glycosyltransferase 3A2 (UGT3A2) in Tobacco Target Tissues**

Discipline: Life Sciences
Subdiscipline: Pharmacology

Ana Vergara*, *Washington State University*; Christy J. W. Watson, *Washington State University*; Gang Chen, *Washington State University* and Philip Lazarus, *Washington State University*

Abstract: The UDP-glycosyltransferase (UGT) family of enzymes play a key role in the detoxification of tobacco carcinogens. While the UGT 1As, 2As, and 2Bs are known to detoxify polycyclic aromatic hydrocarbons (PAHs) using UDP-glucuronic acid, the UGT3A subfamily has been understudied in the detoxification of PAHs. UGT3A2 is functionally distinct from other UGTs in that it uses UDP-glucose and UDP-xylose as cosubstrates, and previous studies have shown it is active against 1-hydroxypyrene (1-HP), a biomarker for PAH exposure. The purpose of the present study was to determine the kinetic parameters of UGT3A2 against PAHs and determine glycosylation in human tissues. Microsomes prepared from UGT3A2 overexpressing HEK293 cells exhibited glycosylation activity against PAHs including benzo[a]pyrene (B[a]P)-7,8-diol, B[a]P-9,10-diol, DB[a,l]P-11,12-diol, and 5-methylchrysene-1,2-diol with K_m’s ranging from 96 to 1250 µM using UDP-glucose. The K_m’s were significantly lower when using UDP-xylose with K_m’s ranging from 120 to 168 µM for the same substrates. To determine the physiological significance of sugar-dependent glycosylation, activity assays were performed in tissues where UGT3A2 is expressed using 1-HP as substrate. Using UDP-glucose as the cosubstrate, glycosylation rates of 3.5, 5.2, and 13 pmol·min^{-1}·mg^{-1} microsomal protein were observed for liver, intestine and kidney microsomes, respectively. The rates were higher using UDP-xylose, with rates of 22, 9.3, and 20 pmol·min^{-1}·mg^{-1} microsomal protein for liver, intestine and kidney, respectively. Liver exhibited the highest rate ratio for UDP-xylose/UDP-glucose. These data suggest that UGT3A2 plays an important role in the detoxification of PAHs in tobacco target tissues, with UDP-xylose as the preferred cosubstrate in tissues.

THU - 134 **Profiling Astrocyte-Specific Transcriptional Changes after Ischemic Stroke**

Discipline: Life Sciences
Subdiscipline: Neurosciences

Victoria Hernandez*, *Stanford School of Medicine*; Kendra Lechtenberg, *Stanford School of Medicine* and Marion Buckwalter, *Stanford School of Medicine*

Abstract: Ischemic stroke is a leading cause of death and long term disability. Neuroinflammation after stroke can significantly affect stroke outcomes, as it can induce tissue repair, but can also exacerbate cell death. After stroke, astrocytes enter a reactive phase of astrogliosis, which is characterized by astrocytic proliferation, formation of an astrocytic scar, and release of pro-inflammatory cytokines. However, the exact astrocytic signaling pathways regulating neuroinflammation after stroke are unresolved. A barrier to understanding this has been the challenge of parsing the astrocytic response from that of infiltrating inflammatory cell types in the brain after stroke. To address this, we used the RiboTag technique to obtain astrocyte-derived transcripts after stroke. By crossing the RiboTag and Aldh1l1-CreER mouse models, we expressed a hemagglutinin tag on ribosomes only in astrocytes, enabling immunoprecipitation of astrocytic ribosomes and isolation of actively translating astrocytic mRNA. Targeted gene expression analysis showed that astrocyte transcripts obtained from stroked mice (N=6) using this technique were highly significantly enriched in astrocyte-specific genes such as GFAP (19.66 fold higher) and de-enriched in characteristic genes from other brain cell types, such as Cx3cr1 (15.79 fold lower) and Tubb3 (24.86 fold lower) compared to whole cortex transcripts. We verified by immunohistochemistry that this tag is expressed by 95% of astrocytes following recombination, and 95% of tag-expressing cells also express GFAP. Our data indicates that the RiboTag technique can effectively profile the astrocyte translatome after stroke. Using this technique, we will comprehensively define the astrocyte-specific translatome response at specific time points after stroke.

THU - 135 Social Transmission of Maternal Behaviors through Observation

Discipline: Life Sciences
Subdiscipline: Neurosciences

Naomi López Caraballo*, *New York University School of Medicine* and Robert Froemke, *New York University School of Medicine*

Abstract: Our laboratory studies the mechanisms by which social experience leads to neuroplasticity to promote learning and pro-social behavioral changes. We focus on maternal care by mice, enabling reliable measurements of various social behaviors combined with experimental approaches such as neural recordings and optogenetics. When mouse pups are out of the nest, they emit vocalizations that prompt the mother to fetch them back to the nest. Virgin females do not initially retrieve pups, but usually begin retrieving after several days of co-housing with an experienced mother and pups. To understand the social experiences that lead to virgin co-parenting, we built a new system for combining continuous video-audio-neural recordings from co-housed animals over days. We found that mothers appear to demonstrate maternal behaviors to virgins. To explore the potential for social transmission of maternal behavior, we developed a new paradigm for virgins to learn retrieval through observation. A non-co-housed virgin observes a mother retrieve pups through a transparent barrier that allows visual, odor and auditory cues to go through. Virgin female mice can learn retrieval through observation. Furthermore, our lab showed that the neuromodulator oxytocin has a role in sensitizing the sensorial cortex promoting learning of pup retrieval (Marlin et al. Nature 2015). Sensory cortices and hypothalamic-oxytocin-releasing regions seem to be activated during observational learning in virgins, as shown by increased expression of the intermediate-early gene *c-fos*. Our research will help determine on how social experience triggers release of neuromodulators to induce learning of complex and essential social behaviors.

THU - 136 The Antimicrobial Peptide Human Beta-Defensin 2 Is Highly Effective Against *Mycobacterium Smegmatis*

Discipline: Life Sciences
Subdiscipline: Microbiology

Tyler Powell*, *California State University Los Angeles*; Roger Berton, *University of Iowa* and Edith Porter, *California State University Los Angeles*

Abstract: Tuberculosis is a significant healthcare burden due to emergence of multidrug and extreme drug resistant strains of *Mycobacterium tuberculosis* (Mtb). When inhaled Mtb initially interacts with epithelial cells in the airways. Among the infected, most control the infection and only 10% will develop active tuberculosis. Epithelial cell derived factors may play a crucial role in controlling Mtb infections. Epithelial cells are known to secrete antimicrobial peptides including beta-defensins. Our lab hypothesizes that the human beta defensin 2 (HBD2) contributes to the control of Mtb. Using *Mycobacterium smegmatis* (Ms), a non-virulent model organism for Mtb, and a metabolic assay, we found that HBD2 reduces the metabolic activity of Ms to less than 30% of the control at concentration as low as 313 nM. In parallel, biofilm formation was reduced to the same degree. This data is consistent with both, killing, or induction of dormancy. To assess bacterial killing, we wished to employ a protocol that utilizes the fluoroprobes propidium iodide to measure increases in cell membrane permeability and dibac$_4$3 to quantify membrane depolarization. We established a correlation of propidium iodide fluorescence and the fraction of dead Ms showing that we can use propidium iodide fluorescence as a gauge for HBD2 mediated pore formation. Furthermore, preliminary data suggests that under the assay conditions for the depolarization protocol Ms viability is not noticeably reduced within the first 3 h of incubation. We are in the process of testing HBD2 activity with this protocol. This research may lead to novel measure to combat tuberculosis.

THU - 137 Novel Bradyzoite Dense Granule Proteins in *Toxoplasma Gondii*

Discipline: Life Sciences
Subdiscipline: Microbiology

Amara Thind*, *University of California, Los Angeles*; Santhosh Nadipuram, *Cedars-Sinai Medical Center*; James Wohlschlegel, *University of California, Los Angeles* and Peter Bradley, *University of California, Los Angeles*

Abstract: *Toxoplasma gondii* is an obligate intracellular pathogen responsible for causing one of the most prevalent parasitic infections in humans and vertebrates. During the acute infection, *T. gondii* tachyzoites invade their host cells where they form a parasitophorous vacuole (PV) that is necessary for intracellular survival. During the chronic infection, the parasites switch to slow-growing bradyzoites, and a cyst forms around the PV allowing the parasite to persist for the life of the host. To maintain its intracellular niche, *T. gondii* secretes dense granule proteins (GRAs) into the PV space and cyst. Few bradyzoite-specific proteins have been discovered, and their roles in establishing and maintaining the chronic infection are largely unknown.

We hypothesized that the BioID approach using the biotin ligase BirA* fused to MAG1, a bradyzoite-upregulated dense granule protein, could be used to identify other novel bradyzoite GRAs. Using this approach, we identified nine new GRAs that were confirmed by epitope tagging and immunofluorescence assays. Two of these, GRA51 and GRA52, were barely detectable in tachyzoites but readily visualized in bradyzoites, in agreement with their transcriptional profiles. We characterized several of these GRAs by gene deletion. Deletion of GRA53 suggested that this protein plays an important role in parasite replication *in vitro*, and its absence results in lower cyst burden *in vivo*. Disruption of GRA54 produced normally replicating tachyzoites but resulted in fewer cysts *in vivo*. Together, these results show that this BioID approach is an effective way to identify key proteins involved in maintenance of the chronic infection.

THU - 138 In Vivo Electrophysiology in the 14-3-3 Functional Knockout Mouse Model of Schizophrenia

Discipline: Life Sciences
Subdiscipline: Neurosciences

Zachary Jones*, *Florida State University* and Yi Zhou, *Florida State University*

Abstract: Schizophrenia is a chronic and disabling psychiatric disorder that affects millions of individuals worldwide. Patients with schizophrenia exhibit diverse cognitive and behavioral deficits, yet the neurobiology underlying these deficits remains poorly understood. Elucidating the mechanisms of circuit and network level changes that manifest in the schizophrenic brain may provide crucial insights into the development and treatment of this highly intractable disorder. We have recently developed a 14-3-3 functional knockout (FKO) mouse line that exhibits schizophrenic-like behaviors such as hyperactivity, decreased sociability, and memory impairments. These mice transgenically express a 14-3-3 peptide inhibitor to disrupt the endogenous functions of 14-3-3 proteins in the brain. 14-3-3 proteins have been implicated in schizophrenia both in patients and in animal models. Our goal was to determine whether our 14-3-3 FKO model recapitulates the dysfunctional network activity seen in patients with schizophrenia. In this study, monopolar electrodes were bilaterally implanted into the prefrontal cortex (PFC) and hippocampus (HPC), and local field potentials were recorded

under various behavioral conditions. Compared to their wild-type littermates, FKO mice show reduced low frequency power and elevated high frequency power in the HPC and PFC, consistent with reported patient data. In addition, these mice show reduced phase-amplitude coupling within the HPC and reduced coherence between the HPC and PFC. Several of these aberrant patterns of activity are attenuated by acute treatment with the atypical antipsychotic drug clozapine. These findings suggest that 14-3-3 proteins mediate synchronized neural activity *in vivo* and thus may represent and important target for schizophrenia treatment.

THU - 139 Molecular Organization of the Octopus Visual System Using a Single-Cell RNA-Sequencing Approach

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jeremea Songco*, *University of Oregon*; Judit Pungor, *University of Oregon*; Dylan Farnsworth, *University of Oregon*; Denise Piscopo, *University of Oregon*; Cristopher Niell, *University of Oregon* and Adam Miller, *University of Oregon*

Abstract: Octopuses, like vertebrates, have camera-like eye structures despite the two lineages having diverged evolutionarily over 500 million years ago from a common ancestor that lacked a central nervous system. Furthermore, anatomical evidence suggests that octopuses and vertebrates may have similar neuronal cell types within their visual system. This begs the question, how has evolution solved the problem of creating a complex visual system? The recently sequenced octopus genome highlighted specific genomic novelties, such as expansions in the protocadherin family of cell adhesion molecules, which may underpin unique solutions to creating a visual system. However, little is known regarding the molecular determinants of visual system organization in octopuses. Using single cell RNA-sequencing in the *Octopus bimaculoides*, we analyzed the optic lobes of juvenile octopuses and aimed to identify the genes and types of neurons that create the octopus visual system. Preliminary analysis has identified ~20 different neuronal cell types based on their unique transcriptional profiles. An examination of the genes that define each cell type identified upregulations of protocadherin genes and differential expression of novel genes that do not have homologs outside of cephalopods, generating hypotheses about the unique aspects of the octopus visual system. This is the first study to begin to illustrate the molecular determinants underlying visual processing in the octopus, which can, in turn, provide insight into cell fate and development of the optic lobe as well as evolutionary influences on visual processing.

THU - 140 Brain-Targeting Prodrug Design for Thyrotropin Releasing Hormone

Discipline: Life Sciences
Subdiscipline: Neurosciences

Daniel Delacruz*, *University of North Texas Health Science Center*; Vien Nguyen, *University of North Texas Health Science Center*; Laszlo Prokai, *University of North Texas Health Science Center* and Katalin Prokai, *University of North Texas Health Science Center*

Abstract: Thyrotropin releasing hormone (TRH) has many neuromodulatory effects throughout the brain, however, treatment using this peptide induces unwanted peripheral side-effects. Based on our novel prodrug design that synergistically employs lipoamino acid residues (LAAs) and a brain-enzyme sensitive linker for prolyl oligopeptidase (POP), we have developed a set of lead compounds in silico. Prodrugs with different LAAs and POP-sensitive linkers were designed in silico for docking with POP's binding site and to calculate their logP (clogP). Computational assessments of lipophilicity and POP-binding affinity of our virtual prodrugs led to the selection of a representative prodrug termed Prodrug (1), for synthesis and in vitro membrane affinity studies to predict brain access from circulation. Prodrug (1) was compared to TRH in membrane affinity using immobilized artificial membrane chromatography (IAMC). IAMC is an established method to predict membrane affinity, such as blood-brain barrier (BBB) permeability, using chromatographic columns comprised of immobilized synthetic lipids that mimic biological membranes. Prodrug (1) showed a significantly increased membrane affinity characterized by the IAM Chromatographic Hydrophobicity Index (CHIIAM) value compared to that of highly hydrophilic parent peptide. Overall, based on the predicted excellent binding of Prodrug (1) to POP's binding site and its favorable membrane affinity, we expect that this prodrug will efficiently be able to deliver TRH into the brain and it may serve as a template for fine-tuning the prodrug constructs for efficacious brain delivery of this neuropeptide.

THU - 143 Testing the Ring Species Hypothesis with RAD-Sequencing and Minion Genome Sequencing in the California Endemic *Calochortus Venustus* (Liliaceae)

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Adriana Hernandez*, *Cornell University*; Jacob Landis, *University of California, Riverside* and Chelsea Specht, *Cornell University*

Abstract: Ring species are an ideal demonstration of incipient speciation, in which a founding population spreads and adapts in localized subpopulations separated across a divide and forming a ring such that when the farthest extending subpopulations come into contact they can no longer successfully interbreed. *Calochortus venustus*, a California-endemic lily, displays striking variation in floral pigmentation with spatial distribution suggestive of a ring species experiencing sequential change in phenotypic variation from the founding population. Petals of individuals within a population can range in color from deep red to white, with variation in petal spots as well, while terminal populations have the least variation in floral color. Preliminary analyses of 25 samples in northern and southern populations indicate that there is strong genetic differentiation, but further exploration of gene flow is necessary to test the ring species hypothesis. Leaf tissue from 200 individuals spanning the geographic range were collected in 2018 and 2019 for DNA extraction, each with quantified data on floral phenotype. In order to test for genomic signatures of selection and speciation, a draft genome was assembled using long reads from an Oxford Nanopore minION. A RAD-Sequencing approach is then used to test the ring species hypothesis by testing the association of recorded floral phenotypic features with particular genotypes, inferring population structure, and characterizing the evolutionary history among the identified populations. These findings will be used to provide insights into how polymorphic traits may be best maintained - or how and why they are lost - across the California landscape.

THU - 144 Regulation of Body Weight and Composition By Dietary Histidine

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Victoria Flores*, *University of Wisconsin-Madison*; Alexandra Spicer, *University of Wisconsin-Madison*; Nicole Cummings, *University of Wisconsin-Madison*; Eunhae Park, *University of Wisconsin-Madison*; Deyang Yu, *University of Wisconsin-Madison*; Shany Yang, *University of Wisconsin-Madison*; Matthew Wakai, *University of Wisconsin-Madison*; Kristen Malecki, *University of Wisconsin-Madison* and Dudley Lamming, *University of Wisconsin-Madison*

Abstract: The increasing prevalence of obesity is a serious threat to global health, placing many humans at risk of many diseases. An intervention is urgently needed to put an end to this epidemic. We and others have demonstrated that a low protein (LP) diet promotes leanness and glycemic control in lean and obese rodents. In a clinical trial, LP diets also promote leanness and glycemic control in humans. However, the specific dietary components altered in a LP diet that promote metabolic health have not been fully characterized.

We previously determined that reduced consumption of dietary essential amino acids mediates the metabolic response to a LP diet. We report our finding that dietary histidine plays a key role in the metabolic response to a LP diet. Specifically restricting dietary histidine by 67% promotes rapid weight loss of C57BL/6J mice, with an overall reduction in adiposity. This effect is not mediated by decreased food consumption, but instead is associated with increased energy expenditure.

To determine the relevance of our findings to the human obesity epidemic, we analyzed population health and nutrition data gathered from over 600 Wisconsin residents. We find that the variation in dietary histidine levels helps to explain differences in body mass index (BMI). Overall, our data suggests that dietary histidine is an important regulator of body weight and composition in both mice and humans and suggests that dietary guidelines and clinical interventions based on reduced levels of histidine may be an effective means to intervene obesity.

THU - 145 From Post-Weaning to Adulthood: Effects of Aging and Long Term Exercise on GDNF Expression, Structural Plasticity and Innervation in Skeletal Muscle

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Alberto Cintron-Colon*, *Western Michigan University* and John Spitsbergen, *Western Michigan University*

Abstract: Exercise has been linked with many beneficial effects on the nervous system, including neuroprotection, increased neurogenesis, decreased apoptosis, and enhanced maintenance of NMJ structures. GDNF is a potent survival factor for somatic motor neurons that innervate skeletal muscle, but as age increases, levels appear to decline. Our hypothesis is that skeletal muscle in aged, sedentary rats will have lower GDNF protein content and that exercise, in the form of voluntary running, will increase GDNF protein content and increase the size of NMJ structures. Samples were taken from sedentary and exercised Sprague-Dawley rats between 4 weeks and 18 months of age. Exercised groups had access to running wheels; and age-matched sedentary controls were housed in cages without access to running wheels. Tissues were processed for measurement of GDNF protein content via ELISA. Immunohistochemical analysis was performed to detect co-localization of GDNF with NMJ structures. GDNF protein content was significantly increased ($p \leq 0.05$) in tissues from exercised animals, and decreased with progression of age in sedentary control animals. There was a significant increase in length and area of stained end plates in muscles from exercised rats. GDNF staining suggests a higher presence in tissues from exercised rats. Results demonstrate a complete story of what occurs with neurotrophic factors as age progresses from post-weaning to adulthood and how physical activity affects at various stages of life. Data suggests that a regimen of increased exercise enhances production of GDNF, causes structural plasticity changes in NMJ elements and possibly lead to enhanced neuromuscular function.

THU - 146 Itaconate and Immunometabolism in Ischemic Stroke

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Thomas Vigil*, *University of Michigan*; Ryan Frieler, *University of Michigan* and Richard Mortensen, *University of Michigan*

Abstract: Stroke is the fifth leading cause of mortality in the United States and the leading cause of permanent disability in older adults. Immunometabolic changes have been shown to be a key factor in determining the immune cell response in disease models. The immunometabolite itaconate is produced by aconitate decarboxylase 1 (Acod1) and has been shown to inhibit inflammatory signaling in macrophages. In this study, we explore the role of Acod1 and itaconate in cerebral ischemia/reperfusion injury. ***Our central hypothesis*** is that Acod1 and itaconate are critical elements in determining immunometabolism in macrophages (and potentially other cell types) and these factors can be targeted to modify stroke. Specifically, we propose that itaconate is protective and anti-inflammatory.

We assessed the effect of exogenous itaconate treatment and loss of endogenous itaconate (Acod1 knouckout) in a transient ischemia/reperfusion occlusion stroke model. Mice received a transient 90-minute middle cerebral artery occlusion followed with 24-hours of reperfusion. Stroke lesion volume was measured by MRI and brain tissues were collected for gene expression analysis. Acod1KO mice showed significant increases in lesion volume compared to control mice, however no differences in pro-inflammatory mRNA levels were observed. Exogenous itaconate administration showed no differences in lesion volume and had no differences in pro-inflammatory gene expression.

These data suggests that endogenous Acod1 is protective in cerebral ischemia/reperfusion injury. These effects however do not appear to be driven by changes in inflammatory gene regulation. Further studies to identify the mechanism of protection are needed.

THU - 147 Novel Drug Combinations for Multiple Myeloma

Discipline: Life Sciences
Subdiscipline: Pharmacology

Susana Najera*, *Johns Hopkins University*; Beverly Mock, *NIH*; Snehal Gaikwad, *NIH*; Sayeh Gorjifard, *NIH* and Andrew Taylor, *NIH*

Abstract: Multiple myeloma (MM) is a heterogeneous cancer formed by malignant plasma cells in the bone marrow. Despite recent advanced therapeutic treatments such as proteasome inhibitors, liposomal formulations, and histone deacetylase inhibitors, multiple myeloma is still considered an incurable disease due to the frequency of acquired drug resistance. Previous studies have demonstrated that the deregulation of MYC, a pro-oncogenic transcription factor occurs in about 70% of MM patients. Thus, identifying drug combinations that target MYC could prove to be a promising avenue for the treatment of this disease. Here, we utilized an NCATS MIPE high-throughput screening platform of approximately 1900 small molecules in 47 MM cell lines treated for 48 hours at 11 doses to discover new targeted agent combinations for treating MM. Following normalization, drug sensitivity and curve classification were obtained for each individual agent in all MM cell lines. In silico correlation analyses with Palantir's Foundry data integration platform revealed 44 candidate combinations of compounds which were active in at least 25 cell lines. Candidate combinations were then evaluated in L363 human MM cells for their expression of MYC via immunoblot analysis. Of the 43 combinations, ten reduced MYC expression. Four different combinations of Heat Shock Protein 90 (HSP90) and interleukin-2-inducible kinase (ITK) inhibitors were analyzed. The effect of an HSP90i/ITKi combination in decreasing L363 cell survival was evaluated via MTS analysis of L363 cells for 48 hours. Together these data provide insight into new potential compound combinations for MM and may further reveal mechanisms of combined drug sensitivity in MM.

THU - 431 The Alpha-Band Component of EEG Modulates the Time Course of Spatial Perception

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Andrew Zavala*, *University of Oregon*; Paul Dassonville, *University of Oregon* and Jeff Petersen, *University of Oregon*

Abstract: Although the vestibular system plays a large role in creating the reference frame used to judge the spatial orientation of an object, the context of a visual scene also provides cues. However, these cues can sometimes be misleading, as in the case of the rod-and-frame illusion (RFI, Asch & Witkin, 1948), where a tilted frame distorts the sense of vertical and causes an enclosed line to appear tilted in the opposite direction. A recent study of the time course of the illusion demonstrated that the magnitude of this effect is influenced by the timing of the illusion's components, suggesting that the orientation judgment of the enclosed line occurs during a specific temporal window of spatial integration (Petersen & Dassonville, SfN 2018). This period may be analogous to the perceptual gating that has been hypothesized to occur in synch with the alpha rhythm of the EEG (Ronconi et. al., 2017). If this is the case, we hypothesize that alterations of the alpha rhythm (using a series of flashes to entrain alpha at slightly slower, 8 Hz, or faster, 12 Hz, frequencies) should alter the magnitude of the RFI for lines flashed just before the frame appears. Preliminary findings indicate that a slower alpha (and the resulting longer gating window) leads to an enlarged illusion, whereas a faster alpha (and shorter window) leads to a smaller illusion. This suggests that the time course of perception is dependent on the sensory gating associated with the alpha rhythm.

THU - 432 PAWS: Promoting Anti-Stress and Well-Being in Students

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Minerva Orellana*, *San Francisco State University* and Leticia Márquez-Magaña, *San Francisco State University*

Abstract: College students experience increased stress which impacts learning and overall health. Stress causes memory loss, increases risk of depression, and promotes the development of chronic diseases. To mitigate student stress, college campuses are implementing stress management interventions, including the use of therapy dogs. While these improve self-reported stress, the biological impact remains unknown. The objective of this study was to determine the effects of a therapy dog intervention on biological markers of stress among college students. Diverse undergraduate students (n=64) were recruited and randomized into either an intervention group (therapy dogs) or a control group (stuffed animal). We obtained measures of stress at baseline and post-interaction. Self-reported stress was assessed using the perceived stress scale (PSS). Saliva samples were collected to quantify levels of stress-related hormones oxytocin and cortisol, using an enzyme linked immunosorbent assay. At baseline, the participants displayed moderate perceived stress. Although oxytocin levels declined, we observed an improvement in self-reported stress and cortisol in both groups. The control group displayed a 13.9% decrease in salivary cortisol post-interaction, while the intervention group displayed a 16.6% decrease. This study was the first of its kind to measure biological markers of stress to determine the efficacy of therapy dogs as a stress intervention among college students. Surprisingly, we detected favorable changes in self-reported stress and salivary cortisol in both groups. These findings suggest that therapy dogs, and perhaps cost-effective alternatives such as stuffed animals, may alleviate stress for students. This can in turn lead to improved learning and healthier students.

THU - 435 **Ua Mau ke Ea o Kō Mākou ʻĀina: Trailheads to More Sustainable Community Forestry Futures in Hawaiʻi**

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

La'akea Low*, *Oregon State University* and Meagan Jones, *University of Hawaiʻi Maui College*

Abstract: This project aims to identify ways in which community forestry programs – guided by the central tenets of EA – may contribute to human and non-human systems in Hawaiʻi. Development of Hawaiʻi's forest ecosystems, while boons to biodiversity, often occur within sacred sites and conservation districts. Concerns related to environmental justice, livelihoods, and climate change have induced a heightened sense of urgency in respect to sustainably managing Hawai`i's environmental, economic, and social capital. This project examines potential strategies in achieving more sustainable community forestry futures for Hawaiʻi nei in three ways: 1) by using Pukui's three-tiered definition of the Kānaka Maoli concept of EA, 2) conducting a review of the community forestry literature, and 3) conducting participant observation research during 2017 and 2018 through the University of Hawaiʻi Maui College (UHMC) Kekaulike Internship Program (KIP). Community forestry program research sites included the Puʻu Kukui Watershed Preserve (PKW) in 2017 and the Leeward Haleakalā Watershed Restoration Partnership (LHWRP) in 2018. Results of this project suggest that the Kānaka ʻŌiwi concept of EA may serve as a critical framework for effectively implementing sustainable community forestry programs. These programs are capable of providing a multitude of ecosystem services applicable to both human and non-human systems across Ko Hawaiʻi Pae ʻĀina.

THU - 850 **Interactive Effects of Iron and Light Limitation on the Molecular Physiology of the Southern Ocean Diatom *Fragilariopsis Kerguelensis.***

Discipline: Other
Subdiscipline: Other Professional Fields

Carly Moreno*, *University of North Carolina at Chapel Hill* and Adrian Marchetti, *UNC*

Abstract: The polar diatom *Fragilariopsis kerguelensis*, is ubiquitous in Southern Ocean waters and is a major responder to iron fertilization. In addition to large gradients in iron availability, *F. kerguelensis* must cope with variations in light availability. We performed a comparative transcriptomic analysis of *F. kerguelensis* grown under varying iron and light conditions in order to investigate the molecular underpinnings for the physiological response to iron and light limitation. Iron limitation reduced growth rates more than low light; however, there was not an additive effect of iron and light limitation on growth rate. The low iron treatments (saturating and low light) had the largest transcriptomic response, with 169 differentially expressed KEGG module annotations compared to the control (iron replete, saturating light); however, expression patterns were more similar in low light treatments (high and low iron). Under interactive iron/light co-limitation, amino acid pathways, ribosome, sulfur metabolism and carbon fixation metabolic pathways were overrepresented. Transcripts of an aquaporin, a proteorhodopsin, and plastocyanin and flavodoxin, were overrepresented to the greatest extent in the combined low iron/low light treatment, indicating there may be an additive effect of iron and light limitation at the gene level. Iron and light replete cells demonstrated increased expression of ferritin, carbonic anhydrase, and numerous iron-dependent proteins. This transcriptional analysis reveals mechanisms that may underpin the ecological success of this diatom in low iron and light environments, highlighting the important role of diversified photosynthetic isoforms, iron acquisition, unique ROS detoxification mechanisms, and metabolic shifts in amino acid recycling and carbon metabolism.

10:00 AM – 12:00 PM

Thursday Undergraduate Posters

THU - 100 **Is the Cell Signaling Response from Exercise Enhanced with *Ex Vivo* Sulforaphane Treatment?**

Discipline: Health
Subdiscipline: Medicine

Nadja Jones*, *Northern Arizona University* and Tinna Traustadottir, *Northern Arizona University*

Abstract: Among the top causes of death in the United States are cardiac disease, Alzheimer’s disease, diabetes, and stroke. Development and progression of these diseases can be reduced through diet and exercise. Understanding the cellular mechanisms that produce these effects will allow us to maximize their benefit. An important cell signaling pathway that is expressed during exercise occurs via the transcription factor Nrf2. The chemical sulforaphane (SFN), found in broccoli and other cruciferous vegetables, has been shown to also induce the Nrf2 pathway. In the present study, we hope to understand how the interaction between exercise and SFN impacts the protective effects of exercise. We expect that SFN and exercise will synergistically increase cellular defenses. Recreationally active men (42 ± 6y, n=12) cycled for 30-min at 70% of their maximal oxygen consumption (VO2 max) measured at a prior visit. Blood was drawn pre- and 15-min post exercise. Peripheral blood mononuclear cells were isolated, counted, and incubated *ex vivo* ±SFN (2.5μM) for 2-hrs and 24-hrs. Cells were harvested and re-counted. Protein abundance was measured via Western blotting for GCLc, NF-κB and Nrf2. There was no significant difference between cell viability pre and post incubation. Preliminary data show high variability in changes to the exercise response. This indicates that SFN may not be as potent for some individuals as it is for others or that individual reliance on this pathway may vary. We hope that these data will help pave the way for future supplementation studies and the therapeutic application of SFN.

THU - 101 **Recovery after Experimental Traumatic Brain Injury Is Not Impeded By Intermittent Administration of the Antipsychotic Drug Risperidone**

Discipline: Health
Subdiscipline: Medicine

Carolyn Lomahan*, *University of Pittsburgh*; Isabel Bleimeister, *Safar Center for Resuscitation Research*; Tracey Lam, *University of Pittsburgh*; Gina Bao, *University of Pittsburgh*; Jeffrey Cheng, *Safar Center for Resuscitation Research*; Corina Bondi, *Safar Center for Resuscitation Research* and Anthony Kline, *University of Pittsburgh Physical Medicine & Rehabilitation Safar Center for Resuscitation Research University of Pittsburgh*

Abstract: Numerous studies have reported that once daily administration of the antipsychotic drug (APD) risperidone (RISP) hinders recovery after traumatic brain injury (TBI). However, it is not known whether intermittent dosing would produce similar detrimental effects. The significance and clinical relevance of providing APDs intermittently is that not all patients require daily

treatments to manage TBI-induced agitation. Intermittent (vs. daily) administration of RISP will be significantly less disruptive to motor and cognitive recovery after TBI. Isoflurane-anesthetized adult male rats were subjected to either a controlled cortical impact of moderate severity or sham injury and then were randomly assigned to groups receiving intraperitoneal injections of vehicle (VEH; 1.0 mL/kg;n=10 for TBI and n=5 for sham) or RISP (0.45 mg/kg; n=10 for TBI and n=5 for sham) 1x, 3x, or 7x per week until the completion of behavioral testing, which consisted of motor and cognitive training on post-operative days 1-5 and 14-19, respectively. The behavioral data were analyzed by repeated measures ANOVA followed by Newman-Keuls post-hoc test to determine group differences. The group receiving RISP 7x week showed greater motor and cognitive impairment compared to those receiving RISP 1x or 3x per week, or VEH [$p<0.05$]. Moreover, no differences were observed between the intermittent RISP groups vs. VEH [$p>0.05$]. The lack of significant differences between the intermittent RISP groups and VEH controls support the hypothesis. A potential clinical ramification is that RISP may be safe to manage agitation after TBI, but only when used intermittently.

THU - 103 Development of a Biomarker for Parkinson's Disease

Discipline: Health
Subdiscipline: Medicine

Daphne AlcalaZuniga*, *University of Texas Rio Grande Valley*; Upal Roy, *The University of Texas Rio Grande Valley* and Deepa Roy, *University of Texas Rio Grande Valley*

Abstract: Parkinson’s Disease (PD) is one of the most common neurodegenerative disorders. Progressive neuron cell death eventually leads to difficulties with motor coordination. Previous research has suggested that an impairment of the dopaminergic system can be a common cause of Parkinson’s disease, however little is known about how the disease progresses.

Dopamine (DA) is a neurotransmitter important for coordination of movement. Recent studies have hypothesized that the oxidation of the neurotransmitter to toxic species can contribute to the selective neurodegeneration observed in PD. In earlier articles, a variant of the DJ-1 protein has been identified as a possible factor of hereditary autosomal recessive PD. Furthermore, this protein is thought to aid the regulation of oxidative stress, although the mechanisms through which this takes place are not fully understood.

An *in-vitro* cell model from SK-N-MC and SH-SY5Y cells will be treated with rotenone at different concentrations for a period of 4 weeks to imitate the chronic condition of Parkinson’s disease. A series of in vitro characterization was done including PCR, cytotoxicity assay, and reactive oxygen (ROS) species assay to determine the effect of DJ1 expression in in vitro PD condition. Results indicated that there was significant effect on DJ1 expression in rotenone treated SK-N-MC cells. Overall data indicated that there is significant down regulation of DJ1 gene in presence of rotenone. Based the data, we conclude that DJ1 can potentially serve as a marker for PD in neuronal cells.

THU - 104 Microplastics May Cause Low-Grade Inflammation and a Shift Toward Glycolysis in Macrophages

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Harrison Moss*, *Undergraduate Pipeline Network, University of New Mexico*; Seth Merkley, *Clinical and Translational Science Center, University of New Mexico Health Sciences Center* and Eliseo Castillo, *Division of Gastroenterology and Hepatology, Department of Internal Medicine, University of New Mexico School of Medicine*

Abstract: Plastic pollution has resulted in the exposure of all living organisms to microplastics, however, the potential risk of microplastic ingestion on human health is currently unknown. In this study, we sought to address this gap in scientific knowledge regarding the health risk of microplastic exposure. We utilized both *in vitro* and *in vivo* models to understand the physiological effects of microplastics in the gut and in macrophages. Macrophages are innate immune cells with phagocytic and antimicrobial activity, are highly concentrated in the intestine, and can sample the intestinal lumen; therefore understanding their role in propagating or mitigating microplastic-driven pathologies is critical. We analyzed murine bone marrow-derived macrophages (BMMs) for microplastic-induced changes in mitochondrial oxygen consumption rates and extracellular acidification rates as measures of oxidative phosphorylation and glycolysis, respectively. BMMs became more glycolytic and less oxidative as compared to unstimulated and LPS-stimulated controls. A glycolytic phenotype is associated with an immunometabolic active state. Additionally, BMMs had increased cell surface expression of costimulatory molecules further demonstrating an activated state. Lastly, microplastic ingestion over an 8-week period in C57BL/6 mice resulted in increased body weight compared to control mice. In conclusion, we advance a novel hypothesis that microplastics cause low-grade inflammation possibly through the activation of macrophages. Low-grade inflammation can lead to Metabolic Syndrome, which describes a set of risk factors such as high blood pressure, high blood sugar, and weight gain that can lead to obesity, diabetes, and cardiovascular disease.

THU - 105 Selection for Estrogen Sensitivity in Feral *Xenopus Laevis* living Downstream from a Golf Course

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Andrea Meraz*, *University of California, Berkeley* and Tyrone Hayes, *University of California, Berkeley*

Abstract: The presence of endocrine-disrupting chemicals (EDCs) in the environment due to industrial and agricultural practices is a threat to our health and the ecosystem. Atrazine, is an herbicide used heavily on golf courses. It is also an EDC that induces estrogen production in animals, including humans. African Clawed frog (*Xenopus laevis*) tadpoles exposed to estrogenic compounds during early development develop female-typical reproductive morphology. Sensitivity to these estrogenic compounds, however, varies among populations. We examined two feral populations collected from a creek that is bisected by a golf course to investigate whether there was a difference in sensitivity between populations collected from upstream and downstream of the golf course. We tested this hypothesis by breeding pairs collected from both sites and exposing their offspring to either 3 ng/mL of estradiol or delivery vehicle. Groups of 30 tadpoles were housed in aquaria with three mouse aquaria dedicated per treatment per pair. When exposed to estrogen, the ratio of male : hermaphrodite : female metamorphs was 61:17:87 (63% with ovaries) in the upstream population and 14:10:143 (92% with ovaries) in the downstream population compared to 49% and 51% with ovaries upstream and downstream, respectively. There was a statistically significant difference between both groups (G-test; $P < 0.05$) and the controls, and estrogen sensitivity was higher in downstream populations. The animals are currently being genotyped to determine sex-reversal ratios and their gonads will be histologically examined to confirm the development of ovarian or testis-typical histology.

THU - 106 Polymeric Nanodepots to Enhance Antibody-Dependent Natural Killer Cytotoxicity Against HIV Reservoirs.

Discipline: Life Sciences
Subdiscipline: Pharmacology

Armando J. Ruiz-Justiz*, *University of Puerto Rico at Ponce*; Allan Bowen, *George Washington University* and Rohan Fernandes, *George Washington University*

Abstract: Natural killer (NK) cells represent a promising immune cell subset for HIV/AIDS and cancer because of their ability to elicit antibody-dependent cellular cytotoxicity (ADCC) against target cells. Because many studies have demonstrated the potential of latency-reversing agents (LRAs) in HIV reactivation (as part of a latent HIV reservoir eradication strategy), we synthesized polymeric polylactic-co-glycolic acid nanodepots (PLGA-ND) encapsulating an LRA and a broadly neutralizing antibody (bnAb) for use in conjunction with NK cells to eradicate latent HIV reservoirs. The PLGA-NDs were selected as a vehicle because PLGA is degradable, stable and FDA-approved. This nano-immunoengineering approach to enhance the NK activity could lead to a novel therapy for HIV since antiretroviral therapies (ART) inhibit the replication and transmission of the virus but cannot lead to a cure. We hypothesized that PLGA-NDs will gradually

release the LRA to induce the HIV reactivation and NK stimulation, allowing the bnAb to recognize the virions on the membrane of the reactivated HIV cells, thus inducing coordinated eradication of the HIV reservoirs via NK-based ADCC. The properties of the PLGA-NDs were measured over several days using dynamic light scattering (DLS) and the encapsulation efficiencies of the LRA and the bnAb were quantified by ELISA and BCA assays. Further, the HIV reactivation by the LRA and the NK cytotoxicity was determined using flow cytometry. Our findings indicate the potential of PLGA-NDs for encapsulating LRAs and bnAbs to enhance an NK cytotoxic response, serving as an effective nano-immunotherapeutic platform for treating latent HIV.

THU - 110 **Chimeric Autoantigen Receptor (CAAR) T Regulatory Cell Therapy for Patients with Neurologic Symptoms Expressing Kelch-like Protein 11 Autoantibody**

Discipline: Health
Subdiscipline: Medicine

Hugo Pontes*, *University of Washington*; Sasha Gupta, *University of California, San Francisco*; Milos Simic, *University of California, San Francisco* and Michael Wilson, *University of California, San Francisco*

Abstract: Paraneoplastic neurological disorders (PNDs) are immune-mediated diseases that can affect the central nervous system (CNS), assumed to be the result of a misdirected anti-tumor immune response. Prior work identified 13 patients with history of seminoma and a similar constellation of neurological symptoms including vertigo, ataxia, and diplopia without a clear pathology. An autoantibody specific for a domain of the kelch-like protein 11 (KLHL11) was identified for these patients using the new technology of peptide phage display. Despite treatment with anti-CD20 monoclonal antibodies to deplete all B cells, patients can continue to progress. This prompts to our hypothesis that this is a T-cell driven disease that may be best treated through the dampening of the immune system. Our strategy is to engineer a chimeric auto-antigen receptor (CAAR) in T regulatory cells specific to the KLH11 B cell receptors (BCR) to dampen the adaptive T cell response. To do this, we performed an in vitro antigen-specific B cell expansion using the KLHL11 protein from patients. The patients' memory B cells are first extracted from serum. Then, using a toll-like receptor in addition to the KLHL11 protein, the proliferation of KLHL11-IgG producing B cells was stimulated, thus expanding the population of the antigen-specific B cells. This protocol establishes a platform for which then we can test if our CAAR T regulatory cells are able to suppress the immune response through the release of anti-inflammatory molecules upon antigen-specific activation. Overall, we hope this can then result in a targeted therapeutic option for these patients.

THU - 111 **Diagnostic Utility of Multiplex PCR-Based Assay on Pleural Fluid of Children with Parapneumonic Empyema.**

Discipline: Health
Subdiscipline: Medicine

Paola Fonseca-Romero*, *Universidad Ana G. Mendez- recinto de carolina*; Shannon Nielsen, *University of Utah*; Nicole Pershing, *University of Utah*; Krow Ampofo, *University of Utah* and Anne Blaschke, *University of Utah*

Abstract: Pneumonia is a common cause of serious illness in infants and children. Parapneumonic empyema (PE) complicates pneumonia when purulent fluid collects in the pleural space and can require prolonged antibiotic therapy. PE is primarily caused by infection with bacterial pathogens including *Streptococcus pneumoniae,Staphylococcus aureus* and *S. pyogenes*.Culture of blood and pleural fluid is used to identified causative organisms; however, culture can be low yield if patients have received antibiotics. We aim to further understand the epidemiology of PE by utilizing a PCR-based assay for pathogen detection. Pleural fluid (PF) specimens were collected from children with PE. Demographic, clinical and microbiologic data was abstracted from the medical record. PF specimenswere tested with the BioFire BCID Panel, a multiplex PCR-based assay detecting 19 bacterial pathogens.We collected 121 PF specimens from children with PE. A bacterial pathogen was identified by culture in 32% of patients. We performed PCR on 19 PF specimens. Nine PF specimens were culture positive; PCR identified a concordant organism in 8 cases. Ten PF specimens were culture negative, PCR identified a pathogen in 6 cases. *S. pneumoniae* was identified in 42% (8/19) of cases, followed by *S. pyogenes*in 21% (4/19) and *H. influenzae*in 5% (1/19) cases.PCR is a rapid and specific method for detection of pathogens in pleural fluid. PCR-based diagnostics expands our understanding of the epidemiology of PE in children. This methodology will help improve treatment of PE by improving the speed and accuracy of pathogen identification.

THU - 112 **Latina Breast Cancer Patient Awareness in Financial Resources: Healthcare Providers' Perspective**

Discipline: Health
Subdiscipline: Public Health

Jocelyne Lemus*, *University of Illinois at Chicago* and Yamile Molina, *University of Illinois at Chicago*

Abstract: Little is known how existing financial assistance programs address these unique needs and Latinas' awareness of them. To address this gap, we conducted 10 semi-structured interviews with healthcare professionals to understand: 1) Latina patients' unique economic needs; 2) availability of financial programs to address these needs; and, 3) Latinas' awareness of these programs. Staff from ALAS-Wings and the University of Illinois at Chicago used purposive sampling strategies to recruit 10 healthcare personnel familiar with financial aspects of cancer care for 60-minute semi-structured interviews. The average age of participants was 43.7 years, 80% identified as female, 50% identified as Latinx, and 50% had graduate degrees. The average number of years participants had engaged breast cancer patients in treatment and survivorship care was respectively 5.7 and 4.97. In terms of costs, healthcare professionals perceived that Latinas specifically struggled with non-medical costs (e.g., transportation, living utilities), for which there was economic support from a few foundations (Pink Fund, Patient Advocate Foundation, American Cancer Society). However, healthcare professionals did not believe Latinas were aware of financial programs due to shame/embarrassment and language barriers. Healthcare professionals perceived that these barriers and the prioritization of surviving resulted in delays in seeking financial supports. Our findings highlight the importance of healthcare professionals that are able to explain the availability of resources to Latina breast cancer patients in linguistically and culturally astute strategies immediately following diagnosis and throughout treatment. This resources will help increase Latinas' awareness and utilization of resources for non-medical and other costs.

THU - 113 **Namitunatya: Evaluating Readability of Printed Cancer Materials for Hopi Men**

Discipline: Health
Subdiscipline: Public Health

Jordan Ojeda*, *Northern Arizona University* and Priscilla Sanderson, *Northern Arizona University*

Abstract: Only 37.5% of AI/ANs nationally are up to date with CRC screening. The Hopi men have requested for cancer support screening services and influenced the goal of this study, which is to create 8th grade reading level cancer materials that may help to increase the rates of colorectal cancer screening among the Hopi men. In order to accomplish this, we ask the question, "What are the readability levels of our printed men's cancer information materials?" A survey will be conducted with the Hopi Community Advisory Committee (CAC) to answer this question. The CAC are Hopi men from the age 35 to 70 years old and reside on the Hopi Reservation in Arizona. The purpose of the project will be discussed with the men and those that voluntarily consent to the project will join. The cancer media materials that were created in Fall 2018 will be shown to those taking the survey and they will be asked to rate how effective they are for Hopi men on the reservation. This conclusion will be based on various criteria that analyze the cultural appropriateness and reading level of the materials. After completion, the survey data will be analyzed and the SMOG readability formula will be also be conducted on the materials to determine their reading level. The implication of this project is that it may help with providing tailored colorectal cancer and cancer screening information for Hopi men and may cause an increase in cancer screenings for Hopi men in their community.

THU - 114 Evaluation of Culturally Consonant Incentives Used in a Community-Based Chronic Illness Self-Management Program

Discipline: Health
Subdiscipline: Public Health

Brianna BullShows*, *Montana State University, Bozeman* and Alma McCormick- Knows His Gun, *Messengers for Health*

Abstract: Messengers for Heath is a nonprofit organization based on the Apsáalooke (Crow) reservation that uses a community based participatory research approach to address health issues on the reservation. Project partners designed a culturally consonant intervention for community members to assist with chronic illness (CI) self-management. The key to improving CI management is the capacity for effective self-care, as most people with CI's spend more time managing their care in the community, as compared to time in spent in the hospital or ambulatory care setting. As a part of a community-based and community-led CI self-management program developed for community members, we developed incentives related to the different topic areas of the program. A couple of the incentives given out included the *Counting Coup Journal,* exercise bands, *Living a Healthy Life* book. These incentives were distributed during the gathering Participants completed an evaluation of the different incentives, indicating how often they used the incentive (ranging from not at all to all the time) and adding comments about the incentives. Some incentives were used more than others and participants offered helpful comments about the use and helpfulness of the different incentives. A limitation of this evaluation was that not all participants completed the evaluation of incentives and some of the participants did not receive all of the incentives. Conducting an evaluation of the usefulness of these incentives can help to improve our program and be used for other CI self-management programs in the future. All the incentives and incentive surveys will be provided.

THU - 115 Risk Perception of Navajo Communities Along the San Juan River Following the Gold King Mine Spill

Discipline: Health
Subdiscipline: Public Health

Morgan Farley*, *University of Arizona*; Paloma Beamer, *University of Arizona* and Karletta Chief, *University of Arizona*

Abstract: On August 5, 2015, 3 million gallons of acid mine drainage was accidently released from the Gold King Mine Spill (GKMS), eventually reaching the San Juan River which the Navajos greatly depended on for subsistence, cultural, and spiritual practices. Although water and soil samples collected 3-9 months after the Spill show no severe environmental impacts, the extent of emotional and spiritual impacts were unknown. Objectives of this project were (1) to assess perceived risk of activities related to the San Juan River and (2) to measure perceived health effects resulting from contact with the San Juan River. It was hypothesized that the GKMS would increase the communities' perceived risk of the San Juan River and associated health effects. Household questionnaires were administered to 59 Navajo homes in three communities dependent on the San Juan River. Results show that the average risk perception of engaging in 11 different activities were substantially higher after the spill (4.24) compared to engaging in those same activities before the Spill (2.08) when using a scale from (1) "Very Low Risk" to (5) "Very High Risk." Additionally, 42% of respondents perceived it would be "likely" or "almost certain" that they would develop physical health effects due to contact or usage of material from the San Juan River after the Spill. This data shows that the GKMS had significant long-term emotional and spiritual impacts on the Navajo people. Next steps include community healing efforts to help reduce stigma and restore trust within the Navajo community.

THU - 116 Qualitative Investigation: Analysis of Adolescent Pregnancy in Ecuador

Discipline: Health
Subdiscipline: Public Health

Keren Herrán*, *University of Maryland, Baltimore County*; Tania Calle, *Williams College*; Karla Cairo, *Universidad San Francisco de Quito* and Iván Palacios, *Universidad San Francisco de Quito*

Abstract: According to the newspaper El Universo, Ecuador has the second highest rate of adolescent pregnancy in Latin America. The country's Multisectoral Policy for the Prevention of Pregnancy in Girls and Adolescents estimates that 26% of all births in Ecuador are the result of teenage pregnancy. The World Health Organization's 2018 Adolescent Pregnancy fact sheet has stated that adolescent pregnancy is a major health risk due to its contribution to both maternal and child mortality, and its reinforcement of vicious intergenerational cycles of poverty.

Health centers in the rural outskirts of Quito requested a qualitative study on local adolescent mothers to better understand the social determinants that causes these pregnancies. Hence, our research question: how does sexual education knowledge, professional aspirations, partner relationships, family dynamics, and other social factors play a role in fostering adolescent pregnancy? The two field work research techniques being employed include focus group discussions, in the provinces of Pifo, Lumbisi, and El Quinche, and in depth interviews with key informants. Validation of collected information will occur through the strategy of triangulation. We will be applying grounded theory for data analysis through analyzing transcriptions via open, axial, and selective coding using NVivo software.

Preliminary results in El Quinche indicate that lack of privacy in health clinics when obtaining contraceptives and taking lightly sexual education workshops are factors that contribute to unwanted pregnancies in adolescents. Ultimately, gaining a better understanding of the causes of adolescent pregnancy can inform the formulation of more effective interventions in Ecuador and beyond.

THU - 117 Genetic and Molecular Basis of Social Behavior

Discipline: Life Sciences
Subdiscipline: Neurosciences

Nazaret Montejanon*, *California State University, San Bernardino* and Philip Washbourne, *University of Oregon*

Abstract: Animals use social interactions for many purposes: communication, warning of predators, and for mating. Yet, not much is known about the underlying mechanisms that control social behavior such as the neural circuits and genes involved. Testing social behavior in the zebrafish, a highly social vertebrate species, will allow researchers to not only gain a better understanding of these mechanisms but may also shed light on the social deficits in those affected by autism spectrum disorder and schizophrenia. Using a forward genetic approach in zebrafish we propose to identify random mutations in genes that affect phenotypic differences in social behavior. Further, by targeting a specific neuronal population in the ventral telencephalon, which is known to be important for social behaviors, we can examine how mutants might alter these neurons and change zebrafish social behavior. This specific cluster of neurons express the transcription factor *lhx8a* and express both GABA and Acetylcholine, which is consistent in mammals, and it is hypothesized that this gene is responsible for determining the neurotransmitter phenotype of these neurons. We will examine how mutations in the *lhx8a* gene, and other genes, could affect the neurotransmitter fate and how this ultimately impacts the role played by these neurons in social behavior. This work has a potential to give us a broader understanding of the genetics that underlie the development of basic social behaviors that are shared across vertebrates.

THU - 119 A Comparative Analysis of HIV Knowledge between Men Who Have Sex with Men Living in La Romana, Dominican Republic and Latino Men in Chicago, USA

Discipline: Health
Subdiscipline: Public Health

Natalie Jaramillo*, *University of Illinois at Chicago*; Maximo Brito, *University of Illinois at Chicago*; John Flores, *University of Illinois at Chicago* and Shaveta Khosla, *University of Illinois at Chicago*

Abstract: The prevalence of HIV is much higher in men who have sex with men (MSM) than the general population both in the Dominican Republic (DR) and in Chicago. The purpose of this study is to assess and compare the HIV knowledge among Latino MSM in Chicago to a Dominican MSM cohort. In 2013, participants were recruited in La Romana, DR via snowball sampling and direct recruitment. The participants had to: be at least 18 years or older, be a resident of La Romana, and have had sex with a man in the past 12 months. Participants were interviewed about demographic information, sexual risk behaviors, and HIV knowledge. Currently, this research is in the process of recruiting Latino MSM in Chicago by direct recruitment and snowball sampling, with the following inclusion criteria: be 18 years or older, be a resident of Chicago, self-identify as Latinx, have had sex with a man in the past 12 months, and have an HIV-negative or unknown status. In the Dominican cohort, of the total of 100 participants, 95% reported consistent condom use effectively prevents HIV transmission, and 97% knew of treatment for HIV-positive individuals. Results for the Chicago cohort are preliminary; I anticipate this cohort will have higher levels of HIV knowledge comparatively. So far, 2 persons have been interviewed and 20 community-based organizations that work with LGBTQ+ and/or Latinx populations have been contacted. The gaps in HIV knowledge of these cohorts should be addressed so that HIV prevalence can be reduced in Latino MSM.

THU - 120 Acceptability and Feasibility of Using Video Visits for Weight Management Care

Discipline: Health
Subdiscipline: Public Health

Natalia Rodriguez*, *University of Texas Houston Health Science Center School of Public Health and School of Biomedical Informatics* and Monisha Arya, *Baylor College of Medicine*

Abstract: The development of mobile health (mHealth) and telehealth technology has revolutionized the way healthcare is delivered. Services available via mHealth applications (apps) have facilitated clinical communication and expanded the information available to patients and providers. There is a need for studies to assess patients' perspectives on access to health care and education through mHealth video visits. The purpose of this study was to assess patients' interest in weight management care through video visits. In 2018, patients enrolled in weight management programs at a weight management outpatient center in Houston, Texas were invited to participate in a ten-question paper survey. The majority of the questions focused on the acceptability of video visits and the feasibility of participating in video visits for weight management care. There were 45 survey participants. A majority (77.8%) expressed an interest in weight management care offered through video visits. This was further supported by a majority of patients being familiar with the hospital mHealth app that provides video visits. A majority of patients (64.4%) also expressed an interest in participating in future pilot studies for video visits for weight management care. Our study of patients in a weight management program found that patients would be interested in video visits to supplement existing in-person weight management programs. It is important to consider video visits as an alternative means of patient access to care and education. These findings are important because they support future efforts to pilot video visits for weight management care.

THU - 121 Determining the Preferences and Functional Use of Highlighting in Text-to-Speech (TTS) Systems for People with Aphasia

Discipline: Health
Subdiscipline: Public Health

Natasha Morales*, *Boston University* and Sarah Wallace, *Duquesne University*

Abstract: Aphasia is a disorder caused by brain damage that impairs one's understanding and use of language, context, and speech expression, which consequently decreases quality of life. Although people with aphasia (PWA) have impaired reading comprehension, studies have shown that text-to speech (TTS) systems allow some PWAs improved reading comprehension through its multimodality features (i.e., presentation of written and auditory information). However, there is little evidence discerning the exact TTS features enhancing or inhibiting word decoding. The purpose of the study was to determine participants accuracy and preference when varying one TTS system feature, highlighting. The participants reviewed 36 stories across three sessions and answered multiple choice-questions related to their content. The stories were presented through different conditions involving word-by-word highlighted text, highlighted sentences, and no highlights. Consequent data collection will measure reading comprehension through post-test multiple choice questions and modality preference was measured through ranking and through open-ended questions. We hypothesized that there would be greater preference for highlighted words as it might facilitate word tracking and consequent contextual understanding. This project compared people from the overall data set with consideration of demographic factors, language skills, comprehension accuracy, and preferences. The preliminary results suggest that there seems to be a preference for highlighted sentences as it facilitates word tracking and word decoding, but data is still being collected. The outcome of this study will provide evidence based recommendations for changing TTS features to maximize the benefits available for PWAs, regardless of their medical profile.

THU - 122 Demographic and Psychological Associations with Zika Preventive Behavioral Intentions

Discipline: Health
Subdiscipline: Public Health

Jazmine Abril*, *University of New Mexico*; Angela Fagerlin, *University of Utah*; Brian Zikmund-Fisher, *University of Michigan*; Victoria Shaffer, *University of Missouri*; Laura Scherer, *University of Colorado*; Megan Knaus, *University of Michigan* and Aaron Scherer, *Univeristy of Iowa*

Abstract: There are multiple behaviors people can engage in to prevent the spread of infectious disease during an epidemic, yet they often do not engage in these behaviors. In this cross-sectional study, we sought to determine the public's willingness to engage in Zika preventive behaviors across three time points during the Zika pandemic of 2016. National representative samples were recruited through an online survey company (Survey Sampling International) across three different time points: Time 1 was March 2016, Time 2, was August 2016, and Time 3 was March 2017. Participants read through a short description of the Zika Virus developed by the Centers for Disease Control and Prevention then completed questions regarding their preventive behavior intentions (e.g., wearing long sleeve clothes, avoiding going outside), psychological characteristics (e.g., trust, perceived risk, worry), and demographics (e.g., gender, age, race/ethnicity). We hypothesized that behavioral intentions would be highest at Time 2 and that demographic and psychological characteristics would be associated with behavioral intentions. Our preliminary data has supported our hypothesis in relation to the role of behavioral intentions over time. Additionally, our results indicate a positive association between anxiety, perceived susceptibility, and perceived severity with greater behavioral intentions. However, more research is needed to further explore potential moderators of preventive actions, as well as the use of these moderators in possible interventions to increase protective-health behaviors within populations.

THU - 123 Sustainability of a Community-Based Dance Program for Older Latino Adults

Discipline: Health
Subdiscipline: Public Health

Martha G. Garcia*, *University of Illinois at Chicago*; Guilherme M. Balbim, *University of Illinois at Chicago* and David X. Marquez, *University of Illinois at Chicago*

Abstract: Prior research indicates the need for community-based physical activity programs for older Latino adults. Latinos report participating in less leisure time physical activity compared to non-Latino Whites and Blacks. Addressing barriers for sustainability of physical activity programs might increase access for older Latinos adults and promote healthy aging. Our study aims to identify and describe the positive and negative aspects and the sustainability factors of the BAILAMOS^{TM} program, a culturally-relevant, community-based physical activity dance program for older Latino adults. We conducted a qualitative study on the sustainability of the BAILAMOS^{TM} program that was implemented in 12 centers (senior, community, and church based) across Chicago, IL. We interviewed center directors one month post-maintenance program completion (n=10) and at six months post (n=9). Questions focused on sustainability, and positive and negative aspects of the program. Interviews were audio recorded, transcribed, and analyzed using a Grounded Theory approach. Initial findings indicate that sustainability factors included instruction, environment, interest/enjoyment, social interaction, and perceived benefits. Key factors for program discontinuation included competing activities, undesirable weather, and lack of leadership. Positive aspects included age- and culturally-appropriate activity, enjoyable physical activity, and social interaction. Negative aspects included lack of instruction and participant disinterest over time. This study highlights the desire for an instructive, age- and culturally-appropriate physical activity in order to create a sustainable physical activity program for older Latino adults. These findings can help researchers and community centers to design and offer sustainable programs that would increase the overall health of older Latino adults.

THU - 124 Healthcare Seeking Behavior and Perceived Discrimination in a Healthcare Setting Among Men Who Have Sex with Men: A Comparative Study of La Romana, Dominican Republic and Chicago, USA

Discipline: Health
Subdiscipline: Public Health

Carina Alvarez*, *Northwestern University*; John Flores, *University of Illinois at Chicago*; Shaveta Khosla, *University of Illinois at Chicago* and Maximo Brito, *University of Illinois at Chicago*

Abstract: Previous studies have found that 9% of Latinx men who have sex with men (MSM) experienced discrimination in a healthcare setting, and these discriminatory experiences lead to negative effects on physical health (higher levels of CD4 cells and more severe illness experiences). The purpose of this study is to assess healthcare seeking behavior and perceived discrimination in healthcare encounters among Latinx MSM in Chicago and compare them to an MSM cohort in La Romana, Dominican Republic (DR). Our study administered a quantitative survey covering: demographics, healthcare seeking behavior, and discrimination to a cohort of Latinx MSM in Chicago. The survey administered is similar to that of the 2013 DR study. Eligible participants were 18 years or older, Latinx-identifying, assigned male at birth, have had sex with men in the past 12 months, and were HIV seronegative or of unknown status. In La Romana, 73% reported being counseled or tested for HIV, and only 27 (37%) informed their doctor that they are MSM (n=100). Of the 27, four (15%) reported that their physician reacted in a negative or discriminatory manner. We anticipate that participants will report more positive healthcare seeking behavior and less discrimination in Chicago than La Romana. From anticipated results, we hope to learn more how Chicago Latinx MSM's perceived discrimination impacts healthcare seeking behavior, in comparison to the DR cohort. Results from this study could be used to inform future programming to decrease discrimination in healthcare settings in order to improve health outcomes among Latinx MSM.

THU - 125 Influence of Insurance on African-American Communities' Beliefs and Behavior in Regard to Availability of Breast, Prostate, and Colorectal Cancer Screenings

Discipline: Health
Subdiscipline: Public Health

Melissa Nava*, *DePaul University* and Cheryl Knott, *University of Maryland, College Park*

Abstract: Breast, prostate, and colorectal cancer represent major health concerns in African-American communities. Rates of breast cancer in African-American women living in Prince George County, MD, significantly increased in recent years. These disparities that affect these communities emphasize the need for interventions to increase the use of screenings. Those with low socioeconomic status tend to have lower screening participation rates when compared to those of higher socioeconomic status. This status also relates to the type of insurance one holds which can influence their likelihood of participating in interventions. This study focuses on how the type of insurance a person has relates to the likelihood of their participation in a faith-based organization's health workshops promoting breast, prostate, and colorectal cancer screenings.

In Prince George County, MD, 34 African-American churches and 370 participants were recruited. Participants completed a baseline survey and a 12-month follow-up survey. The baseline survey covered demographics, knowledge of breast, prostate, and colorectal cancer, and screening behavior. The 12-month survey captured usage of health services. Full analysis of the data collected is still being conducted. The data will be analyzed using linear regression models. The expected results include finding those with Medicare or Medicaid as their primary insurance are less likely to participate in health workshops administered by their church compared to those with private insurance. These results hold significance because interventions implemented into faith-based organizations can experience more success if the participant understands the health services available through their insurance.

THU - 127 Is Racial Identity Associated with Health Behaviors Among Black Women?

Discipline: Health
Subdiscipline: Public Health

Taylor Bays*, *University of Detroit Mercy* and Dawn Misra, *Wayne State University*

Abstract: Racial identity among Blacks has been studied for the past several decades with most research focused on its association with physical and mental health. A few studies have examined whether racial identity may be related to health behaviors. Using data from the Life-course Influences on Fetal Environments study (2009-2012), we examined the associations between racial identity and health behaviors of Black women in metro Detroit (N=1410; 71% response). Maternal interviews were conducted during the immediate postpartum hospitalization. The Multidimensional Model of Racial Identity (MMRI) included 15 items with 4-point Likert responses. Three subscales represent the significance attributed by the woman to being Black, defining what it means to be Black: centrality, public regard, and private regard. Health behaviors studied were lifetime exposure to cigarette smoking (26.6%) and marijuana (45.6%). 1257 women had complete data on all variables under study. The independent sample T-test was used to compare the mean scores on each MMRI subscale by behavior. Women who reported cigarette smoking during their lifetime compared to nonsmokers did not show statistically significant differences in the mean score on any subscale. Women who reported marijuana use had significantly lower mean scores on the centrality subscale (12.03 vs. 12.29, p= 0.045) as well as on the public regard subscale (13.17 vs. 13.70, p= 0.002). These findings add to an important body of research on racial identity in Blacks and examines an infrequently studied subgroup: Black women, specifically mothers.

THU - 128 Classification of Chemical Hypersensitivity Potential Based on Gene Expression Profiles

Discipline: Health
Subdiscipline: Other Health

Caitlin Mickles*, *West Virginia University* and Stacey Anderson, *National Institute for Occupational Safety and Health*

Abstract: Occupational allergic disease is a serious public health burden that can result in asthma and allergic contact dermatitis and is often a result of exposure to low molecular weight chemicals. The classification of chemical allergens has proven to be difficult since many agents can elicit multiple hypersensitivity pathways. Studies are also demonstrating a role for exposure to non-sensitizing chemicals such as adjuvants and irritants in allergic disease.

The skin plays a major role in the development of allergy due to its complex immunological environment. Preliminary data have shown that cells in the skin can secrete a variety of cytokines, regulatory cells and molecules in response to chemical exposure, supporting an important role in immunological responses.

For these studies, mice were dermally exposed to representative chemicals (sensitizers, irritants, adjuvants) and the expression of cytokines and cellular mediators was evaluated in skin, lymph nodes and blood over time.

Results identified unique expression profiles for select cytokines and molecular mediators. A20 and TLR4 were increased in the skin for the adjuvant but not for the sensitizers or irritant. In the blood A20 was decreased for the sensitizers and S100A8 was elevated for the irritant. Increases in IL-10 were only observed for the sensitizers in the lymph node.

In order to further the development of preventative and therapeutic strategies to combat allergic disease, the underlying mechanisms must be fully understood. The discovery of novel mediators of chemical allergy will broaden the general classification schemes and views of chemical allergy as a whole.

THU - 130 The Combined Effects of Hfd and Short-Term Stress over Microglial Activation and Blood-Brain Barrier Permeability in Male and Female Sprague Dawley Rats

Discipline: Life Sciences
Subdiscipline: Neurosciences

Wilfred Fonseca-Ferrer*, *University of Puerto Rico in Ponce*; Dariangelly Pacheco-Cruz, *Pontifical Catholic University of Puerto Rico*; Lubriel Sambolin-Escobales, *Ponce Health Science University, Ponce Research Institute*; Maria Colon, *Ponce Health Science University, Ponce Research Institute*; Anixa Hernandez, *Ponce Health Science University, Ponce Research Institute*; Gladys Chompre, *Pontifical Catholic University of Puerto Rico; Ponce Health Sciences University, Ponce Research Institute* and James Porter, *Ponce Health Sciences University, Ponce Research Institute*

Abstract: High-fat diet (HFD) consumption and stress are independently associated with microglia activation and the development of depressive-like behaviors. Activated microglia release cytokines, which can increase blood brain barrier (BBB) permeability by reducing the expression of tight junction proteins such as claudin-5 to allow macrophage infiltration. However, little is known about the effect of the HFD combined with stress on the activation of microglial cells and BBB permeability. We hypothesize that combining HFD and stress will increase depressive-like behavior, reduce claudin-5, and increase CNS inflammation. To test our hypothesis, rats received a LFD or HFD combined with short-term unpredictable stress for 4 days in adulthood. One week later, we found no differences in depressive-like behaviors using forced swim test and sucrose grooming test. Following behavioral procedures, rats were sacrificed and the ventral hippocampus was dissected. We are currently using immunofluorescence assay to evaluate the expression of claudin-5 and the microglial marker Iba-1. We are also using real time PCR to evaluate the expression of inflammatory cytokines in the ventral hippocampus. Although the administration of HFD combined with short-term stress did not increase depressive-like behavior, it may still affect microglial activation, permeability of the BBB, or inflammation in the ventral hippocampus. Supported By: *NIGMS/INBRE P20 GM103475-14, NIH-NIGMS #2R25GM082406 and NIM-HD MD007579 (B.R.A.I.N. and M.A.G.I.C. Core).*

THU - 131 Characterization of Arsenic Distribution on the Crow Reservation

Discipline: Health
Subdiscipline: Other Health

Tillie Stewart*, *Montana State University, Bozeman*; Ellen Lauchnor, *Montana State University, Bozeman* and Kyle Paine, *Montana State University, Bozeman*

Abstract: Arsenic (As) is a common heavy metal contaminant of groundwater in many areas of the world due to anthropogenic and naturally occurring geologic sources. On the Crow reservation, health screenings and well water testing has identified areas on the reservation of high concern for arsenic contamination in drinking water sources.

The objective of this research is to assess co-localization of high As levels with potential anthropogenic sources such as livestock dipping stations and the railroad corridor. Soil will be sampled from former cattle dipping locations, the railroad corridor and locations that have been identified as high in As. Our team will take GPS measurements and soil samples and measure arsenic content and other parameters that may impact As toxicity. The soil analyses will be conducted using EPA soil digestion methods. A GIS map including these data layers will be prepared with results. The project will encourage community interest in and knowledge of environmental and public health issues through participation of tribal college students in the project and involvement of the Crow Environmental Health Steering Committee in dissemination of research results.

The findings of this project will improve health of tribal members by increasing knowledge of arsenic exposure risks and how to mitigate those risks. Maps and interpreted results will be presented to the community and to the homes that may be impacted by higher arsenic levels. Efforts will include free well water testing, explanation of identified risks, and discussion of mitigation options.

THU - 132 Validation of NIRS Under Resting and Post-Ischemic Conditions in the Lower Extremity

Discipline: Health
Subdiscipline: Other Health

Elizabeth Trujillo*, *University of Texas at El Paso*; Manuel Gomez, *The University of Texas at El Paso*; Lisa Rodriguez, *University of Texas at El Paso*; Janeth Juarez, *The University of Texas at El Paso*; Francisco Morales Acuna, *The University of Texas at El Paso* and Alvaro Gurovich, *The University of Texas at El Paso*

Abstract: Near-infrared spectroscopy (NIRS) is an optical technique that allows for noninvasive monitoring of in vivo oxygenation and tissue perfusion. Oxygenation may be associated with microvascular blood flow. However, there is a lack of studies focusing on the relation between both. **Purpose:** to determine if tissue oxygenation, measured via NIRS, and microvascular blood flow, measured via venous occlusion plethysmography (VOP) are associated. **Methods**: Eight subjects (5 females) were recruited for simultaneous NIRS and VOP during resting and post 5-min ischemic challenge. Rapid inflation cuffs where placed on the thigh and ankle of the right leg. Along with the cuffs a strain gauge for VOP was placed on the largest portion of the calf and NIRS probes were placed approximately 8 cm below the knee without interfering with the strain gauge. Percent oxygenation (%SO2), oxygenated hemoglobin (OxHb, AU), and deoxygenated hemoglobin (dOxHb, AU) from NIRS and lower-leg blood flow from VOP were obtained at rest and peak post ischemia. Linear correlations between NIRS and VOP variables were obtained for statistical analysis. **Results:** Correlations between resting values of NIRS and VOP ranged from -0.21 to 0.28 (all $p>0.05$), showing no association between NIRS and VOP during resting conditions. There was as significant correlation ($r=0.86$, $p<0.01$) between peak blood flow and peak dOxHb. **Conclusions:** Findings show that NIRS and VOP values under resting conditions are not associated. However, the strong correlation between peak dOxHb and peak blood flow suggests that tissue de-oxygenation from NIRS may be associated with blood flow in post-ischemic conditions.

THU - 141 Large-Scale Astrocyte Calcium Events Signify Distinct Neuronal Processing Shifts during Hyperarousal

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alana Tillery*, *University of Maryland*; Grayson Sipe, *Massachusetts Institute of Technology*; Vincent Breton-Provencher, *Massachusetts Institute of Technology* and Mriganka Sur, *Massachusetts Institute of Technology*

Abstract: Behavior is influenced by global arousal varying from drowsiness to hyperactive “panic-like” states. Pupil diameter dynamics reflect arousal shifts that predict performance on cognitive tasks. Norepinephrine (NE) is a key sympathetic neuromodulator mediating arousal, and its release from locus coeruleus projections throughout the brain correlates closely with pupil dilations. Cortical neurons and non-neuronal glia express NE receptors that may coordinate arousal shifts but the effects of NE on neurons during periods of hyperarousal remain unexplained. Astrocytes, although electrically silent, mediate homeostatic roles such as neurovascular coupling, ion maintenance, and neurotransmitter uptake. During arousal, spatiotemporally large-scale astrocytic calcium elevations (LACEs) occur at the global level potentially indicating widespread changes in neuronal activity. To explore this relationship, we simultaneously imaged pupil diameter and performed two-photon calcium imaging of astrocytes and neurons in the primary visual cortex (V1) of awake mice. We found that intrinsically-generated LACEs occur sporadically when mice were presented visual stimuli, and that LACEs strongly correlated with large-magnitude pupil dilations. Also, neuronal activity was suppressed during LACEs, resulting in a decrease of visual decoding accuracy. Our results indicate neuron-astrocyte networks coordinate a global activity switch signifying hyperarousal and interrupted sensory processing. In the future, we will measure arousal due to locomotion and link this to excitatory and inhibitory neuronal activity, LACEs, and pupil dilation. Describing cellular mechanisms underlying arousal is intrinsic to understanding hyperarousal dysfunction, such as post-traumatic stress disorder, in which aberrant NE release induces decreased cognitive performance and impairment in quality of life.

THU - 142 Investigating the Role of Transcription Factor 4 (TCF4) in Astrocytes and Its Impact on Neurodevelopment

Discipline: Life Sciences
Subdiscipline: Neurosciences

Lillian Murphy*, *California State University, Sacramento*; Laura Craciun, *University of California, Berkeley* and Kaoru Saijo, *University of California, Berkeley*

Abstract: Astrocytes have traditionally been thought of as support cells for neurons. However, growing evidence indicates that they are actively engaged alongside neurons in the formation and maintenance of synapses, and are critical for proper neural circuitry development. Many neurological disorders are characterized by changes in synaptic connectivity, including Pitt-Hopkins Syndrome (PTHS), which is caused by haploinsufficiency of *Transcription Factor 4* (*TCF4*). Previous work has shown that astrocytes highly express *TCF4*, making them potential actors in PTHS. We hypothesize that TCF4 is essential for astrocyte function in neurodevelopment, and that mutating *TCF4* disrupts their normal function, resulting in PTHS. We first aim to assess how a common PTHS-causing point mutation in *TCF4* impacts post-natal neurodevelopment using a mouse model (TCF4$^{R579W/+}$). We used targeted injection of AAV viruses into the prefrontal cortex and hippocampus to sparsely label neurons for morphological analysis. Specifically, we assessed changes in neuronal connectivity by examining the shape and number of labeled dendritic spines. We observed that TCF4$^{R579W/+}$ mice have decreased number of dendritic spines compared to their wild-type (WT) littermates. Next, to determine if observed aberrant neural connections could be correlated to astrocyte dysfunction, we labeled astrocytes in TCF4$^{R579W/+}$ and WT mice using immunohistochemistry to analyze variation in astrocyte number and morphology. To compliment this with *in vitro* work, we also generated human astrocyte cell lines with *TCF4* point mutation (R580W) and knockout of *TCF4*. Our study seeks to be the first to demonstrate how astrocyte-specific mutations in *TCF4* impact neuronal connectivity and subsequently lead to PTHS.

THU - 200 The Effect of Hawaii's Native Versus Non-Native Plants on the Growth of Disease-Transmitting Mosquitoes

Discipline: Life Sciences
Subdiscipline: Microbiology

Kahiwahiwa Davis*, *University Of Hawaii Mānoa* and Matthew Medeiros, *University of Hawaii at Manoa*

Abstract: In nature, mosquitoes mature through their larval phase in aquatic environments with unique chemistry derived from plant detritus and this impacts the capability of a mosquito to transmit disease as an adult. This study aims to identify the effect of native Hawaiian and non-native plant detritus on the growth and disease-transmitting capabilities of *Aedes albopictus*, a globally invasive disease vector. Three native plants with known applications in traditional Hawaiian medicine (*Mamaki, Kuku*i, and *Ohia Lehua*) and one non-native/invasive plant (Strawberry Guava) were used to make infusions and create larval media in mesocosms in which *A. albopictus* transitioned through the larval stages. Two filtered (one inoculated with Asaia culture) and two unfiltered (one inoculated with Asaia culture) mesocosms were created in triplicates per infusion; sterile water mesocosms were used as a control. Mosquitoes were tracked as they transitioned through larval stages. Upon emergence as adults, the size of their abdomen, hindleg, and wing were measured. We found that invasive Strawberry Guava accelerates the emergence rate of *A. albopictus,* resulting in adults that are smaller than those grown in controls and other infusion treatments. Future work aims to uncover how the chemistry of the larval environment influences the colonization of a common bacterial symbiont, *Asaia*. This study informs how variation in natural larval habitats induced by differing sources of plant detritus may impact the capacity of mosquito populations to transmit disease.

THU - 201 Studying the Effect of Emergent Interactions in the Population Dynamics of an Opportunistic Bacterial Pathogen Exposed to Antibiotic Treatment

Discipline: Life Sciences
Subdiscipline: Microbiology

Indra Gonzalez Ojeda*, *University of Puerto Rico at Mayaguez, Chemistry department* and Kevin Wood, *University of Michigan*

Abstract: Understanding the underlying population dynamics of bacterial communities may lead to improved strategies for combating antibiotic resistance, a growing public health threat. Cooperation and competition between microbial subpopulations may govern population survival or extinction in the presence of antibiotics, but these drug-dependent ecological interactions are often poorly understood. In this study, we investigate the effects of beta lactam antibiotics on the population dynamics of *E. faecalis*, an opportunistic bacterial pathogen, using mathematical models and quantitative laboratory experiments in computer-controlled bioreactors. We find that population growth in the presence of drug depends on density-dependent feedback between population size, drug efficacy, and the rate of drug inflow and outflow from the system. This interplay—driven, in part, by local changes in pH as cells proliferate—can lead to surprising dynamics, including populations that approach a stable, intermediate size that corresponds to neither extinction nor maximal proliferation. This work highlights counterintuitive dynamics in the response of simple microbial communities to antibiotic and may lay the groundwork for rationally designed antibiotic treatment strategies that harness the intrinsic ecological interactions within bacterial populations.

THU - 202 Breaking the Wall of Intolerance between *H. Pylori* clonal Colonies

Discipline: Life Sciences
Subdiscipline: Microbiology

Yasmine Elshenawi*, *University of California, Santa Cruz*; Skander Hathroubi, *University of California, Santa Cruz* and Karen Ottemann, *University of California, Santa Cruz*

Abstract: *Helicobacter Pylori* is a Gram negative bacteria that frequently causes gastrointestinal disease and gastric cancers. *H. pylori's* ability to colonize the stomach and survive is dependent on chemotaxis and motility. A common method for studying chemotaxis and macroscopic displacement is the use of motility agar assays. In standard conditions, clonal colonies will migrate until forming a wall to prevent direct colony-to-colony contact through an unknown mechanism. In this study, we explore a genetic determinant for the wall of intolerance between clonal *H. pylori* colonies. A pool of 10,000-clone G27 *H. pylori* library was grown on standard motility agar to identify potential mutants that did not form walls. We successfully isolated twenty mutants that merged under standard motility agar. Interestingly, our preliminary DNA sequencing results have shown that five mutants have transposon insertion in the *hopC* gene. The *hopC* gene codes for an outer membrane protein which was previously shown to be important in cell adhesion and gastric epithelial colonization. In conclusion, we characterized *hopC* as a contributor to the wall of intolerance. Further investigation is being done to determine the role of *hopC* in motility and cell-to-cell adhesion. Future research on *hopC* can lead to anti-adhesive strategies for treating *H. pylori* infections.

THU - 203 A Study to Determine the Importance of Elongation Factor P on Sporulation in Bacillus Subtilis

Discipline: Life Sciences
Subdiscipline: Microbiology

Ananda Rankin*, *Pennsylvania State University*; Heather Feaga, *Columbia University* and Jonathan Dworkin, *Columbia University*

Abstract: *Bacillus subtilis* is a bacterium that forms spores under nutrient limiting conditions. A spore is a highly resistant, dormant cell state and can remain viable, even in extreme environments, for thousands of years. A recent screen for genes important for sporulation identified elongation factor P (EF-P) as a potentially important gene. When the ribosome translates mRNA encoding several proline codons in a row, it stalls and is slow to resume translation of the rest of the message. EF-P is essential for alleviating this stalling and contributes to maintaining the translational capacity of the cell. During sporulation, cells undergo a developmental program which requires the translation of more than 200 new proteins. Since translation is essential to the process of sporulation, we hypothesized that EF-P is especially active during sporulation and is necessary for maintaining the high levels of protein synthesis required for spore development. In this study, the sporulation efficiency of a ΔEF-P mutant was studied to determine whether the deletion of EF-P results in a loss of the expression of sporulation-necessary genes. Sporulation assays, ribosome profiling, and reporter assays indicate that a deletion in EF-P results in a delay in sporulation due to the under-expression of a cascade of early sporulation genes. These data suggest that this mutant has a defect in sporulation, and indicates the importance of several proteins that require EF-P for efficient expression. These data enhance our understanding of the early events in sporulation and also define a physiological role for this highly conserved elongation factor.

THU - 204 Secretomes from Metastatic Breast Cancer Cells, Enriched for a Prognostically Unfavorable LCN2 Axis, Induce Anti-Inflammatory MSC Actions and a Tumor-Supportive Premetastatic Lung

Discipline: Life Sciences
Subdiscipline: Microbiology

Nathalie Nadales*, *California State University Northridge, Department of Biology*; Francesca Sanchez, *California State University Northridge, Department of Biology*; Kayla Meade, *California State University Northridge, Department of Biology*; Analine Aguayo, *California State University Northridge, Department of Biology*; Sarkis Hamalian, *California State University Northridge, Department of Biology*; Toni Uhlendorf, *California State University Northridge, Department of Biology*; Lisa Banner, *California State University Northridge, Department of Biology* and Jonathan Kelber, *California State University Northridge, Department of Biology*

Abstract: Cancer metastasis is responsible for the clear majority of cancer-related deaths. Survival and expansion of cancer cells at secondary sites requires that these premetastatic microenvironments be primed by primary tumor cells and their secreted factors. Efforts to date have been limited by immune-deficient *in vivo* models and/or the need for finely-tuned analysis time points that reduce contributions from early-disseminating cancer cells. In this regard, we developed a tumor cell-free syngeneic breast cancer model for characterizing tumor cell secretome-mediated reprogramming of premetastatic tissues. We demonstrate that secretomes from metastatic breast cancer cells differentially regulate the lung and brain, promoting a tumor-supportive lung microenvironment with both elevated CD73 expression and decreased TNFα expression. Using *in vitro* models of CD73-positive mesenchymal stem cells (MSCs) and macrophages/monocytes, we tested whether MSCs can mediate anti-inflammatory effects of metastatic breast cancer cells. Notably, conditioned media from metastatic Py230 cells reprogrammed the secretomes of MSCs toward an anti-inflammatory state. Mining transcriptome data from Py8119 and Py230 cells revealed a lipocalin 2 (LCN2) axis that is selectively expressed in the metastatic Py230 cells, predicts poor breast cancer patient survival and is elevated in circulating serum of mice chronically treated with conditioned media from Py230 cells. Taken together, these results establish the utility of an immune-competent tumor cell-free model for characterizing the mechanisms of breast cancer cell priming of the premetastatic niche, demonstrate that MSCs can mediate the anti-inflammatory effects of metastatic breast cancer cells and substantiate LCN2 as a promising therapeutic target for blocking breast cancer progression.

THU - 205 A Pan-Lineage Model to Understand Antimicrobial Resistance through Adaptive Selection of Tolerance in *Mycobacterium Tuberculosis*

Discipline: Life Sciences
Subdiscipline: Microbiology

Amy Zamora*, *The Institute for Systems Biology*; Vivek Srinivas, *The Institute for Systems Biology*; Jacob Valenzuela, *The Institute for Systems Biology*; Eliza Peterson, *The Institute for Systems Biology* and Nitin Baliga, *The Institute for Systems Biology*

Abstract: Antimicrobial tolerance (AMT) and frequent emergence of antimicrobial resistance (AMR) extend and complicate tuberculosis's (TB) standard 6-month, four-drug treatment; adding onto its high disease burden. AMT, the ability of bacteria to survive transient exposures of antibiotics at inhibitory concentrations without adjusting susceptibility, gives bacteria the ability to revive infection after treatment. This leads to recalcitrant infections in the host and allows mutations to accumulate in the reviving bacteria. Often, these mutations encompass loci that confer resistance to multiple drugs. Therefore, AMT unintentionally aids in the emergence of AMR, the ability of bacteria to survive and proliferate through increasingly high concentrations of antimicrobials. Despite its implications in preventing a patient's TB treatment, there is still very little known about the mechanisms of obtaining AMT and its relationship with AMR. To better understand this relationship, we utilize and expand the eVOLVER, a continuous culture device, to evolve antibiotic tolerance in the model, non-pathogenic *Mycobacterium - M. smegmatis.* Through such evolution experiments, we observe genetic mutation pathways accompanying tolerant phenotypic adaptation of bacteria to lethal drug exposures, eventually leading to AMR. This technique is further applied across varying geographic lineages of *M. tuberculosis*, the bacteria causing TB in humans. This pan-lineage observation provides us with strain-specific (and thus patient-specific) treatment targets to block the pathogen's adaptation to tolerance and resistance. Such information thus allows us to implement a systems approach for predicting the development of these adaptive traits in TB and provides us with a tool to combat its overwhelming global disease burden.

THU - 206 Cyanophage) Exhibit Differential Infectivity Profiles on Different Hosts within a Genus As Well As across Genera: Implications for the Dispersal of Oxygenic Photosynthetic Machinery and the Evolution of Oxygenic Photosynthesis.

Discipline: Life Sciences
Subdiscipline: Microbiology

Guillermo Leyva*, *University of Arkansas*; Yelimar Jimenez, *University of Arkansas*; Kelsey Bevenour, *University of Arkansas*; Elizabeth Padilla Crespo, *La Universidad Interamericana* and Ruben Michael Ceballos, *University of Arkansas*

Abstract: Cyanobacteria are a diverse phylum of photosynethetic prokaryotes with the ability to produce oxygen. Although there are well-established (albeit competing) theories on how oxygenic photosynthesis may have emerged thus initiating the Great Oxygenation Event (ca. 2.45 billion years ago), the mechanism by which oxygenic photosynthetic machinery (i.e., water-splitting genes) were widely-dispersed remains controversial. Recent evidence suggests that viruses of cyanobacteria, otherwise known as *cyanophage*, have the ability to transfer genes from one host to another through “transduction” or phage-mediated horizontal gene transfer (pHGT). The Ceballos lab (and several other labs) have demonstrated that cyanophage can cross genera and even higher order taxonomic groups. Based on these earlier results, the hypothesis that: pHGT can result in the successful transfer and ‘capture’ of photosynthetic genes – was tested. Using environmental isolates of cyanophage and strains of host from two different families of cyanobacteria, cross-infection assays and genetic/genomic methods were used to determine if pHGT could result in gene capture and expression in a previously naïve host. Early data indicate successful cross-infection and potential gene capture. However, the probability of a captured gene to result in enhanced or novel cell function depending upon infection type (e.g., single phage with a photosynthetic ‘cassette’ versus multiple infections each delivering individual genes) remains unclear. This work, however, does demonstrate the potential of cyanophage to serve as agents of rapid gene dispersal in the environment, which can impact evolutionary trajectories of multiple taxa.

THU - 207 Development of Genetic Chimera of Clostridia to Produce Anti-Bacterial Agents Against Multi-Drug Resistant Microorganism

Discipline: Life Sciences
Subdiscipline: Microbiology

Monai mitchell*, *Claflin University* and Omar Bagasra, *Claflin University*

Abstract: The emergence of multiple drug resistant microorganisms (MDRs), especially methicillin resistant Staphylococcus aureus(MRSA) and oxacillin-resistant Staphylococcus aureus (OMSA) are two leading causes of hospital-acquired infections and have become a serious global problem.

With the antibiotic pipeline drying up and lack of development of new antimicrobials, there is a crucial need to develop new ways to ensure antibiotics work for future generations. One reason for the lack of new antibiotic development is the paucity of new microbes and fungi that can generate them. Our laboratory has developed a novel patented technology to create new microorganisms in vitro that can create antimicrobials. This is done by fusing protoplasts from different Clostridia spp. to create genetically unique chimeras that produce unique chemicals with potent anti-bacterial effects. The objective of this proposal was to use this powerful new synthetic biology technology to create new antibiotics effective against MRSA and other multi-drug resistant microorganisms. Our preliminary data support our objective and demonstrate successful generation of chimeras that exhibit antibacterial effects against MRSA, and MRD E. Coliand P. aeruginosa.

THU - 208 Survey, Isolation and Characterization of Bioluminescent Bacteria from Tropical Waters of Puerto Rico.

Discipline: Life Sciences
Subdiscipline: Microbiology

Joelis Lama*, *University of Puerto Rico at Cayey*; Edwin Vazquez, *University of Puerto Rico at Cayey*; Priamo Pichardo, *University of Puerto Rico at Cayey*; José Silva, *University of Puerto Rico at Cayey* and Nicole Rivera, *University of Puerto Rico at Cayey*

Abstract: Puerto Rico has a rich diversity of ecosystems that includes a dry and a rainforest, a karst region, a cave system, thermal waters, salt flats and bioluminescent bays, among others. There are at least seven bioluminescent bays in the world, three of which are in Puerto Rico. The bioluminescence in these bays is a phenomenon ascribed to a dinoflagellate, *Pyrodinium bahamense*. It occurs when the enzyme luciferase acts on its substrate, luciferin, with the emission of light in the process. There are many other bioluminescent organisms such as fireflies, fungi, mollusks and fish, sometimes by association with bioluminescent bacteria. We isolated more than twenty bacteria from all over the island, and from Vieques and Culebra islands, off the east coast of Puerto Rico. We describe at least twelve bacteria that have been isolated, partially characterized and identified from tropical waters of Puerto Rico. Gram staining and biochemical tests demonstrated that some bacteria exhibited biochemical and morphological differences, as well as significant variations in the amount of light emitted as recorded with a luminometer. 16S rRNA sequence analysis showed that most bacteria were *Vibrio* spp., and at least one was a *Photobacterium* species. DNA sequence analysis showed that at least two have no similarities whatsoever with reported sequences, indicating that they may belong to previously unknown species. This study adds to our knowledge of the rich biodiversity of Puerto Rico, and opens the doors to further studies to determine the potential contribution of these bacteria to the bioluminescence of bioluminescent bays.

THU - 209 Identifying Genes That Play a Role in Long Term Stationary Phase

Discipline: Life Sciences
Subdiscipline: Microbiology

ERIK MARTINEZ*, *California State University Dominguez Hills* and Karin E. Kram, *California State University, Dominguez Hills*

Abstract: *Escherichia coli* can adapt to live in an environment without any additional nutrients for long periods of time. When *E. coli* grows in an environment where nutrients are scarce, they enter long term stationary phase (LTSP), which mimics a natural environment. In order to identify nonessential genes that play a role in survival during LTSP, we competed cells in the KEIO collection and wild type (WT) *E. coli* cells. The KEIO collection is a set of *E. coli* strains, each with a single-gene deletion of a nonessential gene. The KEIO collection represents all non-essential genes – with a total of 3985 strains. We performed competitions during 10 days of incubation, into LTSP. We observed cell growth after one, five, and ten days of incubation. After completing the entire collection, we identified 102 gene deletions that affected the cell's ability to compete with WT. 29 strains with deletions had an advantage over WT cells, whereas the remaining 72 strains had a disadvantage when competed against the WT. Moving forward, we will confirm the phenotype of mutant strains to ensure that no additional factors were influencing the competition. We will then determine why these genes play a role in survival into LTSP by determining their function in long-term cultures.

THU - 210 Effects of Non-Nutritive Sweeteners on Common Bacteria in the Mammalian Gut

Discipline: Life Sciences
Subdiscipline: Microbiology

Dalila Gonzalez*, *Cañada College*; Nicol Laura, *Cañada College*; Nathan Staples, *Cañada College*; Maria Garduño, *Cañada College* and Kaitlyn Burke, *Cañada College*

Abstract: Consumption of non-nutritive sweeteners (NNS) has increased dramatically within the past decade. The FDA has approved over 5 NNS, yet we still do not clearly understand the implications these NNS have on the bacteria in the human gut microbiome. Bacterial homeostasis in our gut is important for efficient digestion. Dysbiosis, bacterial imbalance or maladaptation in the gut, is linked to an increased risk for diabetes and other diseases (Carding et al). Previous research has shown that sucralose causes a decrease in the growth of *Escherichia coli*. We are interested in investigating the effect of this and other NNS in other bacteria species present in the mammalian gut, including whether there are any that can metabolize NNS. We used *E. coli, Klebsiella aerogenes*, *Enterococcus faecalis*, and *Bacillus subtilis*, and quantified differences in growth due to NNS. We supplemented rich growth media with individual and combined NNS and monitored their growth. We discovered that both sucralose and acesulfame k have a bacteriostatic effect on the growth of *E. coli* and *K. aerogenes.* High concentrations of acesulfame K completely stunted growth. Furthermore, these strains cannot grow on minimal media supplemented with NNS as the only carbon source. We plan to investigate the cause of these growth defects, and expand upon combinatory minimal media experiments. The questions this project will elucidate hold promise in improving the health and wellness of humans across the world, as well as helping us better understand the symbiotic relationship we hold with bacteria.

THU - 211 Friends or Foes – Effect of Probiotic Microbiota on Group B Streptococcus

Discipline: Life Sciences
Subdiscipline: Microbiology

Jan Mikhale Cajulao*, *San Francisco State University* and Lily Chen, *San Francisco State University*

Abstract: *Streptococcus agalactiae*, aka. Group B Streptococcus (GBS), is a bacterium found in the cervix of ~25% of healthy women and is a leading cause of neonatal fatalities since it can vertically transfer to fetuses. *Lactobacillus* spp. dominate the vaginal microbiome and inhibit the growth of pathogens. This project explores the potential of using probiotics such as *Lactobacillus* spp. to treat GBS infections. HeLa cells were used as an *in vitro* model for the human cervix to examine the ability of *Lactobacillus rhamnosus* and *plantarum* in inhibiting GBS vaginal epithelium colonization. HeLa cell monolayers were grown on sterile coverslips and infected with GBS, *L. rhamnosus*, *L. plantarum*, or a combination of those species. Cells were fixed with cold methanol and visualized using light microscopy after Giemsa stain to allow for enumeration of adherent bacteria and HeLa cells. Preliminary results show that the amount of GBS that remain adherent to HeLa cells post infection is reduced by presence of *L. rhamnosus* and *L. plantarum*. Also, the number of HeLa cells remaining on a coverslip after infection are reduced in the presence of GBS, and even further reduced when supplemented with Fetal Bovine Serum (FBS) during infection. However, when HeLa cells were simultaneously infected with GBS and either *L. rhamnosus* or *plantarum*, a higher number of HeLa cells remain on the coverslip than when infected with GBS alone. This suggests that GBS pathogenicity *in vitro* is reduced by *L. rhamnosus* and *plantarum* but improved by an ingredient(s) in FBS.

THU - 212 Optimization of Isothermal Amplification Methods in a CRISPR-Based Diagnostic Tool for Detection of Tick-Borne Pathogens

Discipline: Life Sciences
Subdiscipline: Microbiology

Nora Gilliam*, *Indiana University Purdue University Indianapolis*; Gordon Adams, *Broad Institute of MIT and Harvard*; Jacob Lemieux, *Broad Institute of MIT and Harvard* and Pardis Sabeti, *Harvard University*

Abstract: CRISPR-based diagnostic tools have the potential to surpass the limits of current diagnostic tools with efficient, field-deployable technology; transforming tick-borne infection clinical care and clinical diagnosis more broadly. Previous diagnostic tools have either been limited in sensitivity or required consistent and reliable electricity and transportation, which are not always guaranteed in a resource-limited or field setting. SHERLOCK (Specific High-sensitivity Enzymatic Reporter unLOCKing) is a CRISPR-based diagnostic tool that couples isothermal recombinase polymerase amplification (RPA) of target genetic material and detection of the amplified material by CRISPR-Cas13a that can then be visualized on lateral-flow paper to achieve sensitivity and deployability. A remaining challenge is multiplexing to test for multiple possible infections; despite RPA's capability to isothermally amplify target genetic material, this method has been shown to amplify nonspecifically which generates undesired products and introduces design and efficiency challenges for multiplexed amplifications. We hypothesize that the isothermal amplification methods helicase dependent amplification (HDA) and strand displacement amplification (SDA) are multiplexable, compatible with CRISPR-Cas13a detection, and may amplify more specifically than RPA. Preliminary data suggest that HDA can amplify target genetic material from these pathogens and be used in a SHERLOCK assay. Further experiments will elucidate HDA multiplexability and determine whether SDA can be coupled with CRISPR-Cas13a detection and further multiplexed. We anticipate that the outcome of these experiments will lead to further optimization and validation for SHERLOCK technology as a novel approach to clinical detection of tick-borne pathogens.

THU - 213 Identification and Characterization of Secondary Mutations in Antibiotic-Resistant *Neisseria Gonorrhoeae*

Discipline: Life Sciences
Subdiscipline: Microbiology

Marissa Duckett*, *University of Kansas* and Yonatan Grad, *Harvard TH Chan School Of Public Health*

Abstract: *Neisseria gonorrhoeae*, the cause of gonorrhea, is becoming less susceptible to antibiotics. Identifying and characterizing the causes of resistance to individual and combination antibiotic treatments will help improve diagnostics and thus treatment approaches. The current treatment for a case of gonorrhea is dual therapy with ceftriaxone, a cephalosporin class antibiotic, and azithromycin, a macrolide antibiotic, under the hypothesis that treatment with two antibiotics will curb the development of antibiotic resistance. Macrolide antibiotics act by inhibiting ribosomal activity. Resistance can be caused by a G70D substitution in RplD, a ribosome associated protein that abuts the macrolide ribosomal binding site. In lab experiments, a secondary mutation, RplD Q66R, is frequently observed upon selection for resistance to azithromycin, but its function is unknown. The focus of this project is to better understand the development of this and other secondary mutations for other macrolide antibiotics, erythromycin and clarithromycin. If the Q66R substitution arises in laboratory experiments under selection with erythromycin and clarithromycin, the primary resistance mutation, G70D, will be genetically reversed so that phenotypic analysis can uncover more information about the secondary mutation and its contribution to bacterial fitness. Computational analysis of clinical isolates will also be conducted to investigate whether the secondary mutation only occurs in lab strains or in clinical strains as well. The conclusion of this project will aid in improving diagnosis and treatment of gonorrheal infection.

THU - 214 Prevalence of *Enterococcus* Spp. As Contaminants of Sea Water Obtained from Recreational Areas in Puerto Rico

Discipline: Life Sciences
Subdiscipline: Microbiology

Yaidelice Rodríguez Álamo*, *Universidad Ana G. Mendez*; Frances Vélez González, *Universidad Ana G. Mendez*; Jose Santoni, *Universidad Ana G. Mendez*; Orlando Santiago, *Universidad Ana G. Mendez* and Nydia Rodríguez-Bonano, *Universidad Ana G. Mendez*

Abstract: Contamination of coastal bathing waters with *Enterococcus* spp. affects both, human and marine ecosystems health. Recent multiple press reports in Puerto Rico (PR) have informed the public that many recreational areas are not suitable for bathers during the current summer season. These had established that the high count of *Enterococcus* is dangerous for beach goers due to the fact that the bacterium can cause multiple human illnesses. The main objective of our project was to compare the count and prevalence of *Enterococcus* spp. and non-*Enterococcus* bacteria in sea water samples from six highly visited recreational areas in PR. To achieve our objective, water samples were collected and processed using the Membrane Filtration procedure. Then, the filters were placed on the selective medium m-Enterococcus agar (m-E) and incubated for 48 hours at 42°C. Individual colonies that grew on top of the filters were counted, picked and sub-cultured onto brain-heart infusion (BHI) agar and incubated at 37°C for 16-24 hours. To presumptively identify enterococci, we performed the catalase and esculin hydrolysis tests to each isolate. More than 6,270 colonies were recovered from the mE agar plates, yet only 24 were presumptively identified as *Enterococcus* spp. These results also indicated that most of the bacteria isolated from the samples were non-enterococci and are most likely staphylococci. The presence and diversity of *Enterococcus* spp. in sea water is unquestionable but we believed that they are mis-identified, most of the time, as the cause of high-level contamination in the recreational waters in PR.

THU - 215 Flagellar Genes Impact on Bacterial Colonization Efficiency

Discipline: Life Sciences
Subdiscipline: Microbiology

Thricia Zabala*, *San Francisco State University*; Natalie Saldana-Rivera, *San Francisco State University*; Loi Ma, *San Francisco State University* and Joseph Chen, *San Francisco State University, San Francisco*

Abstract: The alpha-proteobacterium, *Sinorhizobium meliloti (S. meliloti)*, serves as a model in order to understand the mutualistic symbiosis between rhizobia and legumes, including agriculturally significant crops such as alfalfa and soybean. During symbiosis, the bacterial cells influence the formation of nodules on the roots of legume hosts, which colonize the nodules and perform nitrogen fixation in exchange for carbon compounds. Here we have shown that biofilm formation by *S. meliloti* enhances host colonization. In a previous mutagenesis screen, we have identified transposon insertions in flagellar genes that reduced biofilm development. As a result, we are currently investigating whether flagellar motility affects symbiosis efficiency. We are currently complementing the mutations using plasmids that are carrying wild-type flagellar genes, to ensure that the motility defects can be accredited to the individual transposon insertions. Moving forward, we then plan on examining the colonization efficiency of these mutants. By understanding the cellular and molecular mechanisms of *S. meliloti* that affect symbiosis, we can gain new insights into microbe-host interactions, which play important roles in both agriculture and bacterial infections in humans.

THU - 216 Non-Motile Pseudomonas Aeruginosa Structure Antibiotic-Resistant Accumulation

Discipline: Life Sciences
Subdiscipline: Microbiology

Brandon Brown*, *Dartmouth Giselle School of Medicine* and Brent Berwin, *Dartmouth Giselle School of Medicine*

Abstract: Pseudomonas aeruginosa is an opportunistic bacterial pathogen that is responsible for infections associated with invasive instrument and operative procedures, chronic infections with persistent lung disease and compromised immune responses, and is also responsible for infections frequently associated with burned wounds. The leading strategy to eradicate Pseudomonas aeruginsoa infections is through treatment with antibiotics, and the resistance increases as the bacteria transitions to a non-motile lifestyle during chronic infections. Motile bacteria are far more adequate than Pseudomonas that lack flagella motility at forming antibiotic-resistant bio-films on surfaces, however it is unknown whether the non-motile bacteria can form anitbiotic resistant aggregates that are non-surface adherent. Our central hypothesis is that non-motile bacteria can form aggregates that will attain antibiotic resistance. In order to test this hypothesis, we tested the DH211, DH228, and DH1312 clinical isolates of Pseudomonas aeruginosa for motility, surface adherent bio-film formation and aggregate formation. Our preliminary data demonstrate that, as predicted, the more motile the strain, the more bio-film it formed. Importantly, regardless of motility, flow cytometry assessment of aggregate formation showed that all strains of bacteria grew as non-adherent aggregates, and these aggregates were resistant to antibiotic Gentimicine. Current efforts are directed at the use of GFP expression to generate florescent bacterial strains to evaluate aggregate formation by microscopy. These studies will expand our knowledge of the mechanisms by which clinical Pseudomonas aeruginosa strains may become antibiotic-resistant.

THU - 217 **Molecular Mechanisms of *E. coli* Susceptibility to the Type VI Secretion System**

Discipline: Life Sciences
Subdiscipline: Microbiology

Eleanor Wang*, *University of California, San Diego*; Kristine Trotta, *University of California, San Francisco* and Seemay Chou, *University of California, San Francisco*

Abstract: Bacteria live in dense biofilm communities that are influenced by contact-dependent signaling mechanisms. For example, the Type VI Secretion System (T6SS) of *Pseudomonas aeruginosa* mediates interbacterial competition to shape the composition of its communities. Upon activation, the *P. aeruginosa* T6SS punctures neighboring bacteria and injects protein toxins (effectors) that compromise a variety of bacterial cell structures. However, *P. aeruginosa* doesn't antagonize all bacterial species with the same degree of lethality and not all T6SS events result in cell death. Our aim is to understand the molecular mechanisms that dictate the susceptibility of recipient cells to T6SS. Our hypothesis is that the variability of these outcomes reflects an evolved specificity of T6SS towards certain target species, which is driven by interactions of T6SS effectors with their targets. To investigate this, we conduct a CRISPR interference-based screen in *Escherichia coli* to identify essential genes that are important for susceptibility or resistance to T6SS. We identify several genes involved in cell wall synthesis that contribute to susceptibility. To further investigate the molecular mechanism behind T6SS lethality we express a cell wall-degrading effector from *P. aeruginosa*, Tae1, in our knockdown strains to generate growth curves and perform microscopy to assess loss-of-function phenotypes for interesting genes. We hope that our results will provide a deeper understanding of bacterial fitness in mixed microbial communities.

THU - 218 **Construction of a cDNA-Based RNAi Library for Genetic Screening in the Human Pathogen *Cryptococcus Neoformans***

Discipline: Life Sciences
Subdiscipline: Microbiology

Paola M. Goyco-Fergelec*, *University of Puerto Rico* and Felipe H. Santiago-Tirado, *University of Notre Dame*

Abstract: *Cryptococcus neoformans* is an environmental yeast with worldwide distribution. In immunocompromised humans, it can cause a variety of life-threatening infections, called cryptococcosis, ranging from pneumonia to central nervous system meningitis. Cryptococcosis used to be a disease mostly restricted to AIDS patients, but due to medical advances, such as chemotherapy for cancer treatment or immunosuppressive drugs for organ transplants, it has expanded to other patient populations. Given the increasing burden of cryptococcal disease and the limited number of antifungal drugs available, there is a real need for new therapeutics. However, in the cryptococcal field, there are few genome-wide genetic techniques and tools that would otherwise increase our understanding of the pathogens and accelerate biological discovery. Addressing this, here we focus on the construction of a complementary DNA-based RNA interference library of *C. neoformans* as a powerful new tool for genetic and molecular studies in this fungus. The construction is based on the use of an RNAi vector where two regulatable promoters flank a piece of cDNA generated from specific conditions related to the question to be addressed. As a proof-of-principle, RNA isolated from cultures grown in rich media at 37 °C was used to generate the library. Various tests involving *URA5* and *ADE2* genes, as well as gel electrophoresis analyses, were done to evaluate the library's complexity and efficiency. We would initially use this library to screen for genes required for high-temperature growth, but it can be tailored for various other genetic screens as well.

THU - 221 **Engineering Split-Peroxidase Systems to Find Novel Neuron-Microglia Interactions**

Discipline: Life Sciences
Subdiscipline: Neurosciences

Matthew Mitchell*, *Midwestern State University*; Saadia Hasan, *National Institutes of Health, Bethesda, Maryland* and Michael Ward, *National Institutes of Health, Bethesda, Maryland*

Abstract: Frontotemporal Dementia (FTD) is a disorder generally carrying a poor prognosis with no current treatments for halting or reversing its life-altering symptoms. While several genetic aspects of FTD have been elucidated in recent years, many of the central disease mechanisms are still largely unknown. One recently implicated mechanism in the progression of FTD is microglia-neuron interactions outside of the synapse. While it is generally accepted that microglia play a macrophage-like role in the brain and are involved in synaptic pruning during neurodevelopment, evidence suggests that they may also be involved in neuronal degradation in late adulthood. To test this theory, we engineered nanobody-conjugated split peroxidase systems (sAPEX and sHRP) using Biotinylation by Antibody Recognition (BAR) methodologies to elucidate new interactions between microglia and neurons in human and rat brain tissue.

We aim to construct peroxidase-nanobody fusions in silica, followed by In-Fusion cloning to generate the plasmid and amplification in E. coli. After purification of the desired plasmid from the bacteria, HEK293T cells will be transfected to express our desired construct. Collected cell media will be used for immunohistochemistry on human and mouse brain slices. We will use confocal microscopy to validate the effectiveness of this method.

Currently, we are transitioning into the HEK293T transfection phase of experimentation. Preliminary diagnostics have confirmed that we have successfully engineering the desired plasmids. Preliminary data using BAR method with intact peroxidases shows promising results, therefore we hypothesize that the split peroxidase system will help uncover interacting interfaces, such as microglia surface and neuronal synapses.

THU - 222 **Lysosomal Trafficking and Distribution in Astrocytes**

Discipline: Life Sciences
Subdiscipline: Neurosciences

Lillian Rose*, *University of California, San Diego*; Natalia Slepak, *University of California San Diego* and Gentry Patrick, *University of California San Diego*

Abstract: Protein degradation is a key process important for regulating cellular homeostasis and preventing disease. However, little is known about the role of degradation in regulating neuronal activity. Our lab is interested in understanding lysosomes, a degradative organelle, in neurons. Lysosomes may be more actively involved in regulating synaptic activity than previously thought. In neuronal culture, a large portion of degradation is conducted by astrocytes, which are a type of glial cell that play an important supporting role to neurons. I seek to characterize the role of lysosomes in regulating synaptic strength and activity by analyzing the distribution and trafficking of lysosomes in both astrocytes and neurons in response to different synaptic activity paradigms. Since we know that astrocytes are heavily involved in rapid uptake of excess proteins and neurotransmitters in the perisynaptic space, we expect that there may be increased localization of lysosomes in astrocytes near synapses. We also think that there may be increased trafficking of lysosomes to these areas when activity is chronically or acutely upregulated. I am transfecting astrocytes with LAMP1-GFP (a lysosomal marker) and using confocal imaging to identify colocalization of astrocytic LAMP1-GFP with neuronal synapses using immunocytochemistry. We use treatments that increase or

inhibit neuronal activity and monitor changes in redistribution. Having a better understanding of degradation mechanisms involved in synaptic activity is important to understanding the overall mechanisms of neuronal plasticity. This knowledge could lead to important discoveries for diseases related to protein build up and synaptic loss such as Alzheimer's and Parkinson's.

THU - 223 Decreased Mitochondrial DNA Copy Numbers in the Synaptic Terminals from Human Huntington's Disease Caudate Nucleus

Discipline: Life Sciences
Subdiscipline: Neurosciences

Nicole Hsiao*, *University of Puerto Rico, Río Piedras*; María del R. Castro, *University of Puerto Rico, Medical Sciences Campus* and Sylvette Ayala, *University of Puerto Rico, Medical Sciences Campus*

Abstract: Synaptic function is highly dependent on mitochondria, and alterations of striatal and cortical synaptic structure and function contribute to neuronal dysfunction and degeneration in Huntington's disease (HD). HD is a neurodegenerative disorder characterized by motor dysfunction, personality changes and cognitive decline. HD is caused by a mutation of expanded CAG repeats in the huntingtin gene that generates a mutated version of the huntingtin (*HTT*) protein. Mutant *HTT* leads to decreased mitochondrial ATP production in synaptosomes; however, how *mHTT* leads to mitochondrial dysfunction is unknown. Synaptosomes are commonly used to study synaptic function and are rich in mitochondria. We hypothesize *mHTT* leads to synaptic dysfunction by reducing the levels of mtDNA copies at the synapse. To test our hypothesis, we measured the abundance of mtDNA molecules in striatal synaptosomes. These were isolated from stage 3 and 4 postmortem caudate nucleus and healthy/control tissue, using quantitative PCR. Results indicated that the abundance of mtDNA molecules was 20% lower in synaptosomes from stage 3 postmortem brain when compared to healthy striatal synaptosomes. Interestingly, synaptosomes from stage 4 patients showed levels of mtDNA molecules similar to those of healthy/controls. These results suggest that mtDNA copy numbers at the synaptic terminals may play a significant role in the maintenance of mitochondrial function and neuronal survival in HD. Supported by NIH grants SC1NS095380 (SAP), R25 GM061838, U54 MD 007600, and R24 - MH 068855 (Harvard Brain Tissue Resource Center).

THU - 224 Human Biodistribution and Dosimetry of ^{11}c-PS13, a Novel Radioligand for Cyclooxygenase-1

Discipline: Life Sciences
Subdiscipline: Neurosciences

Fernanda Juarez Anaya*, *National Institute of Mental Health*; Min-Jeong Kim, *National Institute of Mental Health*; Jae-Hoon Lee, *National Institute of Mental Health*; Prachi Singh, *National Institute of Mental Health*; Jinsoo Hong, *National Institute of Mental Health*; Cheryl Morse, *National Institute of Mental Health*; Michelle Y. Cortes-Salva, *National Institute of Mental Health*; Katharine Henry, *National Institute of Mental Health*; Paolo Zanotti-Fregonara, *Houston Methodist Research Institute*; Jeih-San Liow, *National Institute of Mental Health*; Sami Zoghbi, *National Institute of Mental Health*; Masahiro Fujita, *National Institute of Mental Health*; Victor Pike, *National Institute of Mental Health* and Robert Innis, *National Institute of Mental Health*

Abstract: Our laboratory has previously developed ^{11}C-PS13, a novel PET radioligand for cyclooxygenase-2 (COX-2). This protein is implicated in the pathophysiology of neuropsychiatric diseases, making it a potential biomarker for neuroinflammation. Given that previous monkey studies demonstrated excellent in vivo selectivity for this ligand, we looked at the biodistribution of ^{11}C-PS13 in 15 human subjects using serial whole-body imaging with positron emission tomography (PET). Twelve source organs (brain, heart, liver, gall bladder, stomach, spleen, lungs, kidneys, small intestine, large intestine, lumbar spine, and urinary bladder) were identified on whole-body images. The software program, OLINDA 1.1, was used to calculate radiation doses. The whole-body images were notable for early distribution in the blood pool, accumulation in target organs (e.g., spleen, gastrointestinal tract, kidneys, and brain), and apparent metabolism in the liver. Excretion activity was visible in the gall bladder and small intestine, where activity increased towards the end of the scan, but was not visible in the kidneys. The mean effective dose of ^{11}C-PS13 revealed by the analysis from the 15 healthy volunteers was 4.6 ± 0.6 μSv/MBq, which is comparable to the mean dose of 21 other ^{11}C-labeled tracers (range 3.0-6.8 μSv/MBq, mean 5.1 μSv/MBq). This biodistribution study in healthy volunteers suggests that ^{11}C-PS13 has an effective dose comparable to other ^{11}C-labeled ligands. The present data can be used to guide maximum injected activity in future research studies and advise subjects of the radiation risks associated with ^{11}C-PS13.

THU - 225 Dendritic Changes and Redistribution of Synaptic Proteins during Visual Cortex Plasticity

Discipline: Life Sciences
Subdiscipline: Neurosciences

José Zepeda*, *University of Massachusetts, Boston*; Jacque P.K. Ip, *Massachusetts Institute of Technology*; Taeyun Ku, *Massachusetts Institute of Technology*; Kwanghun Chung, *Massachusetts Institute of Technology* and Mriganka Sur, *Massachusetts Institute of Technology*

Abstract: Synaptic plasticity is the brain's ability to rewire its circuits through modifying connections between neurons. Ocular dominance (OD) plasticity occurs through reorganization of dendritic spines (synaptic sites) causing changes in responsiveness in binocular neurons in the primary visual cortex (V1). OD plasticity can be triggered through monocular deprivation (MD), where one eye is deprived of vision by eyelid suture. The molecular mechanisms for this reorganization during MD are not well understood. We hypothesize that the activity-regulated cytoskeleton-associated protein (Arc) mediates the depression of spines and allows for the reorganization of synaptic connections. To test this, we introduced a plasmid into binocular neurons via single-cell electroporation that encodes for the calcium sensor GCaMP6s, together with a structural marker mRuby2. Using two-photon microscopy, spines were imaged *in vivo* in awake mice to determine their ocular dominance index (ODI). We then imaged at later time points during MD to measure how spine size and their responsivity was affected. Finally, the same neurons were visualized using magnified analysis of proteome (MAP), which evenly expanded tissue by 4X to closely examine Arc at the postsynaptic density. Preliminary data suggests that shrinkage of spine size occurs after 2 days of MD and Arc expression is inversely correlated with spine size. In addition to synaptic plasticity being important for learning and memory in adulthood, many autism spectrum disorders (ASDs) have been associated with mutations in synaptic proteins. Investigation of the molecular mechanisms behind changes in synaptic morphology are therefore important to better understand these disorders.

THU - 226 Association between Gut Microbiota and Autism-like Behaviors.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Michael Ito*, *University of Hawaii*; Kimberly Lactaoen, *University of Hawaii* and Masato Yoshizawa, *University of Hawaii at Manoa*

Abstract: Recent metagenomic analysis have shown a significant correlation between gut microbiota and Autism Spectrum Disorder (ASD) in humans. However, a major challenge for the mechanistic investigation of this association is that we do not have a proxy animal model implementing the gut-brain axis in ASD. One emerging vertebrate model system in ASD research is the Mexican tetra, *Astyanax mexicanus*. The cave-dwelling morph of *A. mexicanus* displays the core symptoms of ASD: repetitive behaviors, loss of social interaction, increased stress hormone, hyperactivity, adherence to particular stimuli, and loss of sleep. The cave morph also exhibits similar trends in overall gut microbiota diversity to ASD patients, with firmicute species depleted. We then hypothesize that particular bacteria are correlated with ASD-related behaviors in a genetic cross derived from surface and cavefish. Here, we used behavioral assays to quantify sleep, adherence, hyperactivity, sleeplessness, and repetitive turning in 8 individuals each from the surface and cave morphs, and 40 F_2 hybrids derived from a pair of surface and cave morphs. We then dissected the guts of assayed fish and are currently measuring gut microbiota composition by sequencing the 16S rRNA gene, and assigning taxonomy using UCLUST as implemented in QIIME analysis. We will then determine specific associations between gut microbiota composition and the range of ASD-like behaviors exhibited by different test fish using standard statistical tests such as MANOVA. We will present the latest data and highlight significant genetic relationships between ASD-like traits and gut microbiota compositions otherwise difficult to present.

THU - 227 The Role of the Auditory Cortex in Learning a New Language

Discipline: Life Sciences
Subdiscipline: Neurosciences

Temerity Bauer*, *University of Oregon*; Erin Petruccione, *University of Oregon*; Melissa Baese-Berk, *University of Oregon* and Santiago Jaramillo, *University of Oregon*

Abstract: In this project, we used the mouse as a model in order to study the role of the primary auditory cortex in learning speech sounds at the neuronal level. We investigated whether the primary auditory cortex is important for the discrimination of sounds that differ in two possible features of speech: voice onset time and formant transitions. In the experiment, we used simple human speech sounds such as /ba/ and /pa/ which differ in voice onset time; or /ba/ and /da/ which differ in formant transitions. The mice train and perform their task for an hour each day and the amount of successes and failures is recorded. In our study, the mice were able to successfully learn the task and associate specific sounds with different reward ports. To determine whether the auditory cortex plays an important role in the ability to discriminate between sounds, the primary auditory cortex is shut down as the mice run trials. We used optogenetics to target cells in the primary auditory cortex and shut them down during trials. Preliminary data indicates that discrimination of a subset of speech sounds is affected by auditory cortex inactivation. As the experiment progresses, we will use optogenetics to test the importance of the auditory cortex in the ability to learn to discriminate between possible features of speech. From this research we will develop an understanding for how sounds are associated with a task or meaning and the importance of the auditory cortex in learning sounds from a new language.

THU - 228 Ethanol Modulation of Surface Expression of the BK Channel Is Isoform Specific.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Eliezer Cartagena*, *Institute of Neurobiology, MSC of the university of Puerto Rico* and Cristina Velazquez-Marrero, *Institute of Neurobiology, MSC of the University of Puerto Rico*

Abstract: Alcohol increases the activity of the large conductance Ca 2+ - and voltage-activated K + channel (BK) at physiologically relevant concentrations. We have previously described two membrane trafficking components that lead to the development of molecular tolerance to EtOH: 1) de-clustering and 2) internalization of the BK channel. Both of these components are seen in neurons and transfected HEK 293 cells. Our laboratory has found that after 6-hrs of ethanol exposure the mRNA of the EtOH-insensitive isoform, STREX, replaces the EtOH-sensitive isoform, ZERO. Here, we extend our studies performed at the level of RNA message to the protein level. We test the hypothesis that the surface expression of BK channel isoforms (Zero and STREX) is differently modulated by exposure to EtOH. We use TIRF imaging, along with electrophysiological techniques, to examine the internalization and de-clustering of these two protein isoforms after incubation with EtOH. Results indicate a distinct difference in EtOH effects on distribution of the two BK isoforms where STREX is not redistributed in contrast to ZERO. We further test BK channel redistribution in hippocampal pyramidal neurons. The results revealed time-dependent modulation in the surface expression of the endogenous neuronal population of BK by EtOH, showing a significant decrease in surface expression after 6-hrs of EtOH incubation. By contrast, this reduction was not seen in GFP-tagged STREX isoform. Interestingly, our results suggest in addition to isoform specificity in response to acute ethanol exposure, the plasticity in response to longer-term ethanol treatment also differs as a function of isoform identity.

THU - 229 Resolving Subtle Mutant and Treatment Effects through Pharyngeal Pumping Variability Assessment in the Nematode *C. Elegans*

Discipline: Life Sciences
Subdiscipline: Neurosciences

Derek Phillips*, *California State University, Long Beach*; Michael Harris, *California State University, Long Beach*; Chris Barrientos, *California State University, Long Beach*; Andy Bui, *California State University, Long Beach*; Mary Co, *California State University, Long Beach*; Sunnay Gill, *California State University, Long Beach*; Lily Ly, *California State University, Long Beach*; Micayla Nguyen, *California State University, Long Beach*; Brianna Ortiz, *California State University, Long Beach*; Ashley Parbo, *California State University, Long Beach*; Iris Rieger, *California State University, Long Beach*; Nathan Suree, *California State University, Long Beach*; Vanessa Valdez, *California State University, Long Beach*; T Vu, *California State University, Long Beach*; Barbara Taylor, *California State University, Long Beach*; Renaud Berlemont, *California State University, Long Beach*; Adrian Tran, *California State University, Long Beach*; Shelby Lim, *California State University, Long Beach* and Ahmad Shilleh, *California State University, Long Beach*

Abstract: In *C. elegans*, feeding is achieved through a well characterized behavior, pharyngeal pumping. This pumping is controlled by two pairs of pharyngeal motor neurons (MC and M3). Each pump cycle corresponds to the propagation of a single pharyngeal muscle action potential, initiated by MC and transmitted across a single cholinergic neuromuscular junction. The eat-2 gene is required for nicotinic neurotransmission at the pharynx. We assessed pumping patterns exhibited by wild type (N2) and a series of eat-2 mutant strains, each identified as possessing deficits in pumping, including: (Strain: genotype) DA465: eat-2(ad465) II; DA1113: eat-2(ad1113) II; DA1116: eat-2(ad1116) II. We also assessed pumping patterns in N2 strain animals incubated in the anthelmintic and acetylcholine receptor antagonist Levamisole ((−)-Tetramisole hydrochloride; 0 – 50 uM). All studies we done in animals incubated in 10mM serotonin in M9 buffer. We recorded electropharyngeograms (EPG) using the recently developed ScreenChip system (NemaMetrix) to detect individual pump events, and analyzed recordings using an algorithm (WormBeat) to distinguish and quantify neuromuscular fidelity of the pharynx. As expected, mutant strains and Levamisole-exposed N2 worms each illustrated pump pattern defects. Results show that the WormBeat algorithm can identify subtle treatment effects and distinguish phenotypic variation between mutant strains. Pump pattern assessment distinguished individual strains and allowed comparison of defect to the Levamisole dose-responses of N2s.

THU - 230 Microglia Involvement in the Development of the Human Fetal Retina.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Kayla Eschenbacher*, *University of Washington, Seattle*; Thomas Reh, *University of Washington* and Akshayalakshmi Sridhar, *University of Washington*

Abstract: During embryonic development of the vertebrate central nervous system, innate immune cells, called microglia, migrate into the retina and brain. Microglia are responsible for phagocytosis, monitoring tissues for pathogens, and inflammatory signaling. Several studies in model organisms show microglia also have roles in neural development, particularly in formation of synaptic circuitry. Defects of neuronal circuitry lead to vision loss; therefore, our project seeks to investigate the role and mechanisms of microglia in human retina wiring, specifically if microglia have similar effects in human retinal development as in model organisms. We first needed to determine when and where microglia are found at different ages. We collected donated tissues from developmental day 40 through 132 to determine the number and distribution of microglia in tissue sections using microglia-specific antibody, Iba1, and confocal fluorescence microscopy. To test whether microglia are necessary for retinal development, we used a fetal retina culturing technique to manipulate microglia populations. Retinal development can be visualized after deletion of microglia using progenitor cell marker EdU and various synaptic antibodies. We have found that microglia are present as early as day 58, prior to the majority of synaptic development, and survive in retinal cultures. Earlier stages are being investigated, and we are determining methods that will deplete microglia to study the effects of their absence on development. In conclusion, we know that microglia are present during synaptic development, and persist during retinal

development. Therefore, microglia are potentially essential for human retinal development and could be targets for future disease research.

THU - 231 Activation of Vta NtsR1 Neurons to Suppress Feeding and Promote Weight Loss

Discipline: Life Sciences
Subdiscipline: Neurosciences

Krystal M. Santiago*, *University of Puerto Rico At Cayey*; Patricia Perez-Bonilla, *Michigan State University* and Gina Leinninger, *Michigan State University*

Abstract: Behaviors that impact energy balance, like the motivation to eat and locomotor activity, are mediated by dopaminergic neurons of the ventral tegmental area (VTA). Yet, dopamine neurons are molecularly heterogeneous and project to different brain sites, and it remains unclear which specific VTA neurons exert behaviors to support weight loss. Neurotensin (Nts) released to the VTA promotes weight-loss behaviors in mice, which is dependent on neurotensin receptor-1 (NtsR1). Interestingly, only a subset of VTA neurons express NtsR1, and these "VTA NtsR1 neurons" only project to the nucleus accumbens (NAc) but not to the other main output of the VTA, the prefrontal cortex (PFC). Therefore, we hypothesize that selective activation of VTA NtsR1 neurons increases activation of downstream NAc neurons and suppresses feeding to support weight loss. To investigate this, we used Cre-dependent Designer Receptors Activated by Designer Drugs (DREADDs) to selectively activate VTA NtsR1 neurons of diet-induced obese $NtsR1^{Cre}$ mice. Chronic (7 days, 2xday) activation of VTA NtsR1 neurons in diet-induced obese mice promoted sustained locomotor activity and decreased food intake. However, activating these neurons did not alter food intake after overnight fasting (when motivation to consume food was increased) or their sucrose preference. Together, these data help reveal how the VTA NtsR1 subset of dopamine neurons contributes to energy balance, and if it might be leveraged to support weight loss to treat obesity.

THU - 232 Genetic Screens for Determining the Mode-of-Action of a Host Pheromone, Ztdo, in an Entomophilic Nematode

Discipline: Life Sciences
Subdiscipline: Genetics

Joanna Maddela*, *California State University, Northridge*; Paramin Sangthonkam, *California State University, Northridge*; Vivian Le, *California State University, Northridge*; Juan Cardenas, *California State University, Northridge* and Ray Hong, *California State University, Northridge*

Abstract: *Pristionchus pacificus*, a nematode species that is associated with the host Oriental beetle, is attracted to the beetle pheromone, ZTDO (Z-7-tetradecen-2-one). Previous chemotaxis research has found that wild-type PS312 exhibit elevated attraction towards ZTDO when intracellular cGMP levels is increased. We investigated a ZTDO-hypersensitive mutant, *Ppa-obi-1(tu404),* which is paralyzed at specific life stages in the presence of the pheromone. This gene is highly expressed in amphid neuron sheaths, part of the primary chemosensory organ, and encodes lipid-binding domains that are hypothesized to have a role in mediating both ZTDO attraction and preventing ZTDO-induced J4 larval paralysis. However, other genes involved in modulating the OBI-1 function remains to be identified.

In order to identify additional molecular factors involved in the reception of ZTDO, we screened 52,000 haploid genomes and isolated mutants that suppress the J4 *Ppa-obi-1* paralysis by ZTDO. This resulted in the isolation of three suppressor mutants: *csu61, csu63,* and *csu64.* Our results show that *csu63* is mildly attracted to ZTDO, similarly to PS312 and thus also suppressing the ZTDO chemoattraction defect of *Ppa-obi-1* mutants. In the future, we would like to investigate how the other two *Ppa-obi-1* suppressors: *csu61* and *csu64* affect *Ppa-obi-1* chemoattraction in the cGMP pathway. Ultimately, the goal of our research is to understand the mechanisms underlying the chemosensory responses to ZTDO to provide better insight into the entomophilic host-seeking behavior.

THU - 233 Search for Genetic Factors Controlling Double Fertilization in Plants

Discipline: Life Sciences
Subdiscipline: Genetics

Christian Neri*, *University of California, Riverside*; Chaolan Fan, *University of California, Riverside* and Adam Lukaszewski, *University of California, Riverside*

Abstract: Interaction between mitochondrial and nuclear genome affects double fertilization in plants. In double fertilization, a pollen grain produces two sperm nuclei: one fertilizes the egg cell to produce diploid zygote, and the other fertilizes the double nucleus producing triploid endosperm. In wheat, a combination of mitochondria in the cytoplasm from *Aegilops kotschyi* and the rye chromosome arm 1RS in the nucleus precludes fertilization of the egg and only the double nucleus is fertilized. This produces haploid embryos in an otherwise normal seed. Haploids, after doubling of the chromosome number, give perfectly homozygous lines, so-called doubled haploids, are highly desirable in plant breeding and genetics. Currently, haploids are produced by either microspore culture or selective chromosome elimination, both quite cumbersome and expensive. Harnessing a mechanism that prevents fertilization of the egg, thus generates haploids on demand, would be very beneficial as crop breeders and geneticists would eliminate the time needed to create homozygous lines by inbreeding. Moreover, nothing is known about genetics of double fertilization. The goal of this project is to locate and identify the genetic locus on rye arm 1RS that affects double fertilization in wheat. We have just discovered that polymorphism for this character exists in rye and we are currently creating populations for genetic mapping of the locus. Once mapped to a specific segment of the DNA sequence, candidate genes can be identified and individually knocked out to verify the function of the gene.

THU - 235 Conservation of Calcium-Regulated Protein, Carp, Involved in Virulence Among Clinical and Environmental Isolates of *Pseudomonas Aeruginosa*

Discipline: Life Sciences
Subdiscipline: Genetics

Sergio Mares*, *Oklahoma State University* and Marianna Patrauchan, *Oklahoma State University*

Abstract: Antibiotic resistant pathogen *Pseudomonas aeruginosa* targets patients with Cystic Fibrosis (CF), burns, wounds, and implants. In the lungs of patients with CF, *P. aeruginosa* encounters elevated levels of calcium (Ca^{2+}). Previously, our lab has shown that elevated Ca^{2+} levels enhance the ability of *P. aeruginosa* to produce virulence factors. We have identified a **Ca^{2+}**–**r**egulated β-**p**ropeller protein, CarP, found to be essential for cell tolerance to high levels of Ca^{2+}, regulation of intracellular Ca^{2}, and production of virulence factors. *carP* plays role in the ability of the pathogen to kill *Galleria mellonella* as a virulence model. Due to the important role that *carP* plays in Ca^{2+} signaling and host infection, we hypothesized that *carP* is highly conserved in *P. aeruginosa* clinical isolates obtained from diverse infection sources. The database homology search retrieved 2269 nucleotide sequences with the sequence identity above 95.55%. Interestingly, 97.7 % of the sequences belong to *P. aeruginosa* strains, suggesting the predominant distribution among *P. aeruginosa*. Protein sequence alignments through MEGA identified minimal to no mutations occurring within the trans membrane region, which did not impact the structure. Further, we amplified *carP* homologs in non-sequenced clinical isolates collected from CF sputum and ocular infections, this verified our *in silico* work. This research has demonstrated that *carP* is highly conserved in *P. aeruginosa* isolated from diverse environments, illustrating its importance in adapting to multiple environments. This gene could serve as a biomarker for *P. aeruginosa* infections, which would speed up identification of this organism thus improving treatments.

THU - 236 Evaluating the Presence of Previously Identified Archaic Introgressed Haplotypes in Contemporary and Ancient Unangan (Aleuts)

Discipline: Life Sciences
Subdiscipline: Genetics

Josie Muskrat*, *University of Kansas*; Tara Marriage, *University of Kansas*; Sarah Alden, *University of Kansas*; Lydia Sykora, *University of Kansas*; Justin Tackney, *University of Kansas*; Kristine Beaty, *University of Oklahoma*; Christopher Barrett, *University of Kansas*; Michael Crawford, *University of Kansas*; Nadin Rohland, *Harvard Medical School*; David Reich, *Harvard Medical School*; Dennis O'Rourke, *University of Kansas* and Jennifer Raff, *University of Kansas*

Abstract: Recent analyses in genomics have shown archaic hominins to have admixed with our species in regions where the populations overlapped. These studies have also shown that certain haplotypes characteristic of these extinct hominins have introgressed into modern human populations over time. Certain contemporary human populations exhibit greater levels of introgressed archaic hominin alleles than others. The objective of this study is to re-evaluate the findings of these studies in contemporary Unangan, a group not previously assessed for these archaic hominin haplotypes, and specifically look for haplotypes shown to be associated with lipid metabolism, *SLC16A11,* and cold adaptation, *TBX15/WARS2*. We used a combination of SNP data arrays and targeted PCR approaches to calculate the frequencies of SNPs associated with these respective haplotypes. We found the introgressed variant of *SLC16A11* to be present at a frequency similar to the global average in both contemporary and ancient Unangan, and *TBX15* to be present at lower frequency in contemporary Unangan than in other Native American populations, but present at 100% frequency in the ancient samples. We discuss the implications of our results in the context of Unangan pre- and post-European contact population history and what they might mean for adaptation to Arctic environments.

THU - 237 NFATc1 As a Novel Atrial Fibrillation Susceptibility Gene

Discipline: Life Sciences
Subdiscipline: Genetics

Alexandra Acuna*, *Nora Eccles Harrison Cardiovascular Research and Training Institute (CVRTI), University of Utah*; Christopher Kauffman, *Nora Eccles Harrison Cardiovascular Research and Training Institute (CVRTI), University of Utah*; Natalia Torres, *Nora Eccles Harrison Cardiovascular Research and Training Institute (CVRTI), University of Utah* and Martin Tristani-Firouzi, *Nora Eccles Harrison Cardiovascular Research and Training Institute (CVRTI), University of Utah*

Abstract: Atrial Fibrillation (AF) is the most common type of cardiac arrhythmia. It is a progressive disease that increases the risk of stroke, heart failure, and sudden death. Familial AF, where several family members are affected by young-onset (<40) AF, has a strong component of heritability. Using whole exome sequencing, we identified a novel mutation (M527L) in the Nuclear Factor of Activated T-Cells 1 gene (NFATc1) that segregates in an autosomal-dominant pattern within a family with a young-onset AF phenotype. To understand the mechanism responsible for the increased susceptibility to AF, we developed a homozygous mutant zebrafish line (Δ31) with a CRISPR/Cas9-induced 31bp deletion in exon 2 of the *nfatc1* gene, predicted to cause a premature stop codon truncating the nfatc1 protein. The Δ31 zebrafish develop atrial arrhythmias at 5-9 weeks (juvenile stage). NFATc1 is a transcription factor important in heart development and pathological hypertrophy, but not previously linked to arrhythmia. We hypothesize that NFATc1 loss of function will impact atria-specific gene expression leading to increased cardiac excitability that acts as the substrate for developing AF. To test this hypothesis, we will use Quantitative Polymerase Chain Reaction (qPCR) to study changes in ion channel gene expression in juvenile Δ31 and wild-type (WT) atria and ventricle. We expect some ion channel genes will be differentially expressed in Δ31 atria compared to WT. This information will provide insight into the mechanism by which NFATc1 contributes to AF in humans and may allow for more accurate treatment for Familial AF patients using precision medicine.

THU - 238 Exploring Single-Stranded DNA As a Novel Gene Therapy Vector

Discipline: Life Sciences
Subdiscipline: Neurosciences

Victoria Helm*, *Cuesta College*; Jie Li, *University of California, Berkeley* and Niren Murthy, *University of California, Berkeley*

Abstract: Gene therapy is an exciting technology with the potential to remedy gene associated diseases by delivering exogenous genetic material into affected cells. However, viral and bacterial vectors used in conventional gene therapy present multiple disadvantages such as permanent random insertion into genomes, as well as triggering immune responses. Thus, safe, yet effective non-viral and non-bacterial vectors are needed. A new method for synthesizing long single stranded DNA (lssDNA) in recent gene knock-in experiments provides a promising solution. LssDNA has the potential to be expressed in cells without random insertion and immune response problems. It is also more compact and flexible compared with equivalent double-stranded DNA and plasmids, making delivery into the nucleus for gene transcription and expression more feasible. This summer, we aim to synthesize two forms of lssDNA containing the GFP and IL-2 genes through in vitro transcription of a PCR product, followed by reverse transcription and evaluate their expression in dividing and non-dividing cells. The Lipofectamine 2000 technique will be employed for transfection and expression will be analyzed using flow cytometry, microscopy, and ELISA. If the GFP and IL-2 genes are expressed successfully, this will highlight lssDNA as candidate for safe and useful new gene therapy vectors. We will also use lssDNA as a template for homology direct repair following double strand break in a CRISPR/Cas9 gene knock-in experiment. Efficient integration of GFP and IL-2 will reaffirm the effectiveness of lssDNA as a repair template for gene knock-in based therapies.

THU - 239 The Brain Derived Neurotrophic Factor Val68Met Polymorphism Interacts with Developmental Ethanol Exposure to Damage the Murine Hippocampus

Discipline: Life Sciences
Subdiscipline: Neurosciences

Megan Barber*, *University of New Mexico*; Jack Martin, *University of New Mexico*; Clark Bird, *University of New Mexico*; Brian Baculis, *University of New Mexico*; Jacob Mayfield, *University of New Mexico*; Glenna Chavez, *University of New Mexico*; Tiahna Ontiveros, *University of New Mexico*; Dorit Ron, *University of California, San Francisco* and Fernando Valenzuela, *University of New Mexico*

Abstract: Prenatal exposure to ethanol damages multiple brain regions, including the hippocampus, which is involved in learning and memory processes. Several factors influence the vulnerability to developmental alcohol exposure, including genetic factors. We explored how a ubiquitous single nucleotide polymorphism within the human-brain derived neurotrophic factor (BDNF) gene (val66met in humans; val68met in mice) modulates the impact of developmental ethanol exposure on hippocampal structure. This polymorphism disrupts activity-dependent secretion of BDNF. We hypothesized that developmental ethanol exposure has a greater effect on hippocampal structure in mice carrying a methionine in position 68. BDNF$^{val/val}$and BDNF$^{met/met}$mice were exposed to air or EtOH in inhalation chambers during the equivalent periods to the second (gestation days 12-19) and third (postnatal days 2-9) trimesters of human pregnancy. The brains of adult offspring (postnatal day 90) were sectioned for histological analysis with Neuro-Chrom FluoroPan Neuronal Marker (Millipore-Sigma, Burlington, MA). The volume of the different hippocampal regions was determined using the Cavalieri's principle using unbiased stereology techniques. Two-way ANOVA found a genotype x treatment interaction in females for the dentate gyrus (p=0.024), CA1 region (p=0.039), CA3 stratum radiatum (p=0.041) and the entire hippocampus (p=0.029); and in males there was an interaction for the CA3 stratum oriens only (p=0.0006) (n=8-12 mice per genotype, sex and treatment group). These findings suggest that the val68met BDNF polymorphism modulates the effect of developmental ethanol exposure on the hippocampus. Supported by NIH grants R37-AA015614 and P50-AA0022534 (CFV), as well as UNM's MARC Program (MJB).

THU - 301 Recombining Antibody's Cdrs to Create a More Potent HIV-1 Monoclonal Antibody

Discipline: Life Sciences
Subdiscipline: Biochemistry

Adonis Rubio*, *Stanford University*; Peter S. Kim, *Stanford University* and Clayton L. Brown, *Stanford University*

Abstract: A leading obstacle in the development of a universal HIV-1 vaccine is the inability to target the breadth of HIV strains given the highly-mutable envelope glycoprotein (Env). Identifying broadly neutralizing antibody (bNAb) responses that target epitopes conserved across the various mutants of HIV-1 will allow the field to design more effective vaccines. One conserved region with the potential for stimulating bNAbs is the gp41 pre-hairpin intermediate (PHI), which is exposed during viral membrane fusion to host cells. The few antibodies that target the PHI demonstrate modest neutralization potency. The best characterized of these is a monoclonal antibody, D5, which was discovered from a phage display library. Other investigators affinity matured D5 using phage display by randomizing complementarity determining regions (CDRs), regions that contribute to the binding of the antibody to its specific antigen. These mutants only demonstrated a 1.5-fold neutralization enhancement when compared to D5 wildtype. Interestingly, each mutant tested was limited by having only one CDR mutated at a time. We hypothesize that by recombining multiple CDR mutations, we could achieve an even more potent antibody. Through antibody engineering and expression via mammalian cells, we have created a panel of 11 different CDR combinations. Using in vitro HIV-1 neutralization assays, we have found that some of these mutant antibodies enhance neutralization while some are less neutralizing than wildtype. Further investigating the enhanced mutants can potentially lead to identifying a more potent D5 mutant which will be instrumental in further developing possible vaccine efforts to prevent HIV-1 transmission.

THU - 302 Structural Basis of Nanoribonuclease Substrate Specificity in Bacteria

Discipline: Life Sciences
Subdiscipline: Biochemistry

George Walters-Marrah*, *Cornell University College of Veterinary Medicine*; Justin Lormand, *Cornell University College of Veterinary Medicine* and Holger Sondermann, *Cornell University College of Veterinary Medicine*

Abstract: RNA degradation is a central cellular process that is catalyzed by an assortment of ribonucleases (RNases) and is an essential function of life. Initiation of RNA degradation and the processive breakdown of RNA is catalyzed by a combination of endonucleases and exonucleases that convert structured and unstructured ribonucleotide polymers into smaller ribonucleotide fragments. The final step of RNA degradation is reserved for nanoribonucleases (nanoRNases), which have been described to degrade oligonucleotides 2-5 bases in length to mononucleotides. Oligoribonuclease (Orn) emerged as a particular nanoRNase that, in addition to its ascribed function as a 3’-5’-exonuclease, also plays a role in protein secretion, virulence, antibiotic tolerance, and c-di-GMP signaling in *Pseudomonas aeruginosa*. The latter function relies on the degradation of pGpG by Orn, which is the by-product of c-di-GMP turnover, and mutants display elevated c-di-GMP expression and increased biofilm formation. Structure-function studies indicate Orn functions preferentially as a dedicated dinucleotidase, which prompted us to re-assess the substrate length specificity of other nanoRNases. Based on an interdisciplinary approach combining structural, biochemical, and functional techniques, we present mechanistic insight into and a structural model for the specificity of nanoRNases for dinucleotides. Our data suggests that RNA degradation is a step-wise process which requires terminal enzymes dedicated to the cleavage of dinucleotides into mononucleotides.

THU - 304 Characterizing the Domains of Cika, a Circadian Clock Protein in Cyanobacteria

Discipline: Life Sciences
Subdiscipline: Biochemistry

Kellie Goodnight*, *University of California, Merced*; Xuejun Yao, *University of California, Merced*; Archana Chavan, *University of California, Merced*; Ning Zhang, *University of California, Merced* and Andy LiWang, *University of California, Merced*

Abstract: The circadian clock is an organism’s internal clock that allows for adaptation to environmental changes in a day-night cycle. Circadian clocks enable cells and organisms to coordinate their physiology with the cyclic environmental changes and provide stable regulation of cellular functions in different environments. Cyanobacteria are ecologically important to the Earth for they help contribute to nitrogen fixation and are the simplest organism known to have a biological clock. Particularly, cyanobacteria use clocks for timekeeping, just how humans use an internal clock to regulate sleep. The cyanobacterial clock consists of three proteins - KaiA, KaiB and KaiC - that generates a cyclic rhythm of protein interactions. The clock receives the environmental signal from input proteins and transmits the time information to the rest of the cell through output proteins for regulation of cellular function. Circadian input kinase A, (CikA) is known to function as an input and output protein that plays a role in timekeeping, entrainment, and signaling. However, the molecular mechanism by which CikA functions is still unclear. CikA contains three domains with different functions; to understand how each domain works, determining structural features of this protein is necessary. This project focuses on isolating each domain of CikA by molecular cloning to determine their structure and function using nuclear magnetic (NMR) spectroscopy and biochemical assays. By using methods such as PCR and NMR, the structural basis of CikA could be determined. Thus bringing us closer to resolving the structural and biochemical basis of rhythmicity of the cyanobacterial circadian clock.

THU - 307 Functional Analysis of RNA Exosome Mutants Linked to Disease Using a *Saccharomyces Cerevisiae* Model System

Discipline: Life Sciences
Subdiscipline: Biochemistry

Liz Enyenihi*, *Emory University*; Anita Corbett, *Emory University*; Samika Joshi, *Emory University*; Sara Leung, *Emory University*; Laurie Hess, *Emory University*; Maria Sterrett, *Emory University*; Munira Basrai, *National Cancer Institute, Genetics Branch*; Ambro van Hoof, *Department of Microbiology and Molecular Genetics, University of Texas Health Science Center-Houston* and Milo Fasken, *Emory University*

Abstract: The RNA exosome is a highly conserved, key component of RNA quality control that both degrades and processes many classes of RNA. Mutations in the human *EXOSC2* gene, which encodes a cap subunit of the RNA exosome, have been linked to a novel syndrome characterized by retinitis pigmentosa, hearing loss, and other symptoms. I aim to analyze the functional consequences of these amino acid substitutions modeled in the budding yeast ortholog of EXOSC2, Rrp4, to investigate the effects on RNA exosome function.

The two variants I have analyzed, *rrp4-G58V* and *rrp4-G226D*, correspond to patient mutations G30V and G198D, respectively. I assessed growth of the mutant strains compared to wildtype yeast cells, which revealed that *rrp4-G226D* mutant cells exhibit a growth defect at 37°C, whereas the *rrp4-G58V* mutant cells are not viable. I used immunoblotting to assess Rrp4 protein levels which revealed that rrp4-G226D proteins are expressed, but at reduced level compared to wildtype Rrp4.

Next, I analyzed RNA exosome target RNA transcripts using quantitative RT-PCR. I detected a statistically significant accumulation of several transcripts in *rrp4-G226D* mutant cells compared to wildtype which indicates that the *G226D* mutation impairs exosome-mediated RNA processing. I will use RNA-Seq analysis to provide a full picture of the RNA targets that are impacted and biochemical approaches to study the assembly of the RNA exosome complex and *rrp4* mutant interactions with RNA exosome cofactors. Taken together, these studies provide insight into how specific amino acid changes could impact RNA exosome function and contribute to disease pathology.

THU - 308 Nuclei Acid-Mediated Engineering of Cardiopoietic Stem Cells

Discipline: Life Sciences
Subdiscipline: Biochemistry

Sinibaldo Romero Arocha*, *Center for Regenerative Medicine, Mayo Clinic*; Tyler Rolland, *Center for Regenerative Medicine, Mayo Clinic*; Mark Li, *Center for Regenerative Medicine, Mayo Clinic*; Timothy Peterson, *Center for Regenerative Medicine, Mayo Clinic*; Raman Deep Singh, *Center for Regenerative Medicine, Mayo Clinic*; Andre Terzic, *Center for Regenerative Medicine, Mayo Clinic* and Atta Behfar, *Center for Regenerative Medicine, Mayo Clinic*

Abstract: Myocardial infarction survivors are prone to developing heart failure. Stem cell therapies targeting cardiac repair, mainly with bone marrow-derived mesenchymal stem cells (BM-MSCs), show signs of efficacy and safety. One example is cardiopoiesis, a platform developed by our laboratory that primes BM-MSCs for cardiac repair. However, the duration of induction and the autologous nature of the source material preclude its adoption in clinical practice. Our laboratory developed a microencapsulated-modified-messenger RNA (M3RNA) platform as an alternative approach to induce cardiopoiesis. The M3RNA is a base-modified mRNA encapsulated in cationic liposome that allows the expression of exogenous proteins in cells. We utilized umbilical cord-derived mesenchymal stem cells (UC-MSCs) as a cell source due to their reported success in enhancing cardiac function in experimental models of cardiovascular disease. We hypothesized that transfection of UC-MSCs with Brachyury M3RNA (a cardiac mesoderm marker that plays a key role in cardiomyocyte differentiation) will induce an engineered CP (eCP) cell lineage comparable to the established CP lineage in vitro. UC-MSCs were transfected with Brachyury M3RNA. Protein expression was measured and quantified using fluorescence microscopy, western blotting, and flow cytometry. UC-MSCs transfected with Brachyury M3RNA demonstrated rapid protein expression at 4 hours post-transfection that reached peak levels at 24 hours. Flow cytometry data revealed 28.90% and 82.60% transfection efficiency at 4 hours and 24 hours post-transfection respectively. Immunocytochemistry supported these findings and demonstrated similar morphology between transfected and non-transfected cells. In the present study, we introduced a novel approach to induce cardiopoises that reduces the time of induction.

THU - 310 Discovering Cyclic Peptomer Virulence Blockers That Suppress Pathogenicity of Antibiotic-Resistant Bacteria

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alejandro Cabrera-Cortez*, *University of California Santa Cruz*; Tannia Lau, *University of California Santa Cruz* and Scott Lokey, *University of California, Santa Cruz*

Abstract: The emergence of multi-antibiotic resistant bacteria is a growing public health threat. The development of new antibiotics has been the customary response, however, new strategies for treatment are necessary. Standard antibiotics may treat infection yet wreak havoc on internal microbiota due to a lack of specificity and provide an evolutionary pressure on bacteria to quickly develop resistance. A common virulence strategy of gram-negative bacteria is to employ the Type III Secretion System (T3SS), a syringe-like structure that protrudes from the pathogen's cell membrane. A possible strategy for mitigation of these bacteria is to target the T3SS's ability to secrete effector proteins with the use of cyclic peptomers. Recently, a library of 20 synthetic cyclic peptomers inspired by the natural product phepropeptin D were screened for the ability to inhibit NF-$_{\kappa}$B activation during *Y. pseudotuberculosis* ∆yop6 infection revealing 8 hits. Modification of these hits has revealed a lead, EpD-12N, that inhibits the secretion of effector proteins with a half maximal inhibitory concentration (IC_{50}) of 8.2 μM. Using solid-phase peptide synthesis, further stereochemical modification have revealed a more potent derivative, 4-EpD-12N, with an IC_{50} of 3.9 μM. Additional screening of 4-EpD-12N for inessential side chains through a sarcosine/alanine scan show that all side chains are crucial for inhibition. Moreover, the inclusion of a hydroxyl substituent at the meta or para position of the phenylalanine residue reduced the potency of the peptide, increasing the IC_{50} to 10μM. Further refinement of the 4-EpD-12N scaffold may lead to a potential treatment against the T3SSs.

THU - 311 Targeting the Copper Binding Site of MEK1 with a Small-Molecule Covalent Inhibitor As a Potential Therapeutic

Discipline: Life Sciences
Subdiscipline: Biochemistry

Angel Vazquez*, *University of Puerto Rico, Rio Piedras Campus*; Diana Iovan, *University of California, Berkeley* and Christopher Chang, *University of California, Berkeley*

Abstract: Copper (Cu) is an essential metal for cellular development and proliferation, being implicated in the mitogen-activated protein kinase (MAPK) pathway. Specifically, Cu was found to activate MEK1 and thus promote cancer tumor cell proliferation, justifying the therapeutic interest in targeting this kinase. A MEK1 inhibitor has the potential to block tumor cell growth and thus provide a survival advantage in several cancers. We seek to identify a potential covalent inhibitor that targets the Cu binding site of MEK1 to prevent further activation. A library of acrylamide compounds has been screened to identify a cysteine-reactive fragment for MEK1. With this screening, a small-molecule has been identified to react with cysteine residues on MEK1. With the use of mass spectroscopy, two specific cysteine sites have been identified to be covalently modified by this small molecule, including the one involved in copper binding. MEK1 cysteine-to-serine mutants have been prepared to understand the activity and reactivity of this small molecule with these specific sites. With the use of gel-based fluorescence labeling assays, intact protein and peptide mass spectrometry, and activity assays, the reactivity of the compound to the cysteine sites was examined to establish the effect on enzyme activity as a function of copper. Understanding the reactivity of this small molecule with MEK1 will inform the potential of such a copper-dependent covalent labeling approach to inhibit MEK1, which can have a high therapeutic application.

THU - 312 Characterization of the Regulation Strategies of Malate Dehydrogenase 1 (MDH1)

Discipline: Life Sciences
Subdiscipline: Biochemistry

Sati Alexander*, *Initiative for Maximizing Student Development*; Joi Weeks, *San Diego State University*; An Hoang, *San Diego State University* and Christal Sohl, *San Diego State University*

Abstract: Cancer cells often reroute or stimulate their metabolism to support proliferation, which requires a change in the activity or regulation of key metabolic residues. Malate dehydrogenase 1 (MDH1) catalyzes the NADH-dependent conversion of oxaloacetate to malate, which can help drive glycolysis through the production of NAD+. MDH1 is amplified in many squamous cell lung carcinomas, the second leading cause of cancer related death, and this amplification is associated with a poor prognosis. The precise role of MDH1 in driving squamous cell lung cancer and the mechanisms that regulate this protein are not yet well understood. Here, we hypothesize that post translational modifications (PTMs) associated with oxidative stress alter the normal enzymatic activities of MDH1. It has been previously shown that MDH1 methylation can suppress glutamine metabolism in pancreatic cancers, and that acetylation of MDH1 alters its activity. Here, we will establish the role of oxidative stress on regulating MDH1 activity via glutathionylation using biochemical and cellular methods. Through monoclonal single cell isolation, we will generate a squamous epithelial lung cancer cell line stably overexpressing MDH1, and will heterologously express and purify MDH1 mutants to examine the influence of PTMs on amplified MDH1. By understanding the regulatory strategies of MDH1, we hope to identify new pathways that may be targeted therapeutically.

THU - 313 Alterations in the O-Glcnac Proteome By the Small Ubiquitin-Related Modifier

Discipline: Life Sciences
Subdiscipline: Biochemistry

Oscar Molina*, *University of California, Los Angeles*; Daniel Ramirez, *Harvard University* and Christina Woo, *Harvard University*

Abstract: Cellular nutrient and stress sensors play a critical role in informing the cell to alter signaling pathways, transcription, and mitochondrial activity to maintain homeostasis. The post-translation modification (PTM) and nutrient sensor, O-linked N-acetylglucosamine (O-GlcNAc), modifies >5,000 different substrates and is an understudied, but key PTM that coordinates cellular responses that determine cellular fate and organismal development. O-GlcNAc Transferase (OGT) is the essential enzyme solely responsible for catalyzing O-GlcNAcylation on a substrate. Misregulation of the O-GlcNAcylation has been linked with chronic diseases such as diabetes and cancer. Like O-GlcNAc, Small Ubiquitin-related Modifier (SUMO) is an essential PTM that serves as a protein switch to regulate signaling and transcriptional reprogramming. Proteomic evidence has suggested that SUMO can be conjugated to OGT at multiple lysine residues, but whether SUMO affects the activity of OGT and leads to alterations in the O-GlcNAc proteome is unknown. Here we suggest that SUMO allows a subset of OGT substrates to be modified primarily through non-covalent interactions mediated by SUMO interacting motifs (SIMs). Site-directed mutagenesis of SUMO conjugation sites and

SIMs on OGT revealed changes in the O-GlcNAc proteome via mass spectrometry analysis. We found that OGT localization changed during heat shock response experiments and in conditions of over-expressed SUMO enzymatic machinery. A crosstalk between SUMOylation and O-GlcNAcylation has not been previously established but our data suggests that these two PTMs could concatenate to regulate cellular activity during specific stimuli.

THU - 314 Determining How the C-Terminus of Casein Kinase 1 Delta Isoforms Influences Its Activity on Substrates

Discipline: Life Sciences
Subdiscipline: Biochemistry

Maria Ayala Hernandez*, *University of California, Santa Cruz*; Rachel Harold, *University of California, Santa Cruz*; Sabrina Hunt, *University of California, Santa Cruz* and Carrie Partch, *Department of Chemistry and Biochemistry, UC Santa Cruz*

Abstract: Circadian rhythms are crucial in dictating the timing of many physiological functions. Dysfunction of the internal clock can lead to metabolic and sleep disorders. The internal clock is mainly driven by a transcription-translation feedback loop which promotes the expression of clock-driven genes, including the core circadian repressor PERIOD 2 (PER2). Casein Kinase 1d (CK1d) is known to regulate the stability of PER2 through phosphorylation. However, there are two different isoforms of CK1d, d1 and d2, which differ in only a few residues of their autoinhibitory C-termini. We recently showed that these isoforms exhibit disparate activity towards a critical regulatory phosphorylation site on PER2, with decreased activity by the d1 isoform relative to d2. Our experiments aim to find how the disordered C-terminus of isoform CK1d1 interacts with the CK1d catalytic domain to influence its activity on PER2 using Nuclear Magnetic Resonance (NMR) spectroscopy. NMR will be used to track intramolecular interactions in CK1d by segmental labeling, where only the C-terminus will be isotopically labeled with NMR active nuclei and the catalytic domain will be NMR invisible. Through these methods, we aim to characterize the auto-inhibitory interactions of CK1d1 by analyzing changes in NMR spectra in the presence and absence of ATP, expecting predominant interactions to occur in the extreme C-terminus where differences between the d1 and d2 isoforms arise. Understanding how CK1d undergoes autoinhibition to control its activity on PER2 is an important component in figuring out the regulation of the internal circadian clock.

THU - 315 Identification of Isolevuglandin, a Highly Reactive Lipid Dicarbonyl, Sites of Modification in Human Apolipoprotein a-I

Discipline: Life Sciences
Subdiscipline: Biochemistry

Leah Rowe*, *University of Arkansas at Pine Bluff* and Sean Davies, *Vanderbilt University*

Abstract: Cardiovascular disease (CVD) is inversely associated with high density lipoprotein cholesterol (HDL-C), but pharmacological interventions aimed to increase HDL-C have failed to reduce disease risk. Evidence suggests that CVD risk more closely relates to HDL function than HDL-C. We have reported that isolevuglandins (IsoLGs), highly reactive lipid dicarbonyls generated by lipid peroxidation, deleteriously alter HDL structure and function, mainly via their modification of apolipoprotein A-I (apoA-I) lysines. The specific lysines of HDL apoA-1 modified by IsoLG in a diseased setting are unknown. Identification of these modified lysines could provide insight on the mechanistic basis for loss of apoA-I function and development of clinical assays to identify people at risk for CVD. We developed a high-resolution mass spectrometric based method to quantify specific tryptic peptides derived from IsoLG-modified apoA-I, as well as unmodified apoA-I peptides. Using reconstituted apoA-I particles, we identified 8 apoA-I lysines modified by IsoLG. By stable isotope dilution LC/MS/MS with parallel reaction monitoring, we found a dose-dependent increase in IsoLG-modified Lys226 when human HDL was modified by IsoLG. Lys94, Lys118, and Lys182 adducts were identified with higher IsoLG modification (3 molar eq. to apoA-I). We identified 8 unmodified tryptic apoA-I peptides containing lysines whose levels decrease after IsoLG modification, suggesting that those peptides are adducted or crosslinked by IsoLG. As a validation of our approach, we were able to detect IsoLG modification of Lys94, 118, 183, and 226 of apoA-I in oxidized human plasma. Current studies seek to validate our findings in clinical samples from patients with atherosclerosis.

THU - 316 Structure and Function of Circadian Clock Protein Kaib Examined with Fluorescence Anisotropy and Multi-Angle Light Scattering

Discipline: Life Sciences
Subdiscipline: Biochemistry

Joseph Palacios*, *University of California, Santa Cruz*; Jeffrey Swan, *University of California, Santa Cruz* and Carrie Partch, *Department of Chemistry and Biochemistry, UC Santa Cruz*

Abstract: Circadian clock proteins are self-sustained oscillatory systems that predict 24-hour day/night cycles in order to coordinate these cycles with physiological changes within the cell. Timekeeping of cellular events in the cyanobacterium *S.elongatus* is organized by the phosphorylation state of clock protein KaiC. Dephosphorylation at specific timekeeping sites initiates when tetrameric KaiB folds into an active state and binds KaiC at an allosterically linked site. Current work has focused on mechanistic details of this process from a biophysical and biochemical perspective. KaiB binding interactions with KaiC-hexamer are typically measured by mutating KaiB residue K25 to cysteine and labeling with a fluorescent dye for anisotropy. We have evidence K25 is involved in cooperative recruitment of sequential KaiB monomers on the KaiC-hexamer binding interface. Furthermore, anisotropy of K25C-labeled KaiB changes as a function of unlabeled KaiB concentration, suggesting the mutation may impact tetramerization. For these reasons, I investigated labeling sites of KaiB to recapitulate native binding interactions. I performed site directed mutagenesis on KaiB to generate different dye attachment sites, examining anisotropy in binding assays against gradients of KaiB or KaiC. Thus far, the KaiB labeling site Q36C appears to have the lowest change in anisotropy with increasing KaiB, while binding KaiC with similar affinity as K25C labeled KaiB. Next, I will examine the labeled KaiB's ability to tetramerize using multi-angle light scattering (MALS) to determine labeling effects on quaternary structure. These findings will inform future experiments on the roles of tetramerization and specific KaiB residues in cooperativity of KaiB association.

THU - 317 Expression and Purification of Human Circadian Protein Hrory for Structural and Functional Studies

Discipline: Life Sciences
Subdiscipline: Biochemistry

Sebastian Sanchez*, *The University of Texas at El Paso*; Alexander Madej, *The University of Texas at El Paso*; Brenda Moreno, *The University of Texas at El Paso*; Yuejiao Xian, *The University of Texas at El Paso*; Supriyo Ray, *The University of Texas at El Paso*; Seung-Hee Yoo, *The University of Texas Health Center at Houston McGovern Medical School*; Zheng Chen, *The University of Texas Health Center at Houston McGovern Medical School* and Chuan Xiao, *The University of Texas at El Paso*

Abstract: The circadian rhythm is an internal biological clock that runs in many living organisms. It regulates the sleep wake/cycle among other physiological states involving metabolism. Long term disruption of this internal clock can cause sleep disorders, metabolic diseases, and high risks of cancer. The circadian rhythm is controlled at molecular level by the transcriptional-translational feedback loop (TTFL) that involve positive transcriptional activators CLOCK/BMAL1 and negative feedback suppressors PERs/CRYs. The Retinoic Acid Receptor-Related Orphan Receptors (RORs) function as ligand-dependent transcription factors which regulate BMAL1 production to improve circadian rhythm stability and robustness. It was shown that the naturally occurring flavonoid Nobiletin can bind to human ROR gamma (hRORγ) and increase its function through yet unknown mechanisms. Understanding the interaction between hRORγ and Nobiletin would provide insights in enhancing the circadian rhythm and ameliorating its related diseases. Therefore, this project focuses on solving the three-dimensional structure of hRORγ/Nobiletin complex to establish the mechanism of their interaction. The hRORγ gene was cloned and expressed using *E. coli* BL21 cells.

Expression protocols were optimized to produce large amounts of hRORγ recombinant proteins. The soluble portion of expressed protein was purified using affinity chromatography and size exclusion chromatography, and shown to be properly folded in our circular dichroism studies. Once the required concentration is reached, the purified hRORγ will be co-crystalized with Nobiletin. The obtained crystals would be used for structural determination using X-ray crystallography. The structural information will shed light on Nobiletin's enhancement mechanism on circadian rhythm and provide guidance in related drug development.

THU - 319 BRCA1 and MicroRNA-182 Expression After Epigallocatechin-3-gallate Exposure in Triple Negative Breast Cancer Cells

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Chante Guy*, *John Jay College of Criminal Justice, City University of New York*; Toni-Ann Bravo, *John Jay College of Criminal Justice, City University of New York* and Lissette Delgado-Cruzata, *John Jay College of Criminal Justice*

Abstract: Catechins are phenolic compounds found in dietary products such as green tea, red wine and cocoa. These compounds act as antioxidants and are also involved in the regulation of cellular processes including cell death, extracellular matrix degradation and multidrug resistance. Epigallocatechin-3-gallate (EGCG) is one of the most common catechins. Previous research has found that EGCG suppresses the progression of breast cancer by decreasing cell proliferation and inhibiting angiogenesis. Levels of microRNAs, small non-coding RNAs involved in regulating gene expression, have been shown to vary after EGCG treatment in breast cancer. Studies have shown that microRNA-182 has been shown to have higher expression levels in triple negative breast cancer (TNBC) cells than in normal cells. Also research has shown that miR-182 promotes proliferation and metastasis in TNBC. In this study we investigated the effect of EGCG in miR-182 expression and levels of its target BRCA1 in TBNC MDA-MB-468 cells. We treated the cells with 25μM and50μM of EGCG for 48 hours. We extracted total RNA and used Taqman assays to determine miR-182 and BRCA1 levels. We found that miRNA-182 levels decreased after EGCG treatment but not significantly (miR-18225μM= 83.4± 39.7% (p=0.381) and miR-18250μM= 70.0± 3.9% (p=0.302) vs. untreated). Interestingly, BRCA1 gene expression increased significantly with EGCG concentrations (BRCA125μM= 166.77±74.50% (p=0.009); BRCA150μM= 150.7± 38.9% (p=0.006) vs. untreated).Our results suggest that BRCA1 expression can be modulated by treatment with EGCG, and that is possible that miR-182 has a partial role in regulating the expression of this gene as a response to treatment.

THU - 321 Aldehyde Dehydrogenase 1 (ALDH1)-Expressing Mammary Cancer Stem Cells Differentiate into Hepatic Stellate-like Cells to Promote Growth of African American Triple Negative Breast Tumors

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Nataly Arias*, *California State University, Dominguez Hills* and Shehla Pervin, *Charles Drew University of Medicine and Science*

Abstract: Breast cancer (BC) remains the second highest cause of cancer deaths among African American (AA) women. A particular type disproportionately affects young AA women who have low incidence but suffer high mortality rates. Very little is understood about the genetic and epigenetic factors that play a role in its development. Our lab examined xenografts from three AA triple negative (TN) human BC cell lines MDA-MB-468, HCC70 and HCC1806 to understand the mechanisms that promotes their aggressive tumor growth. Our study found that the fast-growing xenografts from HCC70 and HCC1806 had an upregulation of ALDH1, a mammary cancer stem cell (MCSC) marker, when compared to the slow growing xenografts from the MDA-MB-468 cell line. We also found that when compared to ALDH (-) cells, ALDH (+) had a higher potency to promote tumor development. To understand the mechanisms by which ALDH1 promotes tumor development, gene expression profiling by microarray analysis was performed on early xenografts. The analysis found an upregulation of gene signatures associated with active hepatic stellate-like cells that express collagen and myosin heavy chain, which were also upregulated proteins in early xenografts. Double immunofluorescence and trichrome staining were used to observe the interactions between collagen, myosin heavy chain, and ALDH1. Trichrome results indicate a high expression of collagen and myosin in the early xenografts. We hypothesize that ALDH1-expressing MCSC differentiate into hepatic stellate cell types. Understanding the pathways that influences MCSC population could help us better understand the mechanisms that promote tumor growth and lead to effective therapeutic interventions.

THU - 322 Immune-Profiling of Syngeneic Modeling of Fallopian tube Derived Ovarian Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Kimberly N. Heath*, *University of Illinois at Chicago*; Laura R. Hardy, *University of Illinois at Chicago*; Daniel Lantvit, *University of Illinois at Chicago* and Joanna E. Burdette, *University of Illinois at Chicago*

Abstract: Ovarian cancer is the most lethal gynecological disease, and fifth leading cause of cancer-related death among women. Ongoing clinical trials for immune therapy to treat ovarian cancer show limited progress. Most *in vivo* studies for ovarian cancer use athymic nude mice xenografted with human cancer cells and lack adaptive immunity. The main syngeneic model used in the ovarian cancer field is called ID8, which derives from ovarian surface epithelium. However, ovarian cancer can also arise from fallopian tube epithelium. In this study, ovarian cancer cells derived from fallopian tube epithelium were injected into immunocompetent FVB/N mice to evaluate the role of the immune system with cells that had alterations including $\text{PTEN}^{\text{shRNA}}$, $\text{PTEN}^{\text{shRNA}}/\text{p53}^{\text{R273H}}$, $\text{PTEN}^{\text{shRNA}}/\text{KRAS}^{\text{G12V}}$, and $\text{PTEN}^{\text{shRNA}}/\text{KRAS}^{\text{G12V}}/\text{p53}^{\text{R273H}}$. H&E staining was performed on the tumors to determine if the adaptive immune response affects gross tumor morphology. The survival times between the syngeneic and xenograft system were compared to determine the role of the immune system on progression of disease. CD3 and CD8 specific antibodies were used to examine the presence of T lymphocytes, and F4/80 antibody was used to examine the presence of activated macrophages. The overall tumor morphology was unaffected by the adaptive immune response. In addition, the presence of adaptive immunity increased the aggressiveness of the models when compared to tumors grown in athymic mice. Finally, there is increased tumor immune infiltration as mutational status increases. These models can be used as a tool for the scientific community to more effectively model the immune response to ovarian cancer or immune therapies.

THU - 323 The Synergistic Effects of Temozolomide and Spak Inhibition on Glioblastoma Proliferation and Tumorogenesis *in Vitro*

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Marlisa Shaw*, *Pennsylvania State University*; Paula Valentina Schiappareli, *Mayo Clinic*; Pierre Alexande Miranda Herrera, *Mayo Clinic* and Alfredo Quinones-Hinojosa, *Mayo Clinic*

Abstract: Glioblastoma (GBM) is the most aggressive primary brain tumor in adults, with a five-year survival rate less than three percent. Due to GBM's heterogeneic nature, treating GBM often results in tumor recurrence. One hallmark of GBM is the ability of tumor cells to invade healthy brain tissue via increased activity of chloride channels and chloride transport, which in turn allows cellular volume change and promotes tumor cell migration. We hypothesize that blocking this pathway using a novel inhibitor of SPAK kinase (YU566) will decrease cell migration and proliferation. Moreover, we wanted to test if the combination of the YU566 inhibitor with the current chemotherapeutic standard-of-care, temozolomide (TMZ), results in a synergistic or chemosensitizing effect. We determined the half maximal inhibitory concentration (IC50) of the SPAK inhibitor and TMZ in three primary patient-derived GBM cell lines using CyQUANT Proliferation Assays. The average IC50 values of the SPAK inhibitor and TMZ were 2uM and 500uM, respectively. To determine drug synergy, we tested 25-drug combinations using concentration ranges centered around each IC50 values. We identified multiple combinations that showed synergistic effects, resulting in decreased cell proliferation. In addition, cell death was determined using Annexin V staining by flow cytometry. Preliminary results show that after 48hrs the combination of the YU566 inhibitor and TMZ induced a significant increase in apoptosis by 6.23 times. Our results indicate that the combination of TMZ and YU566 reduced cell proliferation, inducing cell death. Future experiments include determining effects on cell cycle, cell migration and aggressiveness *in vitro*.

THU - 324 Inhibition of RET Via Blu-667 in an *in Vitro* Model of Neuroblastoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Jessica Gutierrez*, *San Diego State University* and Peter Zage, *University of California, San Diego*

Abstract: Neuroblastoma is the most common extracranial solid tumor of childhood. Despite aggressive treatment, outcomes in patients with high-risk disease remains poor and new therapeutics are needed to address their needs. Rearranged during Transfection (RET) is a tyrosine kinase that is a known oncogenic driver of multiple human tumors. RET is expressed on neural crest derived cells, including neuroblastoma cells, and has been shown to play a role in neuroblastoma proliferation and survival as well. Recent studies have shown RET inhibition to be a promising new therapeutic target in neuroblastoma. BLU-667 is a selective RET inhibitor with a higher potency and specificity for RET than the current inhibitors that have been previously tested. We hypothesize that this increased potency and specificity will result in greater efficacy against neuroblastoma in preclinical models with fewer off target effects. Thus, to investigate this we evaluated BLU-667 at different concentrations against a panel of established human neuroblastoma cell lines to assess its effects on neuroblastoma cell proliferation, differentiation, and viability. We found that inhibition of RET resulted in a significant decrease in cell proliferation and viability *in vitro*. Further, given the increased specificity of BLU-667 to RET, we hope to use western blot protein analysis to establish the specific downstream pathways through which RET inhibition leads to decreased neuroblastoma cell survival, potentially revealing further therapeutic targets.

This research was supported by NCI of NIH: U54CA132384 & U54CA132379. The content is the responsibility of the authors and does not represent the official views of the NIH.

THU - 325 Blocking the Bone Destructive Phenotypes of Osteosarcomas through Gli2 Inhibition

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Jacob Brooks*, *Howard University*; Erik Beadle, *Vanderbilt University* and Julie Sterling, *Vanderbilt University*

Abstract: Osteosarcomas are malignant tumors that present in adolescents between 10-19 years of age and aggressively destroy bone tissue. Once metastatic, osteosarcoma drastically decreases patient survival and quality of life. Aggressive chemotherapy and surgery are the first line treatment for osteosarcoma, highlighting the need for molecular targets. The Rhoades lab has previously shown that the hedgehog molecule, Gli2, promotes tumor-induced bone destruction through PTHrP production.

We hypothesize that Gli2 induces osteolytic gene expression and tumor growth in osteosarcoma and that inhibiting Gli2 will reduce tumor growth and osteolytic gene expression. We will investigate this process by culturing osteosarcoma and osteoblast cell lines for in vitro analyses. We will treat the cell lines with the hedgehog agonist, Purmorphamine, or the Gli2 inhibitors, HPI-1 and GANT58. We will evaluate the effectiveness of the drugs by collecting RNA and proteins from cells to analyze changes in gene and protein expression by RT-PCR and western blots, respectively. We will analyze tumor cell proliferation using colorimetric assays and trypan blue cell counts.

Using RT-PCR, we have shown that osteosarcoma appears to express more PTHrP than osteoblasts. Our western Blots have shown osteosarcoma and osteoblasts express robust amounts of nuclear Gli2, and the osteolytic factor, Integrin β3. We have seen an expression of Gli2's downstream targets, RUNX2 and Gli1. Finally, Osteosarcoma cells have displayed varying proliferative capacities.

Our goal is to develop a better understanding of the pathways contributing to osteosarcoma oncogenesis and to further evaluate Gli2 as a molecular target in osteosarcoma induced bone destruction.

THU - 326 The Role of Autophagy in Radiation Resistance of Pancreatic Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Daisy Palomera*, *University of California, Los Angeles*; Anahita Sehgal, *University of California, Los Angeles*; David Sung, *University of California, Los Angeles*; Amy Dao, *University of California, Los Angeles*; Taha Yazal, *University of California, Los Angeles*; Justine Bailleul, *University of California, Los Angeles* and Erina Vlashi, *University of California, Los Angeles*

Abstract: Patients with pancreatic ductal adenocarcinomas (PDAC) have a <5% chance of survival if their tumors are unresectable. This dismal prognosis is the result of the inherent and/or acquired resistance of PDAC to chemotherapy and radiation therapy (RT). At a molecular level, ionizing radiation (IR) exerts its cytotoxic effect by inducing oxidative stress via the generation of reactive oxygen species (ROS). Cancer stem cells (CSC) are a small subpopulation of tumor cells that are capable of initiating and propagating a tumor and exhibit resistance to most anti-cancer therapies. Autophagy, a form of recycling and scavenging of cellular nutrients, is a survival strategy employed by cancer cells to maintain low levels of ROS. Importantly, autophagy has been shown to be critical in maintaining the CSC population of PDAC tumors. Therefore, we hypothesized that inhibiting autophagy would improve the response of PDAC to RT, partly through the depletion of the RT-resistant CSCs. Using small molecule inhibitors of autophagy, we show a significant sensitizing of PDAC CSCs to RT, as well as the bulk of tumor cells. Response to radiation was determined via a combination of methods, including ATP-lite viability assays, classical clonogenic survival assays, and tumorsphere assays. The *in vitro* radiosensitization of PDAC cells was also confirmed with *in vivo* animal models of human PDAC. Together, these results strongly support the premise that autophagy inhibition in combination with RT can potentially improve the prognosis for PDAC patients.

THU - 327 Modeling Neurofibromatosis Type 2 in Zebrafish *(Danio Rerio)*

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Christina Rouhotas*, *Northeastern Illinois University*; Maria Garcia, *Northeastern Illinois University*; Ezekiel Oluyadi, *Northeastern Illinois University* and Jorge A. Cantú, *Northeastern Illinois University*

Abstract: Neurofibromatosis Type 2 (NF2) is a hereditary disease that causes the growth of bilateral, benign tumors on the auditory-vestibular nerve (cranial nerve VIII). The disease is caused by mutations in the *NEUROFIBROMIN 2 (NF2)* gene which encodes the cytoskeletal protein, Merlin. The zebrafish (*Danio Rerio*) genome encodes two homologues of the NF2 gene, named *nf2a* and *nf2b*. To study the function of these genes in zebrafish, we generated two knockout strains with targeted mutations. For this study, we injected single-celled zebrafish embryos with Cas9 nuclease and a single-guideRNA targeting either the first exon of *nf2a* and or the fourth exon *nf2b*. We verified the presence of insertions and/or deletions (indels) in the gene using a heteroduplex mobility assay on a subset of 6-8 embryos per group of injected embryos. Groups with indels in greater than 60% of the analyzed embryos were raised to adulthood for further genetic analysis, tail fin genotyping, and breeding. We hypothesize that zebrafish missing one or both Merlin/NF2 homologues will develop Schwann cell-derived tumors (schwannomas) in the cranial nerves, mirroring those present in patients with Neurofibromatosis Type 2. These fish will be useful as a model of Neurofibromatosis Type 2 and help us better understand the function of the Merlin protein and its role as a tumor suppressor.

THU - 328 Investigating the Genetic Diversity of Immune Genes in Non-Native Populations of American Bullfrogs (Lithobates catesbeianus)

Discipline: Life Sciences
Subdiscipline: Genetics

Luisa Segovia*, *Humboldt State University* and Karen Kiemnec-Tyburczy, *Humboldt State University*

Abstract: The American Bullfrog (Lithobates catesbeianus) is a highly invasive species that has successfully colonized different habitats around the world. Our project's objective was to isolate and characterize the genetic diversity of a rapidly evolving immune gene in an invasive bullfrog population in California's Sutter National Wildlife Refuge. The level of immune gene genetic variability in a population may help determine how resistant a population is to pathogens and how persistent an invasive population may be over time. Our hypothesis is that our focal population harbors high genetic diversity, consistent with its presence in Northern California for decades. To test our hypothesis, we amplified a Major Histocompatibility Complex (MHC) gene using polymerase chain reaction (PCR) and cloned the alleles from each frog. We then assessed individual heterozygosity, number of alleles in population and genetic diversity of those alleles using standard population genetic metrics. Finally, we compared the genetic diversity within this bullfrog population to that found in other frog populations, including both native and non-native populations. We found that the levels of diversity in our focal population were similar to the levels found in native populations of other species and higher than in native species that have undergone population declines.

THU - 329 A *Drosophila* Model for Human Intellectual Disability: Functional Links between a Conserved Poly(A) RNA-Binding Protein and m^{6}a Methylation Machinery

Discipline: Life Sciences
Subdiscipline: Genetics

Brianna Brown*, *Emory University*; Binta Jalloh, *Emory University*; John Christopher Rounds, *Emory University*; Anita Corbett, *Emory University* and Kenneth Moberg, *Emory University*

Abstract: The human brain is a complex system that is comprised of billions of neurons. The establishment, maintenance, and plasticity of these connections requires precise spatial and temporal control of gene expression, which is achieved through the activity of RNA binding proteins. One RNA binding protein recently linked to a form of autosomal recessive, non-syndromic, human intellectual disability is ZC3H14. A major question is why mutations in this ubiquitously expressed gene cause intellectual disability, a brain-specific disease. We employ the fruit fly *Drosophila melanogaster* as a model to study this protein. We generated flies hypomorphic for the *Drosophila* orthologue of ZC3H14, dNab2. These flies show multiple phenotypes that provide insight into the function of dNab2/ZC3H14. We then performed RNA-Seq comparing *dNab2* mutant and control wildtype fly heads. This analysis reveals a number of intriguing candidate dNab2 targets. In initial studies, we focused on aberrant splicing of the *Sex Lethal*(*Sxl*) gene, which is required for sex determination and could thus be the molecular basis for sex skewing in *dNab2* mutants. My project tests the hypothesis that *Ime4* and *dNab2* show genetic interactions by analyzing flies that are homozygous *dNab2* mutants that also lack one copy of the *Ime4* gene. Interestingly, I discovered that deleting one copy of *Ime4* in the *dNab2* mutant flies results in increased viability, normalized sex ratios, and proper *Sxl* splicing and protein expression. This supports a model linking the functions of dNab2 and Ime4 and their involvement in co-regulating critical RNA targets.

THU - 330 Effective Population Size Variation in Two Species Under Ecological Competition Models

Discipline: Life Sciences
Subdiscipline: Genetics

Stefany Nunez Zavala*, *California State University San Marcos*; Arun Sethuraman, *California State University San Marcos* and Jeff Jaureguy, *California State University San Marcos*

Abstract: Species often interact in nature - they compete for the same resources, or one species depredates the other, or in some cases, species co-evolve with each other in a symbiotic relationship. The most common indicator of the size of each species is a population census number, which often overestimates the amount of genetic variation within a the species. Effective population sizes (Ne), however, quantify the rate of change in allele frequencies over time, and are better indicators of the genetic variation in a population due to natural processes that affect census sizes, such as bottlenecks, and selection due to interactions between two species. Here we explore the variation in effective population sizes in two species under the Lotka-Volterra system of first-order differential equations of census size variation, under models of (a) competition (predator-prey), (b) mutualism, (c) commensalism, (d) parasitism, and (e) symbiosis. We assume a simple model of census size variation under genetic drift and population size fluctuation, to solve for effective population size, and hence the population-scaled mutation rate (Q=4Nem), where mis the mutation rate per genetic locus per generation in a species. Our work obtains theoretical expectations for the amount of genomic variability that would be expected under genetic drift and species-species interactions.

THU - 331 Role of 5' UTR *MYH3* Variant in Distal Arthrogryposis

Discipline: Life Sciences
Subdiscipline: Genetics

Kim Ha*, *University of Washington, Seattle*; Michael Bamshad, *University of Washington, Seattle* and Kathryn Shively, *University of Washington, Seattle*

Abstract: Distal Arthrogryposis (DA) syndromes are a group of rare genetic disorders characterized by multiple congenital limb contractures with a wide breadth of phenotypic severity. However, there is little information to explain these different levels of severity. A study by Cameron-Christie (2018), found that individuals with recessive Spondylocarpotarsal Synostosis Syndrome were compound heterozygous, that is, there was the presence of two different variant alleles at a specific gene locus, for a coding variant in the gene Myosin Heavy Chain 3 *(MYH3)* and a non-coding variant found at the location c.-9+1G>A (rs557849165) on *MYH3*. We are interested in discovering if individuals with DA and *MYH3* variants are carriers for this variant, c.-9+1G>A, to explain more severe phenotypes seen. We hypothesize that rs557849165 has a role in phenotype severity of individuals with DA. We screened our cohort of individuals with DA and *MYH3* variants in the previously unscreened non-coding region of exon 2 using Sanger sequencing. To do this we used amplification and purifying techniques including: Polymerase Chain Reaction (PCR), PCR Clean, BigDye Terminator kit, and Sephadex plates. Electropherograms were then analyzed using CodonCode Aligner. We did not detect the variant in any individuals screened in our first cohort. Individuals that did not previously produce results for analysis are being re-screened for the same variant. Further investigation is being conducted on additional DA candidates to better identify the genotype-phenotype relationship of various forms within DA1, DA2A, and DA2B and better understand the effects these variants have on these individuals with DA.

THU - 400 Misperception of Misogyny in Hypermasculine Rap Music

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Joshua Alvarado*, *The Colorado College*; Robert Welch, *The Colorado College*; Tomi-Ann Roberts, *The Colorado College* and Kevin Holmes, *The Colorado College*

Abstract: Over one-fifth of rap songs contain themes of misogyny or gender inequality. Previous research has shown that listening to misogynist rap music increases sexually aggressive behavior among men. Other forms of rap music, while not explicitly misogynist in content, communicate hypermasculine attitudes that may be misperceived as misogynist. The present study investigated this possibility. Participants (*N* = 93 U.S. Amazon Mechanical Turk workers) listened to excerpts from nine rap songs that were either (a) explicitly misogynist, (b) hypermasculine but not misogynist, or (c) neither misogynist nor hypermasculine (control). After each excerpt, participants rated the degree to which the song promoted misogyny and other negative attitudes (racism, classism, materialism, and homophobia), as well as the overall valence and intensity of the song, on 11-point Likert scales. The results showed that misogyny ratings differed across song types, even when controlling for all of the other rated dimensions. Unsurprisingly, the explicitly misogynist songs were rated highest on misogyny, but critically,

the hypermasculine/non-misogynist songs were rated as significantly more misogynist than the control songs. These results suggest that hypermasculine rap music is perceived as misogynist even in the absence of explicitly misogynist content. Future research in our lab will investigate whether such music in turn primes sexual objectification of women, and perhaps even sexual aggression. If so, media that communicates hypermasculine themes may serve as a powerful yet insidious vehicle through which misogynist attitudes are propagated. Our findings will have implications for promoting positive conceptions of masculinity that are not confounded with misogyny.

THU - 401 **The Impact of Discrimination on the Health of African Americans**

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

David Ifediba*, *University of California, Riverside* and Carolyn Murray, *University of California, Riverside*

Abstract: In 2015 and 2016, the overall life expectancy for the United States population decreased from 76.3 years to 76.1 years (Khazan, 2017). The increase in death rates for African American males, between the ages of 25 and 34, was so dramatic that it lowered the life expectancy for the entire US population. Previous literature has demonstrated that high levels, or sources, of threat to an individual's social wellbeing increases the release of stress hormones, such as proinflammatory cytokine activity and cortisol levels. In addition, release of these stress hormones were associated with experiencing discrimination, subsequently resulting in negative impacts on general health (Dickerson, Gruenewald & Kemeny, 2004). The present study examines the relationship between different types of discrimination (e.g., daily, major, and anticipated) and levels of health reported by African Americans and Caucasians. The study used telephone interviews, home visits, and self-administered questionnaires to poll 605 adults, who were born between 1959 and 1967 and then followed to age 50. Participants were asked questions in regards to their daily, major, and anticipated experiences of discrimination. Results indicate that African Americans, when compared to Non-African Americans, experienced more discrimination and worse general health. A proactive African-centered mental health approach is recommended.

THU - 402 **Individual Differences in Facial Emotion Recognition in Psychosis Risk**

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Leslie Zuniga*, *University of Illinois at Chicago*; Kristen HAUT, *Rush University Medical Center* and Briana Galindo, *Rush University Medical Center*

Abstract: Individuals with schizophrenia demonstrate impaired emotion recognition that is associated with poorer social functioning. However, the relationship of emotion recognition to functioning in CHR prior to the onset of a psychotic illness is unclear. Limited research focusing on emotion recognition in CHR individuals. It is unclear if performance differs based on the type of emotion presented and the impact of clinical and demographic factors is unknown. This examines the effect of individual differences on the performance of a facial-emotion processing task in CHR individuals. We hypothesize that individual differences on gender, age, iq and symptoms may be related to differential performance on the task. 69 individuals who meet CHR criteria performed a facial emotion recognition task using morphed faces that combine an emotional expression with a neutral face. Subjects were rated on a number of CHR symptoms following a clinical interview. Significant differences in accuracy depending on the emotion expressed (F=29.48, p<.001) and CHR individuals are significantly more accurate on positive emotions compared to negative emotions (t=-9.91, p<.001). There were no significant correlations between symptoms and task performance. These results suggest that while CHR individuals show differing performance based on the type of emotion, performance differences cannot be attributed to basic demographic differences or symptom levels. These findings suggest that research on emotion processing CHR individuals may need to account for differential effects of emotion type as well as of IQ by gender. Further research is necessary to understand the individual differences that impact emotion recognition performance in CHR individuals.

THU - 403 **Are Ratings of Women's Body Attractiveness and Health Associated with Markers of Fertility: Waist-to-Hip Ratio, Waist-to-Stature Ratio, and Body Mass Index?**

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Amanda Golden Eddy*, *California State University, Fullerton* and Jessie Peissig, *California State University, Fullerton*

Abstract: Evolutionary psychologists hypothesize that men's mate preferences for attractive and healthy women are based on waist-to-hip ratio [WHR], waist-to-stature ratio [WSR], and body mass index [BMI] because these characteristics are informative of fertility (i.e. estrogen levels) (Jasienska, 2004); however these hypotheses are largely unsubstantiated (Jones, et al., 2018).

In the current study, participants provided saliva samples, which were analyzed by SALIMETRICS LLC. Participants' body characteristics (e.g. waist, hip, height, and weight) were measured to calculate their WHRs, WSRs, and BMIs. Photos of their bodies were presented to a separate set of participants, who were randomly assigned to rate the photos using either an attractiveness or health Likert-like scale from 1-7, with 1 being very unattractive/unhealthy and 7 being very attractive/healthy. This study revealed a significant positive correlation between attractiveness ratings and health ratings (r= .895,p< .000), which has been established for faces but not bodies (Thornhill & Moller, 1997). Preliminary correlations between health ratings and estradiol concentrations showed nonsignificant positive correlations (r= .098, p> .739). Although non-significant, the correlation between attractiveness ratings and estradiol concentrations is higher (r= .303, p> .292), suggesting that with more participants this may reach significance. Moreover, WSR (r= -.589, p< .027), and BMI (r= -.617, p< .019) showed a significant negative correlation to attractiveness ratings, however WHR was not significantly correlated to attractiveness ratings (r= -.428, p> .127), suggesting that WSR and BMI may be better correlates of attractiveness than WHR.

THU - 404 **Effects of Familismo on Academic Motivation in High-Achieving Latinx College Students**

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Jonathan Azpeitia*, *Pomona College, Department of Psychology* and Guadalupe A. Bacio, *Pomona College Departments of Psychology and Chicana/o-Latina/o Studies*

Abstract: Given their increased enrollment but low rates of graduation in higher education, it is critical to assess factors that academically motive Latinx college students. Familismo suggests that the family is the most important unit in Latinxs' lives – deriving support from, acting in reference, and feeling an obligation to the family. Familismo has been found to predict positive academic outcomes, such as academic motivation. Endorsements of familismo have been found to differ by immigrant generation and gender, however, their interactive effects have not yet been explored. The current study aims to investigate how the interaction of immigrant generation and gender may moderate the relation between familismo and academic motivation. This study collected data from 176 Latinxs attending elite liberal arts colleges Southern California. Participants (66% women) completed a series of self-report measures on familismo and academic motivation. As expected, analyses showed that immigrant generation moderated the relation between familismo and academic motivation, and in turn, these associations differed by gender. That is, only 1st/1.5-generation Latinos and 2nd-generation Latinas experienced the academic benefits of familismo. Further analyses revealed that family support was the dimension of familismo responsible for the observed relations. Implications of these findings suggest that institutions of higher education must acknowledge how cultural values influence academic motivations, while also recognizing how immigrant narratives and gendered familismo influence these effects. These findings provide a counternarrative by focusing on the factors that predict academic motivation in high-achieving Latinx college students rather than focusing on the factors that hinder educational success.

THU - 405 The Role of High School Ethnic Diversity on Health and Academic Outcomes during the Transition to College

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Karina Barragan*, *California State University, Northridge*; Lucy Gonzalez, *California State University Northridge* and Yolanda Vasquez-Salgado, *California State University Northridge*

Abstract: Despite measures taken, after the ruling of *Brown vs. Board of Education*, there continues to be an alarming rate of schools that lack in ethnic diversity. Previous studies have found that diversity in school settings matter because it aids individuals in becoming less socially vulnerable (Graham, 2018). This effect is strongest among ethnic minority groups, such as Latinx middle and high school students (Juvonen et al., 2018). The purpose of our study was to extend this work by examining whether ethnic diversity of high school attended relates to health (mental, physical) and academic problems during the transition to college. We also examined whether these relations would be moderated by ethnic background. We hypothesized that students that attended high schools with lower diversity would experience higher rates of health and academic problems during the college transition. Additionally, we hypothesized that these relations would hold strongest among Latinx students. Participants completed an online survey at the end of their first year in college (N = 170, M_{age} = 18.75; Latinx: 27%). Simpsons' (1954) Diversity Index was utilized to calculate ethnic diversity.Our results indicated that attending high schools with higher diversity was associated with lower health and academic problems (r's ranged from -.16 to -.25, $p < .05$). In addition, when examined by ethnic group, the effects only held for Latinx students (r's ranged from -.27 to -.46, $p < .05$), demonstrating moderation. Several findings held after controlling for SES of high school attended. Our findings illuminate the importance of ethnic diversity.

THU - 406 Exploring the Relationship between Nativity Status, Experiences with Deportation, and Alcohol Use Among Latinx Men Who Have Sex with Men (MSM) in Los Angeles

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Jasmine Hernandez*, *University of California, Los Angeles*; Steven Shoptaw, *University of California, Los Angeles* and Pamina Gorbach, *University of California, Los Angeles*

Abstract: Prior research has shown alcohol use disorder is strongly associated with adverse life circumstances, among men who have sex with men from ethnic minority backgrounds, especially Latinx men who have sex with men (LMSM). Previous findings vary as to whether native-born or foreign-born status is a predictor for higher levels of alcohol use. Other studies urge that experiences with deportation needs to be further assessed because it may be associated with higher levels of alcohol use among LMSM. The current study examined whether foreign-born LMSM who have experienced deportation reported higher levels of alcohol use when compared to U.S.-born LMSM. A cross-sectional analysis was performed using baseline data from the mStudy, a longitudinal study examining alcohol and drug use among male-identified Latinx and African-American/Black MSM in Los Angeles. Results indicated U.S.-born LMSM were significantly more likely to report higher levels of alcohol use than foreign-born LMSM, thus providing evidence for the *immigrant paradox,* whereby U.S.-born individuals tend to have worse developmental outcomes than those who are foreign-born. Future research should explore how native-born status is a risk factor for higher levels of alcohol use among LMSM, as well as identify protective factors among foreign-born LMSM that decreases their risk. These results may inform mental health professionals and researchers on how to better address appropriate preventive measures in reducing alcohol use disparities among LMSM, as well as to place a greater focus on new policy implementation of a program to support vulnerable populations such as LMSM.

THU - 407 Postpartum Depression: A Psychosocial and Health Literacy Perspective

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Daniel Saravia*, *California State University, Northridge*; Teresa Wagner, *UNT Health Science Center* and Amit Aggarwal, *UNT Health Science Center*

Abstract: Postpartum Depression (PPD) is a major contributor to maternal morbidity in the U.S (Robertson, Grace, Wallington, & Stewart, 2004). One in nine mothers is diagnosed with PPD (Ko, Rockhill, Tong, Marrow, & Farr, 2017). Specifically, a 2011 Texas state report estimated that 10.2% of mothers reported PPD symptoms. Additionally, PPD symptoms were more prevalent among Black mothers (11.9%) than White mothers (9.4%) (TXDSHS, 2011). Lastly, extensive research shows that low-income and ethnic minorities are less likely to seek professional assistance than White individuals (Kurtz, 2005; Song, Sands, & Wong, 2004).Mothers often do not recognize abnormal emotions occurring during the postpartum period which signal PPD (Abrams, Dornig, & Curran 2009). Limited mental health literacy (MHL) hinders mental health (MH) service utilization and recognition of PPD symptoms. Research illustrates that mothers with PPD exhibited symptoms but lacked knowledge about PPD, MH services available or how to access services. (Abrams et al., 2009; Holopainen, 2002).

The current study aimed to determine whether mothers received appropriate PPD instruction by examining data collected from one-on-one interviews with a diverse sample of mothers residing in North Texas. Twenty-one new mothers were interviewed as part of a pilot study on postpartum health literacy. Interviews were transcribed and coded conducting applied thematic analysis using the Integrated Model of Health Literacy. 33% of participants indicated a lack of PPD education provided at discharge. Results illustrate the need for providers to give more comprehensive postpartum instruction on PPD to facilitate diagnosis, understanding and obtaining PPD MH services.

THU - 408 Does Fraction Understanding Involve Consistency across Multiple Visual Models?

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Yeo Eun (Grace) Yun*, *Northeastern Illinois University*; Christian Palaguachi, *Northeastern Illinois University*; Steven Montalvo, *Northeastern Illinois University*; Ashley Lebron-Vazquez, *University of Illinois, Urbana-Champaign*; Breckie Church, *Northeastern Illinois University*; Shereen Oca Beilstein, *University of Illinois, Urbana-Champaign* and Michelle Perry, *University of Illinois, Urbana-Champaign*

Abstract: In the United States, many children struggle with the mathematical concept of fractions. Previous literature shows that conceptual understanding of fractions is critical to obtain flexibility in mathematics and to achieve higher academic success. Previous theories about the development of mathematical understanding suggest that complex understanding of fractions requires explicit linking of multiple representations (including symbols and concrete models). The goal of this research was to identify and describe children's understanding of fractions through use of different representations (e.g., fraction circles, number lines, drawings) obtained through a structured, open-ended interview. In the interview, 23 7 to 10 year old children were asked to show and explain the meaning of certain fractions (e.g., ¼). In addition, children individually completed a 14-item diagnostic worksheet and, based on this assessment, were categorized as having low- or high-fraction understanding. The types of models children relied on during the interview were examined and were matched to the their explanation of the fraction. Results showed that the high-fraction children were more likely to express fraction understanding correctly and consistently across multiple models whereas low-fraction children tended to convey correct understanding inconsistently across models. Implications include understanding how children might explicitly link multiple representations of concepts to improve academic success especially for those with educational disadvantages. This will help level the playing field of educational disparities.

THU - 409 Discrepancies Between Teacher- And Child-Reports On Proactive And Reactive Aggression: Does Prosocial Behavior Matter?

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Sofia Mildrum Chana*, *University of Kansas*; Elisabeth C. Tampke, *University of Kansas* and Paula J. Fite, *University of Kansas*

Abstract: Previous research has demonstrated that informants differ on their reports of childhood aggression subtypes (i.e., proactive goal-oriented aggression and reactive, impulsive aggression). Further research is needed to understand how reporters' discrepancies may be moderated by other variables, as well as how these associations may change over time. This project examines discrepancies between teacher and student reports of proactive and reactive aggression as well as how teacher perceptions of prosocial (i.e., positive, helping) behavior moderates reporters' discrepancies of aggression in a sample of elementary school-age youth over an academic year (fall and spring). No difference in the magnitude of reporters' discrepancies across time was found ($ts=1.486$ & -0.868, $ps>.05$). Correlations indicated an association between informant reports of reactive ($rs=.152$ & $.309$, $p<.05$) but not proactive aggression ($rs=.083$ & $.080$, $p>.05$). Further, analyses indicated that prosocial behavior didn't moderate the associations between reports of proactive aggression ($\beta s=.089$ & $.034$, $ps>.05$). In contrast, at low levels of prosocial behavior, teacher and child reports of reactive aggression weren't statistically related ($\beta=.063$, $p=.345$), but at high levels of prosocial behavior, teacher and child reports on reactive aggression were positively associated ($\beta=.350$, $p=.007$) in the fall semester. Findings suggest that teachers and students are more similar in their reports of reactive than proactive aggression, particularly when teacher perceptions of prosocial behavior are high. Implications and future directions are discussed.

THU - 410 Investigating the Impact of Education on the Relationship between Depressive Symptoms and Mental Health Service Utilization Among Diverse Samples

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Patricia Orozco*, *California State University, Northridge*; Daniel Saravia, *California State University, Northridge*; Crystal Venegas, *California State University, Northridge*; Jose Arreola, *California State University, Northridge*; Isabel Lopez, *California State University, Northridge* and Jonathan Martinez, *California State University. Northridge*

Abstract: Individuals diagnosed with depression often fail to seek treatment (WHO, 2012), particularly ethnic minorities (Beyers et al., 2012). Additionally, those with lower education demonstrate negative mental health help-seeking attitudes (Jagdeo et al., 2009). This study examined the moderating effect of education on the relationship between depressive symptoms (DSx) and mental health service utilization (MHSU); and the differences between U.S vs. non-U.S. born participants.A subsample of 3,727 adult participants (2,983 U.S. born and 716 non-U.S born)were evaluated from the Collaborative Psychiatric Epidemiology Surveys. DSx and education were hypothesized to positively predict formal MHSU. Moreover, the relationship between DSx and MHSU was hypothesized to differ based on education. Regression analyses revealed significant, positive main effects for DSx and education on MHSU for the overall sample (OR=1.23, $p<.001$; OR=1.45, $p<.001$, respectively), and U.S. born sample (OR=1.26, $p<.001$; OR=1.63, $p<.001$, respectively). Greater DSx and education significantly predicted a greater likelihood of formal MHSU for the U.S. born sample. There was no significant interaction between DSx and education on MHSU in the overall or U.S. born samples. However, there was a significant interaction for non-U.S. born sample (OR=.847, $p=.028$). Follow-up simple main effects revealed that higher MHSU was associated with lower education, whereas lower formal MHSU was associated with higher education. While higher education was considered a proxy for greater mental health literacy (MHL), education effects encourage follow-up analyses examining the role of MHL. Namely, examining the moderating effects of specific MHL indicators on the relationship between DSx and MHSU among racial minorities.

THU - 411 Associations of Emotional Support and Cultural Factors with Benefit Finding Among Spanish Speaking Latina Breast Cancer Survivors

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Maria Reyes*, *California State University Monterey Bay*; Cristian Escalera, *National Institute on Minority Health and Health Disparities*; Jackie Bonilla, *National Institute on Minority Health and Health Disparities*; Jasmine Santoyo-Olsson, *University of California, San Francisco*; Carmen Ortiz, *Círculo de Vida Cancer Support and Resource Center* and Anna Nápoles, *National Institute on Minority Health and Health Disparities*

Abstract: Benefit finding, the perception that positive contributions resulted from the experience of traumatic events, is understudied among Latina breast cancer survivors. This study examined the extent to which emotional support and cultural factors are associated with benefit finding among Latina breast cancer survivors. Analyses used baseline data from an RCT of a stress management program delivered to 151 Spanish-speaking Latinas with non-metastatic breast cancer. All data except for breast cancer variables were obtained via in-person interviews. Predictors were emotional support and cultural factors of spirituality (meaning/peace, faith) and fatalism. Outcomes were two dimensions of benefit finding (personal growth, social relations). Age, breast cancer variables, marital status, and intrusive thoughts were covariates. Generalized linear regression models examined bivariate and multivariate associations of predictors with outcomes of personal growth and social relations. Variables that were associated with either outcome at $P<0.15$ at the bivariate level were retained in multivariate models. Mean age was 50.5 years (SD=10.9; range=28 to 81 years). Mean time since breast cancer diagnosis was 3.8 months (SD=2.7). In bivariate models, emotional support and all cultural factors were associated with personal growth and social relations at $P<0.001$. Controlling for covariates, emotional support ($p<0.001$), meaning/peace ($p<0.05$), and faith ($p<0.05$) were positively associated with social relations. Only emotional support ($p<0.001$), was positively associated with personal growth, controlling for covariates. Interventions that enhance emotional support and spirituality could increase benefit finding among Latina breast cancer survivors.

THU - 412 Correlations of Identity and Medical Mistrust in Latino Sexual Minority Men

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Isaiah Jones*, *San Diego State University* and Aaron Blashill, *San Diego State University*

Abstract: While much has been done to explore medical mistrust (MM) in ethnic minorities and men who have sex with men (MSM), there is a deficit of literature for MM in the Latino MSM (LMSM) community. This population may be less likely to trust health care providers and more likely to face multi-minority stressors, stigma, and discrimination related to MM. This study aims to explore the typical profile of LMSM experiencing MM, and the mental and physical health correlates that they may be facing. Exploratory analysis was conducted using data collected from 151 LMSM to examine the demographic, behavioral, and psychological correlates of MM. Participants were recruited through various MSM dating apps and websites to complete an online survey concerning sexual, psychosocial, and demographic topics. The majority of participants were young adult (mean age=24) gay (68.2%), white (55.3%), and college educated (74.5%), with some form of medical insurance (90.7%). MM (using the Group-Based Medical Mistrust Scale) was largely associated with greater depression ($r=.29$ $p<.001$), drug use ($r=.53$ $p<.001$), unstable housing ($r=.33$ $p<.001$), being bisexual ($r=.30$ $p<.001$), and machismo ($r=.44$ $p<.001$) versus caballerismo ($r=-.46$ $p<.001$). LMSM experiencing MM reported more substance use and unstable housing. Bisexual and machismo men reported more MM than gay or caballerismo men. This may suggest that cultural factors and personal beliefs held by LMSM, rather than demographic characteristics commonly related to discrimination, are key to understanding MM. Future studies examining how culture and acculturation influence MM may be promising avenues toward reducing mistrust and increasing general care.

THU - 413 Under Pressure: Rapid Presentation of Multiplications and Memory for Arithmetic in Bilinguals

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Paola Montufar Soria*, *University of Texas San Antonio*; Vanessa Cerda, *University of Texas San Antonio* and Nicole Wicha, *University of Texas San Antonio*

Abstract: Students typically learn arithmetic facts, such as multiplication tables, through verbal rehearsal in one language. Math cognition models suggest that bilinguals engage different verbal memory systems when performing arithmetic in each language, while bilingual models suggest that both languages are simultaneously active. Behaviorally, bilingual students generally prefer to use the language they were taught in (LA+), rather than their other language (LA-), to do math. In fact, previous studies have shown that bilinguals are faster and more accurate in retrieving arithmetic facts in LA+ than LA-. This suggests that the verbal memory for arithmetic facts may be dependent on the language in which the math facts were encoded. We tested whether bilinguals process arithmetic facts differently in their two languages by recording event-related potentials (ERPs) as Spanish-English bilingual adults verified multiplication facts presented in their LA+ or LA-. Using this task, our lab has not found evidence of qualitative or quantitative differences in the way bilinguals process arithmetic across languages. Here, we removed the interstimulus intervals (ISIs) from our original verification task to test whether rapid presentation of multiplication problems reveals differences in the way bilinguals process arithmetic facts in each of their languages. Preliminary results suggest that bilinguals are slower and less accurate at verifying the correct multiplication answer, but the brain response doesn't appear to be different between languages.

THU - 414 Evaluations of EEG Systems Utilizing Mindfulness Task

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Aileen Kangavary*, *California State University, Northridge* and Stefanie Drew, *California State University, Northridge*

Abstract: It is critical to further understand how new imaging devices with high mobility may contribute to research in cognitive neuroscience and to explore the applications of these imaging devices in general. The purpose of the present study is to make comparisons between two commercially available electroencephalographic (EEG) systems, the Emotiv Insight and the InterAxon Muse, while utilizing a mindfulness task. We hypothesize that the Interaxon Muse will have better spectral sensitivity showing an increase in alpha waves as it is marketed for mindfulness usage. Participants are instructed to keep their attention on their breathing patterns with their eyes closed for 5 minutes, clearing their mind and listening to relaxing music. A spectral analysis will be conducted by averaging the Alpha, Beta, Gamma, and Theta band frequencies recorded from each headset, which will be analyzed as separate dependent variables using a 4 (electrode) × 2 (headset) MANOVA. We anticipate an increase in slow alpha oscillations in the frontal area and an increase in the presence of frequencies corresponding to the theta band (4-8 Hz) and the lower end of the alpha band (8-10 Hz), which are indications of mindfulness. This research is applicable to practitioners that have patients using mindfulness techniques, which can then inform the field about utilizing EEG systems that are commercially available, applicable, and less costly than hospital grade systems.

THU - 415 Chronic Administration of Alcohol and the Brain: A Role for Δfosb?

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Tania Lugo*, *California State University Dominguez Hills*; Philip Vieira, *California State University Dominguez Hills* and Stacy Zamora, *California State University Dominguez Hills*

Abstract: Pathogenesis of substance use disorder (SUD) is presumed to be caused by alterations in gene expression in the mesocorticolimbic pathway of the brain. ΔFosB, a transcription factor that induces and represses gene expression, is a purported 'molecular switch' of SUD, supporting long-term neurobiological changes that underlie addiction. ΔFosB is shown to be induced by drugs of abuse in several brain regions associated with reward processing and decision making, including the nucleus accumbens (NAc), ventral tegmental area (VTA) and the prefrontal cortex (PFC). Overexpression of ΔFosB has been linked to behavioral responses such as compulsive drug-intake and drug-seeking. Drugs that induce ΔFosB include, amphetamine, cocaine, alcohol, methamphetamine, morphine, nicotine and D9-tetrahydrocannabinol. Yet, there are limited amount of studies that use alcohol to investigate ΔFosB induction. The proposed study is designed to investigate the expression of ΔFosB in the NAc, VTA and PFC in response to chronic administration of alcohol. Brain slices will be taken from male and female Sprague-Dawley rats exposed to alcohol (alcohol-treatment) and those not exposed to alcohol (vehicle-treatment). Concentrations of ΔFosB protein and *ΔfosB* mRNA in the mentioned brain regions will be assessed via immunohistochemistry and quantitative PCR techniques. The data generated by this work may better inform treatments for SUD as a result of chronic alcohol consumption.

THU - 416 Does Tacs during an Auditory Spatial Attention Task Stave Off Vigilance Decrement?

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Alyssa Randez*, *University of Texas at San Antonio*; Jeffrey Mock, *University of Texas at San Antonio* and Edward Golob, *University of Texas at San Antonio*

Abstract: Focusing attention over long durations reduces performance and is known as vigilance decrement. Human attention control is governed by two neuronal networks: a dorsal attention network (DAN) responsible for directing attention towards a task/goal and a ventral attention network (VAN) that automatically reorients attention towards unexpected stimuli. Communication between the right inferior frontal gyrus (rIFG) and right temporoparietal junction (rTPJ) is vital for this reorienting of attention. Previous electroencephalogram studies suggest theta coherence (4 Hz) between rIFG and rTPJ along with blood flow in the medial cerebral artery (MCA) decreases during the vigilance decrement. This study will investigate how facilitating information transfer between the rIFG and rTPJ with 4 Hz transcranial alternating current stimulation (tACS) influences the vigilance decrement. tACS produces a frequency-specific electrical current between two scalp electrodes which can interact with neural brain activity. For behavioral measures, an auditory spatial attention task will include discriminating between two tones ("go") and not responding to a distractor sound ("no-go"). Reaction time, accuracy and MCA blood flow will be quantified. We hypothesize that maintaining the baseline coherence power between the rIFG and the rTPJ with tACS will stave off the vigilance decrement. Expected results should show less of a decrease over time in accuracy to go trials, no-go distractors and blood flow during tACS stimulation when compared to sham tACS stimulation. These findings will help understand the neuronal mechanisms underlying the vigilance decrement, which could possibly lead to discovering ways for counteracting performance deficiency.

THU - 417 Interviewer Gender Effects in the Afrobarometer Survey

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Carla Garcia*, *University of Central Florida* and Cristina Bodea, *Michigan State University*

Abstract: The number of political science publications utilizing surveys conducted in developing countries has more than doubled in the past decade. However, there is a limited understanding of the unique methodological challenges faced by survey researchers in the developing world. US-based research suggests that characteristics of the interviewer influence survey responses (the "interviewer effect"), though this theory has not been widely tested in the developing world. To work towards bridging this gap, this study investigates the research question, how does interviewer gender influence survey responses in the Afrobarometer survey? The Afrobarometer is a public opinion survey of democracy and governance in Africa, the results of which are used widely in academic research. We use Round 6 of the survey, which was administered in 2014-2015 to over 53,000 respondents across 36 countries. Using logistic regression models, we analyze how interviewer gender affects responses to a question regarding women's political participation. We compare these results with a model analyzing the effect of interviewer gender on questions unrelated to gender issues. We find that respondents of both genders are more likely to report support for women in politics when interviewed by a woman, consistent with social desirability theory. We also expect to find that women interviewers elicit higher non-response rates, as predicted by social power theory. We expect the effects to be small overall, but vary in magnitude across countries and regions. We anticipate that this study will have valuable implications for the future collection of accurate, unbiased survey data in the developing world.

THU - 418 Patient-Provider Relationships in Breast Cancer: Implications for Latina Breast Cancer Survivors' Mental Health

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Kryztal Pena*, *University of Illinois at Chicago*; Yamile Molina, *University of Illinois at Chicago*; Jocelyne Lemus, *University of Illinois at Chicago*; Corazon Avila, *University of Illinois at Chicago* and Perla Chebli, *University of Illinois at Chicago*

Abstract: We want to understand the impact on Latina breast cancer survivor’s mental health stemming from the relationship between health providers and breast cancer patients.

Latinas are commonly under-treated for breast cancer and its sequelae, including for depression, which can impact their quality of life post-treatment (Maly, 2010). This study aims to characterize Latina breast cancer patients’ perspectives on how patient-provider relationships can impact cancer outcomes.

Staff from ALAS-Wings and the University of Illinois at Chicago used convenience-based sampling to recruit 19 Latina breast cancer survivors for 2 focus groups. Participants had to be over the age of 18, identify as Latina/Hispanic/Chicana, diagnosed with breast cancer, and have undergone a lumpectomy or mastectomy within the past 5 years. Inductive content analysis was done.

The majority of Latinas had negative experiences with their provider due to lack of empathy (e.g. difference in authority between a patient and provider, lack of guidance) and miscommunication. Those with negative experiences reported more stress throughout diagnosis and treatment. Latinas with positive experiences demonstrated no stress related to experience with provider and were clear on next steps in their treatment process.

Our results suggest that providers’ relationship with patients influences patients’ mental health during treatment. Future interventions should educate health personnel on cultural sensitivity and collaborative decision-making to avoid contributing to Latinas stress during diagnosis and treatment.

THU - 419 Presidential Leaders: Is There an Overconfidence Effect?

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

DIANA Baldovinos*, *Washington State University* and Julie Kmec, *Washington Statue Univesity*

Abstract: What is the significance of overconfidence? Studies have shown that people who hold high power positions (e.g., scientists, legal scholars, negotiators, CEOs) in management, positions tend to be overconfident (Galasso, 2014). Overconfident individuals attain higher status and power within their organizations, whether their confidence was justified by actual ability or not (Anderson, et al., 2012). Past studies have found high risks of damaging consequences with people in power being overconfident (Kennedya, et al., 2003), such as financial deficits—and yet these people tend to display overconfidence across many spheres (Dunning, 2005). The present study will use *overconfidence effect* as a theoretical framework. Essentially, this theory can be used to examine participants’ overconfidence by measuring where they lie on a scale. Our participants are college students who are presidents of club organizations. The surveys are targeted across many of the 430 undergraduate student organizations on campus. (1) To begin, we measured where presidents lie on overconfidence through an experimental survey. (2) Subsequently, we gave surveys to active members to gauge their satisfaction and perception of effectiveness in the organization. The literature shows correlation of negative consequences, especially with financial damages, within organizations that have people in high power positions who are overconfident. The question to be answered will be “how do these presidential leaders ranking on the overconfidence effect scale influence the organization?”. The results can be applied to a plethora of leadership aspects of high power through the process of various institutions such as education, government, sports, and or corporations.

THU - 420 The Effect of Race on Harsh Parenting, Adverse Childhood Experiences, and Child Development

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Samaria Stovall*, *University of Colorado at Denver* and Katherine Casillas, *University of Colorado at Denver*

Abstract: Adverse childhood experiences and corporal punishment have both been linked to negative child outcomes, but rarely is race taken into account as a moderator. Corporal punishment focuses mostly on physical punishment. Currently, the literature suggests that for White children, corporal punishment usually leads to child aggression and negative behavior, even when looking at parental warmth as a moderator. However, Black and minority families may use corporal punishment to lead to positive child outcomes in order to prepare them for the harshness of society. We propose an analysis of archival data from the effective home visiting program, SafeCare Colorado to investigate race as a moderator of corporal punishment and child outcomes. SafeCare is a program for intervention and prevention of child abuse and neglect for at-risk families, and we will gather and analyze demographic information, adverse childhood experience scores, and Parent-Child Conflict Tactics as they are interrelated. Results from this study will help inform home visitors on best intervention strategies based on racial differences in corporal punishment.

THU - 421 Self-Efficacy in Applying to Graduate School Is Key

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Kerstin Rewerts*, *Aurora University* and Meaghan Rowe-Johnson, *Aurora University*

Abstract: Applying to graduate school can be a daunting task. First-generation, low-income, and minority undergraduate students experience barriers in completing applications to graduate school. The purpose of this study was to determine the impact of “Applying to Graduate School” curriculum on students’ postgraduate school application self-efficacy. Participants attended four workshops based on Social Cognitive Career Theory. The workshops covered topics such as searching for postgraduate schools, acquiring letters of recommendation, preparing for the GRE, creating a resume/curriculum vita, writing personal statements, conducting parallel processing, and properly preparing for the interview process for potential job offers. Pre- and post-workshop data revealed that there was an increase in levels of self-efficacy after undergraduate students completed the Graduate School Search, Resume/CV Construction, and GRE Preparation workshops (pre-test M = 121, post-test M: SD = 14.2). Ideally, these results can provide the foundation for further research regarding the limitations of students reaching higher levels of education as well as finding further ways to assist students in their goals of pursuing postgraduate school.

Keywords: Undergraduate, Self-Efficacy, Postgraduate Application, Applying to Graduate School

THU - 422 When a Perpetrator Wears a Disguise: Exploring Conditions That Improve Eyewitness Identification.

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Kendra Paquette*, *California State University, Fullerton*; Jessica Barragan, *University of California, Irvine* and Iris Blandón-Gitlin, *California State University, Fullerton*

Abstract: When a witness perceives a perpetrator in disguise, what can the police do when testing that witness’s memory with a lineup? Basic face recognition research suggests that if people are tested with faces that include the original disguise (e.g., wigs, eyeglasses), memory would be better compared to when test faces have disguises removed. Related research shows that when a target face has a distinctive feature (e.g., nose ring, tattoo, scar), it is much better to digitally replicate the attribute in all the test faces than to remove the feature from the target. Thus, we hypothesized that replicating the disguise of a suspect during a photographic lineup would improve eyewitness accuracy compared to the no-replication condition. We experimentally manipulated three variables. At the time of an event, witnesses saw disguised or undisguised targets. At the time of a recognition test, witnesses made identifications from disguised or undisguised lineups. Lineups either contained the target (target-present) or a designated innocent suspect (target-absent). A receiver operating characteristic (ROC) analysis indicated that witnesses (*N* = 696) do show a significant improvement in discriminability when identifying a suspect in a replication condition. However, pairwise comparisons revealed that disguised lineups also increased false alarms (identifications of innocent suspects). Supplemental analyses indicated there were more choosers in the disguised lineup condition than in the undisguised condition. This finding suggests that disguised lineups may induce a liberal choosing criterion resulting in an increase in correct identifications and false alarms. This line of research can be used reduce eyewitness misidentifications.

THU - 423 Exploring Racial/Ethnic Differences in the Mediating Effect of Internalizing Symptoms on Parent-Child Relationships and Adolescent Substance Use.

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Ayana Culhane*, *Hampton University*; Natasha Duell, *University of North Carolina - Chapel Hill* and Eva Telzer, *University of North Carolina - Chapel Hill*

Abstract: Negative parent-child interactions contribute to adolescents’ internalizing and externalizing symptoms (i.e. depression and substance use). This study explored whether the association between negative parent-child interactions and internalizing symptoms is associated with greater substance use. Further, we predicted racial/ethnic differences in the associations among these variables due to cultural differences in family values. The study participants included 147 adolescents ages 12-15 years (*M*=13.2, *SD*=.648; Female=52.3%) from diverse racial/ethnic groups (Latinx=39.4%, White=34.2%, Black=26.5%). Adolescents reported past-year frequency of negative parent interactions, internalizing symptoms, and substance use. We computed a proportion score of adolescents’ reports of alcohol, marijuana, e-cigarettes, tobacco and prescription drug (not prescribed to them) use. PROCESS for SPSS was used to run a mediation analysis (negative parent interactions=X, substance use=Y, internalizing=M), with race as a moderator of the path from X à M and X à Y. Results for the model without race indicated a significant indirect effect of negative parent interactions on substance use via internalizing symptoms. With race as moderator, the effect of high negative parent interactions on greater internalizing symptoms was stronger for Latinx and Black youth than White youth, but did not differ between Latinx and Black youth. High negative parent interactions was associated with greater substance use for all groups. Findings highlight the significance of racial/ethnic differences in family dynamics as they influence adolescent internalizing symptoms. However, familial factors similarly impact substance use across racial/ethnic groups. This study helps fill gaps in minority research and provides a more culturally inclusive understanding of youth risky behavior.

THU - 424 How Can We Begin to Decolonize Biology? Reckoning with Our Colonial 'past' in the Sciences

Discipline: Psychology & Social Sciences
Subdiscipline: Sociology

Ash Alunan*, *Willamette University* and Emma Coddington, *Willamette University*

Abstract: Scientists carrying white supremacist ideologies have played an active role in the development and sustenance of colonialism. Through the guise of objectivity and the quest for scientific “discovery,” these scientists have actively harmed people living on the margins and in the process limited the scope of scientific findings. To uphold the dominant white supremacist hegemony, colonial ideologies often are legitimized in scientific inquiry. Scientists who enhance imperialist projects use multiculturalism and promises of diversity to promote the scientific community as inclusive. However, the erasure of colonial involvement deepens the trauma experienced by marginalized populations and leads to limited scope, inaccurate findings, and the ongoing normalization of colonial logics and practices. An honest reckoning with our legacy of colonialism and white supremacy is needed to build an inclusive scientific practice. I propose to examine our culture using intersectionality theory, which considers how social determinants such as racism, sexism, and ableism create compounding systems of oppression that impact the experiences and lives of individuals with multi-dimensional identities. To do so, I will employ autoethnography, a qualitative research method, which gives scholarly voice to marginalized experiences. I hope to show how my lived experiences are not isolated, but fit within a larger story of injustice within the scientific community. This research acts as a vehicle to move beyond the rhetoric of diversity and inclusion to the practice of diversity and inclusion. The findings from this research serve to inform a path towards necessary transformation of the scientific community.

THU - 425 "Walking on a Tightrope through Hell:" a Qualitative Investigation of the Lived Experience of Alcohol Withdrawal

Discipline: Psychology & Social Sciences
Subdiscipline: Sociology

Sarah Najera*, *The University of Texas at El Paso, Department of Psychology*; Brianna Holcomb, *The University of Texas at El Paso, Department of Psychology*; Rubi Gonzales, *The University of Texas at El Paso, Department of Psychology*; Eden Robles, *The University of Texas at El Paso, Department of Psychology* and Craig Field, *The University of Texas at El Paso, Department of Psychology*

Abstract: Alcohol withdrawal can be considered a pivotal time in recovery from an alcohol use disorder given that it is a strong motivator for continued drinking. Still, there is a lack of knowledge on such an experience, as current research on the topic is limited to its physical symptoms. The present study was meant to uncover psychological, social, cultural and perhaps spiritual aspects of alcohol withdrawal during recovery from an alcohol use disorder, and how meaning is attributed to the experience. Using a phenomenological theoretical framework, open-ended responses were collected via semi-structured interviews. Hispanic men (n=4) and women (n=2) who were in treatment for an alcohol use disorder in an inpatient facility were interviewed. Data analysis consisted of careful coding and re-coding between members of the research team and resembled a combination of framework and content analysis. Twenty-four codes that we identified during initial analyses were then organized into categories (mental, emotional, social, cultural, spiritual, and meaning) and condensed into themes describing the general lived experience of alcohol withdrawal. Member checking is underway to ensure that results reflect the intended messages of the participants. Current results reveal that participants were heavily impacted by psychological symptoms during their experience of withdrawal, and generally felt isolated and misunderstood by facility staff and other professionals. The significance of this study lies in its potential to further research in recovery and interventions regarding alcohol use disorders and begs a reconsideration of traditional approaches to alcohol withdrawal management as opposed to other substance use disorders.

THU - 426 Using R Shiny As an Active Learning Tool in Statistics and Machine Learning

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Nicole Major*, *Virginia Polytechnic Institute and State University* and Christian Lucero, *Virginia Polytechnic Institute and State University*

Abstract: The fields of statistics and machine learning have become increasingly important since the dawn of the Information Age. Unfortunately, many audiences find these topics intimidating or confusing. Our goal is to develop new approaches to better instruct future scientists, engineers, and policy makers through the use of an active learning environment.

Our educational platform is centered around developing new tools to supplement traditional teaching styles that may prove useful in better instructing different audiences with varying statistical backgrounds. Our primary approach involves the

development of interactive apps using Shiny, an open-source platform from the makers of RStudio. These applications emphasize visual and numerical summaries that help reinforce key concepts that students learn in class. In particular, these apps provide students with greater control of the visualizations without the need for continuous software manipulation. We hypothesize that students will develop a deeper understanding of statistics and machine learning methods and practice better decision making. We also wish to investigate whether these tools help mitigate the "statistical anxiety" that many non-majors suffer when learning statistics.

We have deployed the use of Shiny apps in several undergraduate courses targeted at non-majors. We have chosen to focus upon two metrics (1) a qualitative assessment of the students' confidence regarding how well they feel they know a concept and (2) a numeric assessment that compares the performance on standardized questions for groups who have used the the apps versus those who have not. We'll present our initial findings and discussion regarding the tools and methodology.

THU - 427 Effect of Electrolyzed Reduced Water on the Rumen Microbiome of Ruminally-Cannulated Steers Consuming a Roughage or Concentrate Diet

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Daisy Gonzalez*, *Texas A&M University Kingsville*; Kendrah De Leon, *Texas A&M University Kingsville* and Natasha Bell, *Texas A&M University Kingsville*

Abstract:

Electrolyzed reduced water (ERW) has a negative oxidation-reduction potential (ORP). ORP is a measure of the tendency of a chemical species to become reduced through the gain of electrons and is a common water quality parameter. Current research shows ERW to beneficially effect human intestinal microflora because it provides an optimal environment for growth of anaerobic microorganisms. Effects of ERW in livestock species, specifically cattle, are less understood. The rumen is a complex environment with an ideal habitat for anaerobic microorganism growth. In this study, four ruminally-cannulated steers were assigned to a two period, two treatment crossover design. Treatments are: 1) CON (standard water; pH 6.5-7.0) and 2) HDX (ERW from Herd X, Inc.; pH 8.7-9.5). The study consists of two phases: 1) forage diet and 2) concentrate diet. The goal of these two phases is to determine if ERW has a different impact as a result of diet type. Each phase consists of two 14-d periods. Two hours after feeding, on days 10, 12, and 14, of each period, rumen fluid will be collected via suction strainer for evaluation of microbial populations. Rumen fluid samples will be stored at -80°C until analysis by massively parallel sequencing. Data will be analyzed using QIIME 2.0. Although this study is still in progress, it is anticipated that the rumen microbiome will be altered toward microbes with a preference for higher pH. Understanding how ERW effects the rumen will allow its potential use as a management tool for improving cattle health.

THU - 428 Testing the Protective Effects of Naupaka Kahakai Juice (*Scaevola taccada*) on *Saccharomyces Cerevisiae* Against UV Radiation

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Keanu Rochette-Yu Tsuen*, *Kapi'olani Community College* and Michael Ross, *Kapi'olani Community College*

Abstract: *Scaevola taccada* or Naupaka Kahakai is a native Hawaiian plant that grows commonly in coastal areas. Indigenous knowledge suggests that the fruits of this plant contain UV absorbing compounds. As such, the fruits of this native plant could potentially help reduce the use of commercial sunscreens on Hawaiian reefs. In this study, we will determine if the juice of the fruit of *S. taccada* can protect yeast from harmful UV radiation.The juice of the fruits of the *S. taccada* was collected by squeezing them through a sterile muslin cloth. After being centrifuged, the supernatant of the juice was collected. A nanodrop spectrophotometer was used to generate an absorption spectrum from the extract. The extract was filter-sterilized and added to *Saccharomyces cerevisiae* suspensions at a dilution of ½, 1/10 and 1/100. Suspensions were plated and then exposed to UV radiation at 253 nm for 0 min, 0.5 min, 2 min and 5 min. Absorption spectrum studies indicate that indeed Naupaka Kahakai fruits do contain sun blocking properties, with a calculated Sun Protection Factor (SPF) as high as 20. However, the experiments performed using UVC rays (253 nm) indicated that plates exposed to UV showed no signs of viability. Nevertheless, more experiments will be performed in the future using reviewed protocols and different methods to support or disapprove the original hypothesis.

THU - 429 Foundational Indigenous Knowledge in STEM: Tools for Wayfinding

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Paanaakala Tanaka*, *University of Hawaii at Manoa* and Chad Baybayan, *Imiloa Astronomy Center of Hawaii*

Abstract: Tools used by wayfinders as they continue their practice of voyaging thousands of miles across the ocean unaided by modern instruments is an example of the cultural applications related to STEM. Wayfinding encompasses all the ways in which people and animals orient themselves in a physical and navigate from place to place. Wayfinding is also a term that refers to indigenous navigation methods. It istraditional knowledgethat spans thousands of years and within its practice science, mathematics, and indigenous cultural knowledgeis applied. As an applied researcher the data being presented has been gathered through study under four Hawaiian master navigators, experiential knowledge, and historical research. Central to wayfinding are the physical, mental, and spiritual connections that Hawaiians have with their environment and ancestors. Through my educationalstudyin navigation based on wayfinding, I have completed three voyages between Hawaii and Tahiti on wa'a kaulua (voyaging canoes). The system of navigation used while voyaging, Hawaiian star compass,was created by Nainoa Thompson and is a modern heuristic device with 32 directional points using the rising and setting points of stars. In addition, indigenous navigators use other celestial objects,wind, ocean swells, seamarks, and clouds. These help them understand direction and the presence of land. Throughout the voyage we acknowledge our ancestors in the cultural protocols we conduct.Indigenous knowledge is valuable and these wayfinding tools help navigators traverse the ocean. We gain an understanding of how cultural knowledge is foundational for understanding STEM in indigenous cultures.

THU - 501 Size Matters: Comparative Morphology of Rockfish Urogenital Papilla

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Holly Suther*, *California State University, Fullerton* and Kristy Forsgren, *California State University, Fullerton*

Abstract: Rockfishes are a popular recreational and commercial fishery in California. Rockfish catches account for 20% of the state's commercial harvest, which contributes $550 million dollars annually to California's economy. As an economically and ecologically important fishery, regulatory agencies monitor the status of rockfish populations. However, there is no accurate method to identify sex, data that has important implications for fishery management. The objective of our study is to increase our understanding of rockfish reproduction by characterizing the male urogenital papilla of various rockfish species in order to establish a reliable method of externally identifying sex in the field. Rockfishes [starry (*Sebastes constellatus*), vermilion (*Sebastus miniatus*), squarespot (*Sebastes hopkinsi*), blue rockfishes (*Sebastes mystinus*)] were collected in southern California via hook and line. Gonadal tissues and genital papilla were dissected and preserved, then embedded in paraffin wax. Tissues were sectioned using a rotary microtome, stained, and histologically examined. Additional specimens were borrowed from the Natural History Museum of Los Angeles County for external measurements. We have determined that the morphology of the urogenital papilla is species-specific and can be used to accurately identify males. Our future work includes describing the morphology of additional rockfish species to develop a comprehensive tool for fishermen and agency biologists.

THU - 502 The Effect of Salinity on Growth Rates of Male and Female Juvenile Blue Crab (*Callinectes sapidus*)

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Nicole Doran*, *The Ohio State University* and Michael Kendrick, *South Carolina Department of Natural Resources Marine Resources Research Institute*

Abstract: Blue crab is a commercially important fishery and plays a significant ecological role in estuarine food webs. Previous work has contributed to our understanding of its required habitat for reproductive success, but not much is known about juvenile development or habitat use as it relates to salinity. To begin investigating intrinsic and extrinsic factors that influence development, we assessed the effect of sex and salinity, respectively, on growth rates of juvenile blue crab. Male and female crabs were reared in a controlled environment with either high (25 ppt) or low (5 ppt) salinity. Both sexes grew faster in the low salinity conditions based on percent change in body size. Additionally, an interaction between sex and salinity was observed wherein salinity impacted male growth more substantially than it did for females based on the percent change in wet weight. Understanding the role of salinity on juvenile blue crab development can provide insight to the implications changing environmental conditions resulting from climate change may have on blue crab populations and fisheries in the future.

THU - 503 Ocean Abundance and Distribution of Chinook Salmon (*Oncorhynchus tshawytscha*) Revealed through Genetic Stock Identification

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Isabella McCrory*, *California State University Monterey Bay*; Anne Beulke, *University of California Santa Cruz*; Carlos Garza, *U.S. National Marine Fisheries Service* and Anthony Clemento, *U.S. National Marine Fisheries Service*

Abstract: Chinook salmon (*Oncorhynchus tshawytscha*) are the target of valuable tribal, recreational and commercial fisheries due to their economic value and ecological services. There is a need for improved management of fisheries since many Chinook salmon stocks (populations) haven't met conservation targets in recent years. Salmon are anadromous, meaning they travel up rivers from the ocean to reproduce. Due to their migratory behavior, fish from different stocks mix in the ocean. However, they are visually indistinguishable, leading to uncertainty of stock composition in fisheries and hindering the balance of harvest and conservation management goals. In this work, genetic stock identification (GSI) was used to understand population-specific ocean distribution of Chinook salmon off the coast of California. Commercial fishing vessels sent in fin clips from thousands of individual salmon harvested in 2019. Each fin clip had an associated GPS point of catch, records of fishing effort, and the depth at which the fish was caught. DNA was extracted and 96 single nucleotide polymorphisms (SNP) were genotyped. SNP genotyping has low error rates and the data allow differentiation between Chinook salmon populations, which makes it effective for GSI. In previous GSI work, preliminary results revealed potentially important differences between different salmon stocks off of California. This method is allowing evaluation of the concordance between information on ocean distribution provided by physical tags of hatchery salmon and that of wild salmon with no tags and unknown distribution. The results of this study will help to improve future fishery management.

THU - 504 Developing an IL1-R8 Knock-out (KO) NK Cell Line from Human Induced Pluripotent Stem Cells (iPSC), Using the CRISPR/Cas-9 System.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jack Castaneda*, *California State University Northridge*; Victor Shen, *University of California, San Diego*; Davide Bernareggi, *University of California, San Diego* and Dan Kaufman, *University of California, San Diego*

Abstract: Natural killer (NK) cells are innate immune cells that play a key role in killing stressed cells such as tumor cells and virally-infected cells. Previous studies demonstrate that the receptor IL1-R8, serves as a check point to regulate NK cell activity. IL-1R8 serves as a checkpoint for NK cell maturation and effector function. Its genetic blockade unleashes NK-cell-mediated resistance to hepatic carcinogenesis, haematogenous liver and lung metastasis, and cytomegalovirus infection. These studies used an IL1-R8 deficient mouse model of hepatocellular carcinoma resulting in inhibition of liver carcinogenesis and protection against liver and lung metastasis. This project is aimed to create an IL1-R8 knock-out (KO) NK cell line from human induced pluripotent stem cells (iPSC). Using the CRISPR/Cas-9 system and 2 gRNAs, a large deletion in the intracellular domain of the receptor was introduced, and using a western blot, the protein knock out was confirmed. Initial experiments have shown that when differentiating the KO iPSCs into NK cells, KO iPSCs differentiated slower and seemed to produce more myeloid cells compared to wild-type iPSCs. This may suggest IL1-R8's involvement in both myeloid and NK cell differentiation. Once generated, the mature NK cells will be tested for their cancer killing potential compared to wild type cells in-vitro and in-vivo, as they may provide new avenues for Cancer treatments. If KO cells are not able to be differentiated into NK cells, the role of IL1-R8 in differentiation of other hematopoietic cells will be studied.

THU - 505 Defending the Castle: Soldier Worm Response to Host Injury and Opportunistic Infection Threat

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Jennifer Pena*, *Scripps Institute of Oceanography* and Ryan Hechinger, *Scripps Institute of Oceanography*

Abstract: Some groups of trematode parasitic flatworms have evolved a specialized caste of soldiers to fight off rival trematodes attempting to infect their host snail, effectively supplementing or replacing the host immune system. Beyond this anti-trematode function, soldier trematodes may take over other immune functions from the host. We hypothesize that one such immune function is to defend against opportunistic pathogens that infect a host snail after it is injured in the field.

The California horn snail (*Cerithideopsis californica*) is an excellent model system for addressing this issue. This snail, hosts at least 9 trematode species with soldiers. Further, the snails are injured by birds or crabs that snip off the snail snouts, an injury that would expose the snail to opportunistic pathogen invasion.

We are mimicking snout damage in groups of treatment snails and exposing them to mud with opportunistic pathogens. We are comparing soldier distribution in injured snails to the soldier distribution in control snails. If soldiers have an anti-opportunistic pathogen function, we predict that there will be more soldiers near the snout in experimentally injured snails compared to control snails. Preliminary results are consistent with this prediction, but results are not significant ($n = 13$, $p > 0.20$). Completing our experiments will shed light on whether trematode soldiers have an expanded role to play in the defense of the trematode colony and the 'stolen' host body.

THU - 506 Bust a Move: Movement of Microplastics through Open Water Marine Trophic Levels

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Mayra A. Silva*, *California State University, Fullerton*; Abigail Cho, *California State University, Fullerton*; Jennifer N. Ibarra, *California State University, Fullerton*; Taylor Naquin, *California State University, Fullerton*; Julia B. Teeple, *California State University, Fullerton*; Kevin S. Whittemore A.A., *California State University, Fullerton*; William J. Hoese, *California State University, Fullerton*; Jennifer L. Burnaford, *California State University, Fullerton*; Andres Carrillo, *Cabrillo Marine Aquarium* and Samantha Leigh, *California State University, Fullerton*

Abstract: In the oceans, plastic waste breaks down to smaller particles (microplastics, <5mm) that may be ingested by prey organisms and transferred up trophic levels to their predators, allowing plastic to disrupt marine food webs. We hypothesized that microplastics consumed by brine shrimp, *Artemia salina,* could move up the food chain to predatory moon jelly, *Aurelia aurita*. We provided 90um diameter polypropylene pieces to *Artemia* and compared ingestion of this microplastic to ingestion of fish flakes. We monitored the progression of plastic and fish flakes every thirty minutes for 120 minutes. We found no significant differences in the consumption or the rate of progression through the gut of brine shrimp. We ran four suspension feeding treatments with jellies (plastic alone, *Artemia*,

Artemia and plastic together, and plastic-fed *Artemia*) and two gavage treatments (plastic alone and plastic-fed *Artemia*). We observed jellies twice in a four hour period. Jellies did not eat plastic alone. After two hours we observed plastic in 100% of jellies fed brine shrimp and plastic and 75% after four hours. We observed plastic in 75% of gavage-fed jellies after two hours and 0% after four hours, showing jellies cleared their gut of plastic in four hours. After four hours we observed plastic in 100% of gavage-fed jellies that ate plastic-fed brine shrimp. We demonstrated that plastic can move across trophic levels from brine shrimp to jellies; plastic has the potential to move further up trophic levels in ocean systems.

THU - 507 The Effect of Terrestrial Runoff on Coral Growth and Health

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Alyssa Taitano*, *University of Guam* and Bastian Bentlage, *University of Guam*

Abstract: On the island of Guam, heavy rains during the wet season lead to significant terrestrial runoff that drains into rivers and ultimately the ocean. Sediment runoff has shaped Guam's coral communities in its southern bays into which rivers drain. Here, sedimentation has led to shifts in the composition of coral communities and affects the health of corals. The purpose of this study is to investigate how terrestrial runoff affects coral growth and health. Corals studied are massive *Porites* species that dominate the reef in Fu'a Bay, Umatac, southern Guam, representing the sole large, reef-building coral species in this bay affected by heavy sedimentation. Growth rates and color changes, as a proxy of chlorophyll densities of photo-symbionts, will be tracked over the course of the wet and dry season at two sites that differ in sedimentation rate and turbidity. Monthly photos of replicate coral fragments will be taken to estimate growth rates through time. Further, color-corrected images will be used to track color changes. It is expected that corals growing in high sedimentation habitats have a lower growth rate, reducing rates of reef accretion, than those growing in low-sedimentation habitats. Further, corals growing in turbid waters will be paler than those growing in clear water due to decreased chlorophyll levels and consequently lower photosynthetic activity, ultimately affecting calcification and thus growth rates.

THU - 508 Gene Expression of ABC Transporters in Embryonic *Strongylocentrotus Purpuratus* Following Exposure to the Bacterium *Vibrio Diazotrophicus*

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Isabelle Danforth*, *University of California, San Diego*; Amro Hamdoun, *University of California, San Diego* and Catherine Schrankel, *University of California, San Diego*

Abstract: ABC (ATP-Binding cassette) transporters are a highly conserved family of membrane proteins found throughout the development of organisms. They are responsible for effluxing a variety of compounds, including chemotherapy drugs, signaling molecules and nutrients. Although the role of ABC transporters in adult tissues is well studied due to their importance in human diseases such as cancer or cystic fibrosis, little is known about the role of transporters in early development. In this study, we describe how transporter-associated gene expression of purple sea urchin (*Strongylocentrotus purpuratus*) embryos changes following exposure to the bacteria, *Vibrio diazotrophicus.* We hypothesize that embryos exposed to *V. diazotrophicus* early in development will have greater transporter-associated gene expression in specific tissues throughout development in order to efflux metabolites of *V. diazotrophicus*. Embryos were grown in beakers containing a combination of filtered seawater and *V. diazotrophicus.* Fixed embryos were collected at nine developmental stages for RT-PCR, qPCR and WMISH (Whole Mount In Situ Hybridization). Preliminary data suggests that embryos exposed to *V. diazotrophicus* develop guts more rapidly than the controls. Based on early WMISH results, embryos exposed to *V. diazotrophicus* have greater ABCC4 expression in primary mesenchymal tissue at the blastula stage (48 hours post fertilization). In conclusion, preliminary data has shown a clear difference in both the phenotype and genotype of embryos exposed to *V. diazotrophicus*. Further analysis of collected embryos is required to isolate the location of expression for different transporters, the location of expression, and the quantity of expression throughout development.

THU - 509 Spatial Distribution and Burrowing Behavior of the Invasive Mussel *Arcuatula Senhousia* in a Southern California Estuary

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Annabel Gong*, *University of San Diego*; Nathalie Reyns, *University of San Diego* and Eric Cathcart, *University of San Diego*

Abstract: The Asian mussel, *Arcuatula senhousia,* has successfully invaded estuarine habitats globally, including those in southern California, USA. *A. senhousia* outcompete native bivalves and create byssal thread mats that alter the community composition of soft-sediment habitats. Thus, understanding the abiotic factors that influence the distribution of *A. senhousia* has important ecological implications. During a four-year (2015-2019) field study in Mission Bay, San Diego, California, we collected sediment and mussel samples to identify the spatial distribution of *A. senhousia* within the estuary. *A. senhousia* was more abundant in finer-grain sediment than in coarser-grain sediment. We hypothesized that the spatial distribution of *A. senhousia* in Mission Bay was related to sediment grain-size. More specifically, we tested the hypothesis that *A. senhousia* would burrow more effectively and create more byssal threads in finer-grain sediment than coarser-grain sediment. Mussel burrowing and byssal thread production was examined in a laboratory experiment, using three sediment grain-size treatments that reflected sediment composition in Mission Bay. Mussels burrowed faster, were more completely burrowed, and produced significantly more byssal threads in finer-grain sediment. These results suggest that *A. senhousia* residing in coarser-grain sediment will be more prone to predation than those in finer-grain sediment, as burrowing efficiency and byssal mat production appears stymied in sandier sediments. Our laboratory results also help explain the variability observed in the spatial distribution of mussels in Mission Bay and how anthropogenic alterations to sediment, like dredging, could affect these communities.

THU - 510 Microhabitat Associations of Post-Settlement Juvenile Rockfishes: Utilization of Transient Drift Kelp Adjacent to the Kelp Forest Boundary

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Megan Salomonson*, *Institute for Applied Marine Ecology at California State University, Monterey Bay* and James Lindholm, *Institute for Applied Marine Ecology at California State University, Monterey Bay*

Abstract: The importance of kelp forests for providing habitat and refuge to temperate reef fishes is well-established, including ontogenetic shifts in how kelp is utilized across life histories. It is also known that detached kelp can be clustered at the surface, in deep sea canyons, or on the beach. Less is known about the role of transient drift kelp on the sea floor adjacent to the reefs in relation to fish habitats. This study aims to evaluate (1) the change of drift kelp density over time and space, (2) the effect of drift kelp density on its respective utilization by juvenile rockfishes, and (3) the extent to which the drift kelp contributes to the halo of suitable habitat around the reef. Microhabitat utilization of juvenile rockfishes is documented through transects on SCUBA extending out 20 meters from the reef-sand interface and 12-18 meters in depth in Carmel, CA. Data are collected through five minute underwater visual census (UVC) surveys and recorded imagery through diver-operated stereo video (DOV). Preliminary results show that 54% of observed juvenile rockfishes are utilizing drift kelp at an average of 3.18 meters from the kelp forest boundary while 20% utilize reef outcrops at 4.48 meters, 12% utilize sand at 3.94 meters, 10% utilize reef at 0.13 meters, 3% utilize cobble at 3.13 meters, and 2% utilize attached kelp at 2.10 meters. This suggests that drift kelp is the most utilized habitat beyond the reef and may be extending the halo of suitable habitat around the reef.

THU - 511 A Comparison of Microplastic Concentrations and Polymer Types between an Urbanized and Rural River.

Discipline: Life Sciences

Subdiscipline: Marine Sciences

Cristobal Yanez*, *Virginia Institute of Marine Science*; Bongkeun Song, *Virginia Institute of Marine Science* and Samantha Fortin, *Virginia Institute of Marine Science*

Abstract: Microplastic pollution is a growing concern with negative impacts on aquatic organisms, and concentrating and transporting the emerging contaminants including antibiotics and chemical toxins.. While microplastics larger than .3mm have been examined in many environments, microplastics smaller than .1mm have not been studied with polymer type identification. This study focused on quantifying and identifying these smaller microplastics. We conducted surface water sampling at multiple locations in the James River and the York River, two tributaries to the Chesapeake Bay. Both Nile Red staining and Raman spectroscopy were used to quantify and identify microplastics in both rivers. The preliminary results showed variation in microplastic concentration among different sampling locations in each river, but no significant differences in concentrations were found when comparing the rivers. Primary polymer types in each river are expected to be polyethylene and polypropylene as their low densities allow them to float and they are two of the most common types of plastic.. Discharges of the wastewater treatment plants located in both rivers will be also examined to determine if the plants are the potential point sources of microplastics. Understanding the sources and distribution of microplastics is crucial in order to predict and reduce microplastic loading in aquatic environments.

THU - 512 Exploring Settlement and Survival Patterns of *Pocillopora Acuta* Larvae on Natural and Synthetic Substrates

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Ciara Ratum*, *Hawai‘i Institute of Marine Biology* and Mackenzie Manning, *Kapi‘olani Community College*

Abstract: The global decline of coral reef ecosystem health has intensified reef restoration efforts and research on coral larvae settlement cues. Previous studies have shown that coral larvae exhibit settlement preference based on substrate type and color, as well as the presence of algae, sediment, or biofilms. In this study we first tested settlement success of *Pocillopora acuta* larvae on conditioned (fouled) or unconditioned (clean) substrates. We then tested whether *P. acuta* would show substrate preference when presented with natural and synthetic substrate types. Preliminary results suggest no significant difference in settlement success between conditioned and unconditioned substrates regardless of substrate type. Natural substrates (aragonite tile, coral rubble, and lava rock) promoted significantly higher settlement compared to synthetic substrates (marine debris and acrylic plug), with aragonite tile and coral rubble being the most successful. For the substrate preference experiment, larvae showed no significant preferences for a particular substrate although, similar to trends in the first experiment, natural substrates had higher settlement compared to synthetic substrates. Larval settlement rates peaked on the second day of the ten-day experiment. Mortality rates were high throughout our experiments possibly due to the presence of small predators within conditioned substrates and/or water quality conditions. These results can help inform future coral research endeavors that contribute to the process of restoring reefs that are being lost to bleaching and other human impacts.

THU - 513 Fishpond Foodies: Investigating Feeding Relationships in He‘Eia Fishpond Using Stable Isotopes

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Seaenna Correa-Garcia*, *California State University, Monterey Bay* and Sherril Leon Soon, *Hawaii Institute of Marine Biology*

Abstract: Traditional Hawaiian fishponds were engineered to attract and maintain fish to supplement regular fishing activities. Loko i‘a o He‘eia (He‘eia Fishpond) is an ancient Hawaiian fishpond located on the windward side of O‘ahu. It serves as a meeting place not only for salt and fresh waters, but also as a cultural site of learning, exchange, and subsistence for the community. Understanding nutrient sources and the feeding relationships amongst organisms within the loko can be instructive as fishpond restoration efforts, including invasive algae removal, take place. Stable isotope ratios of water, primary producers, and two probable primary consumers were used to track dissolved nutrient sources to the fishpond and make a targeted evaluation of the foodweb relationships within it. Samples were collected from five sites of interest that were selected based on evidence (empirical and anecdotal) which suggest that these sites either provide nutrients for the fishpond or function as fish aggregation sites. Primary producer collection focused on phytoplankton, two species of invasive macroalgae, and microphytobenthos, while primary consumer collection was restricted to *Cuapetes spp.* (*‘ōpae*) and *Metopograpsus thukuhar* (*alamihi*). Insight into the nutrient pathway through the first two trophic levels of the loko i‘a foodweb may be critically important to fishpond managers as they continue restoration efforts. Results may also offer an understanding of the fishpond’s ability to buffer against high nutrient inputs, including those from anthropogenic activities

THU - 514 Validation of a Sonar Method to Classify Marine Sub-Littoral Habitats in a Coastal Lagoon Near Barrow, Alaska.

Discipline: Life Sciences
Subdiscipline: Environmental Science

Hector Dominguez*, *University of Texas at El Paso* and Vanessa L. Lougheed, *The University of Texas at El Paso*

Abstract: The ecosystems situated along the Arctic coast are recognized as some of the most threatened ecosystems on Earth. With global temperature rising, permafrost is thawing at an accelerated rate, which is resulting in substantial amounts of soil organic carbon being transferred to the coastal Arctic Ocean via coastal erosion and riverine inflow. The objective of this study was to classify and map the nature of the of sediment in a coastal lagoon of the Beaufort Sea (Elson Lagoon, Barrow, AK) and relate this to high spatial resolution sonar data in order to create a detailed map of the sublittoral habitats in the region. Sonar data along with soil samples were collected throughout the lagoon in August of 2015. A SonarMite Echo Sounder (SeaFloor Systems) recorded sonar velocity corrected for the effects of salinity and temperature variations in the water. Sediment samples were collected at 87 sites; each sample was homogenized and dried, with percent organic matter determined after combustion at 500°C. Sediment particle size will be determined on a laser diffraction particle size analyzer. Preliminary results indicate that most of the sampled areas contained a high amount of fine sand, furthermore sonar intensity was negatively associated with organic matter content and percent fine sediment. Our results indicate that sonar may be a viable option to classify sublittoral habitats on a broad spatial scale.

THU - 515 Investigation of Land Use on Soil Carbon and Nitrogen Stocks in a Grassland Ecosystems

Discipline: Life Sciences
Subdiscipline: Environmental Science

Erika Meraz*, *University of Illinois at Chicago*; Nick Glass, *University of Illinois at Chicago*; Eduardo Dias de Oliveira, *University of Illinois at Chicago*; Chris Whelan, *University of Illinois at Chicago* and Miquel Gonzalez-Meler, *University of Illinois at Chicago*

Abstract: Tallgrass Prairies have become one of the most endangered ecosystems due to land use conversion to agriculture. Restoration programs of Tallgrass Prairie such as the Midewin National Tallgrass Prairie (MNTP) could presumably restore part of this ecosystem and its services. These programs also provide opportunities to investigate the dynamics of soil carbon (C) and (N) nitrogen in this recovering ecosystem. Soil C and N stocks were investigated in 2007 and again in 2018 in six areas from MNTP representing different stages of restoration: remnant prairie, restored prairie, unmanaged land (“old field”), row crop, cow pasture, and areas recently converted to cow pasture (“new pasture”). Soil cores were processed for root biomass and analyzed for C and N concentration by elemental analysis. We hypothesized that 1) row crop will have lowest amount of C, N and root biomass, while remnant prairies will have the highest amount of C, N and root biomass of all the land types; and 2) soil C, N and root biomass in restored prairie increases with time (greater in 2018 than in 2007). This research will allow investigation of the mechanisms driving the establishment of the ecosystem services such as C sequestration

in Tallgrass Prairies. It will also improve our understanding of how soil nutrient cycling responds to land-area specific changes. Understanding how soil C and N stocks recover in restored prairie systems will be of extreme importance both locally and globally, especially given the importance of C and N cycling to global climate change projections.

THU - 516 Trends and Relationships of Chlorophyll-a and Sea Surface Temperature in the Salish Sea.

Discipline: Life Sciences
Subdiscipline: Environmental Science

Breana Nguyen*, *Northwest Indian College, Lummi Nation* and Sylvie Arques, *Northwest Indian College, Lummi Nation*

Abstract: Satellite technology continuously collects data that can be used for observation of areas that are prone to harmful algae blooms (HABs). HABs have been an ongoing issue in the Salish Sea with harvest closures due to the HABs being toxic. One of the toxic HABs, known as Paralytic Shellfish Toxin (PST) saxitoxin, accumulates in filter feeders that ingest the phytoplankton known as *Alexandrium cantanella*. PST affects the nervous system, paralyzes muscles and lead to death to humans. Shellfish harvesting has been and still is an important resource of sustenance foods for the 20 Salish Sea tribes that live along the Coast of the Salish Sea. This preliminary research focuses on the use of remote sensing applications to identify HABs and understand the long-term changes that may occur in the Salish Sea due to Global Warming. We used a time series of the MODIS-Aqua, Level 2- NASA Ocean Color data from the past 14 years (2003-2017) to assess the trends and relationship between chlorophyll-a (chlor-a) and Sea Surface Temperature (SST). Correlation between SST and chlor-a was found to be 24.68% and was significant at $p < 0.01$. Which means that SST and chlor-a concentration do not behave differently from each other but other factors must be taken into account in determining the biomass growth. Finally, this research is a first step toward the creation of a predictive model of the HABs in the Salish Sea.

THU - 517 Algal Bloom Modeling and Prediction in Bellingham Bay

Discipline: Life Sciences
Subdiscipline: Environmental Science

Talon Arbuckle*, *Northwest Indian College*; Rachel Arnold, *Northwest Indian College*; Misty Peacock, *Northwest Indian College, Lummi Nation* and Sherry Palacios, *National Aeronautics and Space Administration*

Abstract: Bellingham, Washington is located near the American-Canadian border in the northwestern part of Washington state; it is bordered on its west side by the Lummi reservation, which has nearly 13,000 acres of tidelands. Between Lummi and Bellingham lies Bellingham Bay, which has a history of harmful algae-related closures dating back to 1978. Harmful algae considered for this work are *Pseudo-nitzschia*, *Dinophysis*, and *Alexandrium*, all of which produce toxins; toxins bioaccumulate in bivalves, which in turn cause amnesic shellfish poisoning, diarrhettic shellfish poisoning, and paralytic shellfish poisoning (PSP) respectively. The most common cause of closures in Bellingham Bay is *Alexandrium*, which causes PSP; symptoms in humans include tingling and numbness in cases of mild exposure to death in cases of acute exposure. Harmful algal blooms negatively impact both native and non-native peoples living along or near the Salish Sea. Washington is the leading U.S. producer of farmed bivalves and the longstanding history of shellfish gathering among the Coast Salish Tribes makes this a project that benefits native and non-native people alike. The objective of this work is to identify factors that influence blooms in Bellingham Bay, and build a predictive model for future blooms. The method proposed for doing so is multiple linear regression on a monthly basis, using observations measured by instruments on the Bellingham Bay Buoy. The initial phase shows promise based on model metrics.

THU - 518 Environmental and Economic Perspectives from Local Intag, Ecuador Population on Development Interventions

Discipline: Life Sciences
Subdiscipline: Environmental Science

Hilary Zuniga*, *Washington State University*; Michael Goldsby, *Washington State University* and Caitlin Bletscher, *Washington State University*

Abstract: In international development there is a need to consider the whole system- those in power, the ‘outsiders’ doing the intervening, and those we label as needing help. Interveners’ views of the realities of locals from developing countries and of what should be done are constructed mainly from a distance and can be argued is molded for their convinence (Chambers, 1995). ‘Intervention’ is defined in this research as an attempt to aid in the environmental or economic sectors of the third-world country by implementing solutions with the goal to help either the development of the country, or the welfare and livelihood of locals from the region. This study will draw from existing literature and results from implemented solutions in third-world countries, especially Latin America, and analyze how they compare to the perspectives of local Intag Ecuadorians regarding foreign-based NGO development agencies. Local perspectives on their surrounding environmental and economic wellbeing will be analyzed and compared to the perceived priorities set forth by the development agencies. A series of individual interviews will be conducted through a convenient sampling of Intag adults. The effectiveness of outside interventions when it comes to economic and environmental wellbeing of third-world countries will be explored as well as the perceived ethical dilemmas and moral responsibilities that accompany economic and environmental development work. Identifying and further exploring the effectiveness and ethics behind development in third world countries is crucial in understanding whether ‘good’ is truly being done, rather than perpetuating poverty and harm.

THU - 519 Impact of Biochar As Soil Amendment on the Yield of High Value Crop *Capsicum annuum* in South Central Washington State

Discipline: Life Sciences
Subdiscipline: Environmental Science

Xavier Martinez*, *Heritage University*; Alexander Martinez, *Heritage University* and Jessica Black, *Heritage University*

Abstract:

Biochar is an activated charcoal like product of pyrolysis. Biochar as a soil amendment has been shown to retain nutrients that are essential for plant growth and development. Biochar has the potential to reduce the overuse of fertilizers, which in turn could help improve water quality by binding excess nutrients, such as nitrates, in soil reducing concentrations found in the drinking water of agricultural regions, such as the Lower Yakima Valley in South-central Washington State. Biochar is also thought to increase soil water retention, which can be critical for more arid regions prone to drought. Here, we evaluated the impact of biochar as a soil amendment on the yield of a high value crop, *Capsicum annuum* (bell pepper), by conducting field trials in the Heritage University Research Farm. The primary purpose of this study was to assess plant growth and crop yield differences in *C. annuum* between biochar amended soil and non-biochar amended soil. Two biochar treatment groups, 0.5% and 1% application by weight, were applied to plots. The control group consisted of zero applied biochar. Each biochar treatment group consisted of three plots; the control group consisted of six plots. Each plot consisted of 48 plants. Observed metrics included flower count, crop yield, and plant diameter. Preliminary results indicate a 5-10% crop yield increase. However, these results were likely impacted by difficulties controlling watering timers and excessive weed growth. Ultimately, this research will provide beneficial information about enhancements to current agricultural practices regarding water and nutrient efficiency in crop-growth.

THU - 520 Spotted Sandpiper (Actitis macularius) Habitat Selection on the Elwha River after Dam Removal

Discipline: Life Sciences
Subdiscipline: Environmental Science

Alexandra Trejo*, *Western Washington University*; Celida Moran, *Western Washington University*; Jenny Baxter, *Western Washington University* and John McLaughlin, *Western Washington University*

Abstract: We studied responses of Spotted Sandpipers (*Actitis macularius*) to restoration associated with dam removals on the

Elwha River, Washington. Sandpipers are among the first wildlife to return to restoration sites exposed when reservoirs are drained. As many dams approach the end of their useful lives, the need to understand responses of sandpipers and other wildlife to dam removal is becoming increasingly important. We studied spotted sandpiper distributions and habitat selection relative to availability of five kinds of substrates. We tested the hypothesis that sandpiper habitat selection is determined by substrate texture, with greater use of cobbles and gravel than silt, sand, and vegetated areas. We recorded sandpiper locations and associated substrates in open areas along the larger of the former Elwha reservoirs and a matched valley upriver from direct dam effects. We determined substrate extent and distributions using a systematic sampling grid anchored by random starting point. We used logistic regression models to calculate substrate resource selection functions. Our results reveal a reciprocal relationship of Spotted Sandpipers in Elwha restoration. Sandpipers benefited from extensive open habitats created by dam removal, and they may enhance restoration by distributing organic matter and nutrients to substrates lacking those materials.

THU - 521 Effects of Urbanization on the Microbiome of a Coastal Stream

Discipline: Life Sciences
Subdiscipline: Environmental Science

Alessandro Mazzora*, *Skyline College* and Christine Case, *Skyline College*

Abstract: Streams are ecologically important environments that provide a host of benefits including acting as flood controls, trapping sediment, protecting water quality, and maintaining biological diversity. Urbanization has led to significant changes in streams including channeling, placing them underground in culverts, and allowing road and garden runoff into them. As a result, acidification, eutrophication, hypoxia, and harmful algal blooms have all become serious concerns. Our work aims to determine the effect of urbanization on the microbiota in a stream ecosystem. Mud samples collected from five locations along San Pedro Creek (Pacifica, CA) were inoculated into Biolog Ecoplates to determine carbon substrate utilization. Carbon substrate utilization serves as an indicator of pollutants and microbial metabolic diversity in the creek. Preliminary results indicate a decrease in metabolic diversity after channelization, underground culverts, and storm drain runoff (9.7%) compared to undeveloped headwater regions (96.8%). The Shannon diversity index indicated a 100% decrease in microbial diversity after underground channeling. The presence of denitrifying bacteria is being determined. Results suggest that urban pollutants are selecting for fewer different microorganisms.

THU - 522 Developing a Site Suitability Analysis for Beach Restoration in Santa Monica Bay to Improve Climate Resiliency

Discipline: Life Sciences
Subdiscipline: Environmental Science

Jazmin Quezada*, *Coastal Research Institute, Loyola Marymount University*; Melodie Grubbs, *Coastal Research Institute, Loyola Marymount University*; Karina Johnston, *Coastal Research Institute, Loyola Marymount University* and John Dorsey, *Department of Civil Engineering and Environmental Science, Loyola Marymount University*

Abstract: Nature-based solutions to protect and preserve shorelines are cost-effective, sustainable, and provide a myriad of ecosystem services in comparison to traditional barriers like sea walls and jetties that have been shown to negatively impact beaches. The Bay Foundation is currently implementing four living shoreline and coastal dune restoration projects in the Santa Monica Bay region to improve resilience to sea level rise (SLR) and coastal storms. A key research component to inform this process is developing a regional site suitability analysis (SSA) model to identify and prioritize areas for beach and dune restoration that maximize benefits to the coastline.

The SSA includes three principal components: SLR and Infrastructure, Physical, and Biological. The first component utilizes SLR prediction data from regional models and GIS data on location and types of infrastructure. Physical parameters include dominant wind direction and speed, sand grain size, and beach width and orientation. Biological parameters include percent cover and species of plants, wrack cover, and critical habitat for rare species.

Preliminary results identified the most vulnerable coastal locations (e.g., Hermosa Beach Pier, portions of Venice Beach) that are also adjacent to critical infrastructure for tourism, recreation, commercial areas, and residences and provide some ecological function. Other priority areas identified include critical habitat for the federally threatened Western snowy plover (*Charadrius nivosus*). Next steps for the SSA will identify and prioritize locations for sandy beach restoration along Santa Monica Bay, results of which will be shared with municipalities, beach managers, and coastal agencies.

THU - 523 Impact of Agriculture and Roadways on Fragmented Forests in Michigan

Discipline: Life Sciences
Subdiscipline: Environmental Science

Maria Alvarez Zavala*, *Westminster College*; David Rothstein, *Michigan State University* and Asia Dowtin, *Michigan State University*

Abstract: Human activity can alter the function and characteristics of natural land. In the Midwest there are many human-impacted forest fragments that are surrounded and thus influenced by nearby agriculture land and roadways. Vehicular emissions and waste debris related to urbanization introduce many compounds into the environment which can eventually be deposited on the forest and affect it. Agricultural land use can also affect natural landscapes as high amounts of fertilizers are applied to fields, which can then be redistributed after the fact. In highly populated areas, these processes can then alter or disrupt natural cycles in native forest soils that receive the deposition of human produced compounds. This study aims to characterize forest soil health from two woodlots in East Lansing, MI that are directly adjacent to agricultural land or a major freeway. In each woodlot, soil samples were collected from seven locations along three transects. All samples have been processed for soil acidification, macronutrient (K^+, PO_4^{3-}, Ca^{2+}, Mg^{2+} and Na^+) bioavailability as well as quantification of carbon and nitrogen mineralization rates by native microbes in the forest patches. We expect salt concentrations to be highest near road edges and to decrease farther into the forest site. We also predict that samples obtained from forest edges near agricultural fields will have higher soil acidification as a consequence of macronutrient leaching due to the high use of ammonium containing fertilizers in crops.

THU - 524 Does Egg Attendance Provide a Benefit to the Offspring in the Emerald Glass Frog *Espadarana Prosoblepon*?

Discipline: Life Sciences
Subdiscipline: Environmental Science

Abner Hernandez-Figueroa*, *University of Puerto Rico-Rio Piedras Campus*; Johniah Gomez, *University of Rhode Island* and Johana Goyes- Vallejos, *Biodiversity Institute, University of Kansas*

Abstract: Less that 10% of the world's frog species exhibit some kind of parental care behavior. Parental care is defined as any behavior from the parents that benefits the offspring. In frogs, egg attendance is the most common parental care behavior. In many species where egg attendance has been observed, the benefits are unknown, and therefore it is debatable if it should be called parental care behavior. In the family of the Glass Frogs, many species exhibit egg attendance. For some of them, the benefits are clear, but for some of the species with short-term egg attendance (< 1 day), the benefits (if any) are unknown. We studied the egg attendance behavior of the Emerald Glass Frog *Espadarana prosoblepon* at Las Cruces Biological Station in Costa Rica. Previous studies showed that egg attendance ranged from 10 minutes to over 2 hours. We hypothesized that this variability in egg attendance duration is due to observer effects. We used modified infrared cameras to record the behavior of *E. prosoblepon* with minimal disturbance. Our results suggest that the range of egg attendance time is smaller than previously reported, lasting on average 1 hour and 10 minutes. Future estimates of offspring survival will help to determine if longer egg attendance increases embryo survival. The implementation of new technologies as tools for natural history research, aids in filling informational gaps about behaviors difficult to observe in the wild, and ultimately will help us to understand the evolution of parental care behavior in this clade of frogs.

THU - 525 Assessment and Comparison of Fecal Coliforms and Total Coliforms on Water and Sand Samples from Three Balnearios (Public Beaches) in Puerto Rico: How Climate Change Should be Changing Our Regulatory Standards

Discipline: Life Sciences
Subdiscipline: Environmental Science

Paola González-Colón, *Universidad Ana G. Mendez-Carolina Campus*; Rubén Suro-Valverdi*, *Universidad Ana G. Mendez-Carolina Campus*; Stephen Narvaez-Morales, *Universidad Ana G. Mendez-Carolina Campus*; Solymar Pellot-Lanzo, *Universidad Ana G. Mendez-Carolina Campus*; Carlos Hernandez-Rodriguez, *Universidad Ana G. Mendez-Carolina Campus*; Victor Santiago-Rodriguez, *Universidad Ana G. Mendez-Carolina Campus*; Kiomara Carrero-Garcia, *Universidad Ana G. Mendez-Carolina Campus*; Karina Rodriguez-Perez, *Universidad Ana G. Mendez-Carolina Campus*; Emmanuel Carrion-Donowa, *Universidad Ana G. Mendez-Carolina Campus*; Keishla Paris-Hernandez, *Universidad Ana G. Mendez-Carolina Campus*; Jessenia Morales-Hernandez, *Universidad Ana G. Mendez-Cupey Campus* and Karlo Malave, *Universidad Ana G. Mendez-Carolina Campus*

Abstract: Climate Change affects precipitation, temperature, and other environmental factors on a region over a significant period. Thus, influencing the concentration of bacteria concentration, on public beaches, which is a public health concern. The purpose of this study was to measure the total coliforms (TC) and fecal coliforms (FC) to determine how safe public beaches on Puerto Rico are. Samples of water and sand were collected from the following recreational beaches in Puerto Rico: Escambrón in San Juan, *Balneario* de Luquillo, and *Balneario* de Carolina. The samples were filtered through a cellulose membrane (0.45μm pore size) utilizing a dilution of 1mL of sample to a 99 mL of sterile water. The media used were MacConckey, mEndo and MFC, which are selective to FC and *Escherichia coli*. The colonies were counted after 48 hours; mEndo media formed more colonies than MFC, with a green metallic shade that indicates presence of *E. coli*. We deduced that the higher the temperature, the more TC were found. Sand samples had a higher concentration of TC with an average of 2080 CFU, in contrast to the water samples with an average of 1000 CFU count. Gram negative rod shape bacteria were also identified. The Beach Monitoring Program (BMP) on Puerto Rico established by the Environmental Quality Board (PREQB) and the Environmental Protection Agency (EPA) should consider modifying their protocol to include sand samples on the program as a public health protection strategy. This is a study that's still in progress, and new data will be collected.

THU - 526 A Spatial Investigation of Floodplain Deposition in the Lake Champlain Basin of Vermont

Discipline: Life Sciences
Subdiscipline: Environmental Science

Julyanice Cruz Ramos*, *Saint Michael's College*; Stephanie Drago, *University of Vermont*; Rebeccca Diehl, *University of Vermont*; Beverly Wemple, *University of Vermont* and Don Ross, *University of Vermont*

Abstract: Periodic inundations of lands near streams are physically modified by overflows into floodplains. These allow the water to slow down by absorbing floodwaters and trapping debris and organic material the stream might otherwise transport downstream. This way, cities, communities, and families living downstream receive reduced flooding and improved water quality benefits from floodplain ecosystem services. We studied the role of floodplains in trapping nutrients by coring deposits from 2019 spring floods and installing plots to track flood deposition through summer of 2019. Each plot contains four patches of artificial grass located at a meter away from one another; these are stapled to the ground to prevent them from getting caught in floodwaters. Our sampling locations were in different agricultural sites' floodplains within the Lake Champlain basin of Vermont. The purpose of this investigation is to determine how much material deposits on the floodplain. We measured phosphorus (P) levels using a nitric acid assisted microwave digest procedure and analysis for total P ICP-OES. We also measured levels of carbon content in selected samples using a C/N analyzer. Thicknesses of deposits measured ranged from 0.1cm to 15.4 cm. Spatial patterns of phosphorus and carbon deposition varied across the plots studied. Our data clearly indicates that floodplains in the Lake Champlain basin serve an important role in trapping sediments and nutrients. Measuring the levels of nutrients that the water carries into the streams can help us better understand what changes must be made to improve the Lake Champlain Basin's health and reduce eutrophication.

THU - 527 Assessment and Characterization of Legacy and Current-Use Pesticides (CUPs) in the Maumee and Ottawa Riverine Systems

Discipline: Life Sciences
Subdiscipline: Environmental Science

Elyse Bonner*, *National Oceanic and Atmospheric Administration* and Michael Edwards, *National Oceanic and Atmospheric Administration*

Abstract: The environmental occurrence of legacy and current-use pesticides (CUPs) in the Great Lakes Basin coastal freshwater systems has potential to accumulate in aquatic environments, which pose adverse health risks and toxicological endpoints. Most pesticides, which includes herbicides, insecticides, and plant growth regulators are currently unregulated and continued characterization and screening is needed to identify potential sources and "hot spots" in coastal freshwater matrices (sediment, water and biota). Although these contaminants have been banned in the United States since the 1970's, they are still present in many coastal aquatic environment and their persistence further creates cause for concern. The US Environmental Protection Agency (EPA) registers some CUPs for use with restriction in the United States. However, the potency and persistence of these contaminants creates growing concern and their potential risks warrant further in-depth assessment and characterization. In this study, a multi-matrix approach including *dreissena* mussels, freshwater clams (*corbicula fluminea*) and Polar Organic Chemical Integrative Sampler (POCIS) was used to collect pesticide data within the Maumee and Ottawa riverine systems during the 2015-16 sampling campaign. The data collected was summarized and the results are presented in the form of percent detections (frequency) and magnitude (concentration) in various matrices, as well as the spatial distribution of these contaminants with respect to land-use at site (5Km buffer) and watershed scales (catchment). The results presented will serve as an initial assessment of various suites of legacy and CUPs that had the highest probability of bioaccumulation and detection in tissues as well as POCIS devices.

THU - 528 Updating Historical Shoreline Change Rates of North Kāʻanapali, Honokōwai, and Kahana, West Maui

Discipline: Geoscience
Subdiscipline: Earth Science

Cuong Tran*, *University of Hawaii at Manoa* and Charles Fletcher, *University of Hawaii at Manoa*

Abstract: Tracking shoreline movement across the main Hawaiian Islands provides empirical data to assist in the development of better coastal management practices. The University of Hawaiʻi at Mānoa Coastal Geology Group uses empirical data to calculate shoreline change rates on the islands of Kauaʻi, Oʻahu, and Maui. In this study, 2015 raw satellite imagery, provided by World View 3, was used to update the historical shoreline database of North Kāʻanapali, Honokōwai, and Kahana, West Maui. We calculate 2015 shoreline change rates and analyze differences compared to an earlier database in 2007. The satellite imagery we used was orthorectified using ArcGIS and PCI Geomatica Inc., the low water mark and coastal vegetation line were digitized, and shoreline position locations were measured from transects spaced 20 meters alongshore. These locations were modeled using linear regression to identify long-term rates of change at each transect. Including the 2015 shoreline, the data revealed that 77% of all transects were erosional, compared to 73% in 2007. With regard to beach loss, 2007 experienced a loss of 80 meters whereas the 2015 database showed a loss of 920 meters. The expansion of eroding shoreline over the period 2007 to 2015 is consistent with the expected influence of rising sea level. However, a full analysis that would have identified whether the changes were due to short-term variability or a valid statistical trend was not conducted.

THU - 529 Water Balance of a Traditional Hawaiian Plot

Discipline: Geoscience
Subdiscipline: Earth Science

Andrew Mance*, *Honolulu Community College* and John DeLay, *Honolulu Community College*

Abstract: *Colocasia esculenta*, also known as Taro or *Kalo*, is the stable crop of Hawaiian culture. *Kalo* is also culturally significant as it is considered the ancestor of the Hawaiian people in their cosmogony. It is cultivated two ways, in wetlands (*lo'i*) and dry lowland (*mala*). The study area at Honolulu Community College, currently within urban Honolulu, was once an important location for the cultivation of wet lowland *kalo* but due to the diversion of a local stream and urban development, agriculture was abandoned at this site. In 2011, efforts were made to restore cultivation at the site and convert the study area into a traditional Hawaiian dryland cultivation plot. Currently irrigation with municipal water has proved necessary to prevent crop wilting. A meteorological station was installed adjacent to the plot to measure variables to calculate the water balance, including precipitation, solar radiation, temperature, relative humidity, and wind speed. Precipitation was compared to evapotranspiration calculated using a variation of the Penman-Monteith method. Initial wet season results during an El Nino year indicate lower than average rainfall, and that evapotranspiration greatly exceeded precipitation. The challenges faced at this site regarding water availability due stream diversion represent a local example of a resource conflict experienced across the archipelago that continues to be a relevant social issue.

THU - 530 Predicting Wildfire Favorable Conditions in California at Sub Seasonal Lead Times Using Remote Predictors

Discipline: Geoscience
Subdiscipline: Earth Science

Ciara Dorsay*, *University of California, Berkeley*; Tom Murphree, *Naval Postgraduate School*; Kellen Jones, *Naval Postgraduate School* and Annabelle Norman, *York School*

Abstract: Wildfires that occur at the end of the California dry season (October-December) can be especially destructive as demonstrated by the Camp and Woolsey fires of last year in which 85 lives were lost and thirty billion dollars of damage done. Wildfires occur often, but those resulting in significant financial and personal damages are associated with the offshore Santa Ana winds thought to flow through the Southern California. Despite their reoccurring nature, few sub-seasonal forecasting systems with demonstrated skill exist when predicting the winds. Our goal was to investigate the potential to predict these fire favorable winds at sub-seasonal lead times from a week to over one month. Our primary data came from global multidecadal climate reanalysis datasets. Our primary methods were: (1) analyses of conditional composite anomalies of global climate system variables associated with the strongest offshore and onshore wind periods in California; and (2) correlations of California winds with global climate system variables. Our analyses were designed to: (a) characterize the global anomalies associated with fire favorable conditions in California from October to January; and (b) identify potential predictors of these conditions at sub-seasonal lead times. From these methods and datasets, we were able to correlate offshore winds throughout California to a positive geopotential height anomaly located off the coast of Washington state created by anomalously low convection in the tropical Indian and western Pacific Oceans. We have used these findings to begin developing sub-seasonal prediction systems to prepare for wildfire conditions in California long before they happen.

THU - 531 Investigating Microplastic Pollution in Zaaga'iganing (lakes) on the Gaa-Zagaskwaajimekaag (Leech Lake Reservation)

Discipline: Geoscience
Subdiscipline: Earth Science

colin eagle*, *Leech Lake Tribal College* and Melinda Neville, *Leech Lake Tribal College*

Abstract: Niibi (water) is an important natural resource to the Anishinabeg (first people), especially for the Leech Lake Band of Ojibwe (LLBO) reservation which encompasses hundreds of lakes, including some of largest in Minnesota. The Anishinabeg have been hunters and fishermen for generations, and only recently have been made aware of a new threat to their way of life. Microplastics (MP) refer to a wide range of plastics, polymers, particle sizes, and the negative ecological effects are only beginning to be understood. The first year of MP research at Leech Lake Tribal College established a ubiquitous presence of MP in local lake sediments. This summer, the study will establish the ongoing monitoring effort in order to define the extent of the problem by adding surface water analyses along with continued sediment analysis. Preliminary results have identified low-cost ways of isolating and counting MP from samples, including density separation, vacuum filtration, wet peroxide oxidation, and microscopy. One objective of this field season is to use surface trawling of smaller lakes determine the effect of shoreline development. The efforts to refine MP sampling methods will establish repeatable protocols for future scientists.

THU - 532 Synthesis and Characterization of Pure Nano-Polycrystalline Diamond at High Pressures in Multi-Anvil Press

Discipline: Geoscience
Subdiscipline: Earth Science

Kelsey Nichols*, *University of Hawaii at Manoa* and Bin Chen, *University of Hawaii at Manoa*

Abstract: Nano-polycrystalline diamonds (NPD) have been found authigenically in meteorite impact craters and are industrially produced. Despite the occurrence of both, there lacks systematic investigations into their similarity overlap and most onerously, how to produce large and pure NPD at achievable pressure and temperature conditions. By experimentally investigating the NPD phase stability field for various starting materials, insight can be gained into sample volume optimization under approachable pressure-temperature settings. This would further illuminate the relation between synthetically and naturally derived NPD and its viability in research of planetary materials properties by reaching multi-million atmospheric pressure conditions. Using a 2000-ton multi-anvil press (MAP) graphite and trans-stilbene ($C_{14}H_{12}$) were compressed to 15.5 GPa and heated to temperatures ranging from 2150-2848 K. The run products were analyzed using Raman spectroscopy, X-Ray Diffraction (XRD), scanning electron microscope (SEM), and energy dispersive X-Ray Spectroscopy (EDS). Multiple NPD samples including a single pure diamond were successfully produced. The successful manufacture of these samples can significantly reduce the costs of production resulting in easier and more affordable access.

THU - 533 Physical Properties and Mineral Identificatio of Rock Formations of an Extinct Cinder Cone

Discipline: Geoscience
Subdiscipline: Geology

Mykyta Dementyev*, *Los Angeles City College* and Jayesh Bhakta, *Los Angeles City College*

Abstract: A number of rock samples were collected from the base of the Amboy Crater, which is an extinct cinder cone volcano located in Southern California. From the observations, the rocks have been characterized as mafic, vesicular, extrusive, and fine-grained igneous rocks. Investigation for magnetic susceptibility and the strength of the magnetic field will be performed to investigate magnetic properties of the rocks. Currently, the investigation has shown that Magnetite, a mineral rich in iron ions, composes a major portion of the rock samples and causes the rock to have a magnetic field. Electron microscopy and thin section optical analysis will be performed to identify other minerals composing the rocks. The samples were also investigated using x-ray powder diffraction, which showed the presence of quartz in them. Melt tests will be performed to determine the effect of cooling rate on the crystalline fraction of the material. Further tests for estimating the cooling rate of the rocks during their formation will be performed with varying environmental conditions, such as pressure and temperature. Preliminary results already suggest that our rock samples are a part of a group of Scoria and more precisely as Olivine Basalts. The analysis of the rocks from the cinder cone volcano will help prospective investigators with further analyses of rocks that have similar conditions upon their formation.

THU - 534 Temperature Measurements of the MgO [111] Hugoniot Using Streaked Optical Pyrometry

Discipline: Geoscience
Subdiscipline: Other Geoscience

Junellie Gonzalez Quiles*, *Johns Hopkins University*; Ray Smith, *Lawrence Livermore National Laboratory*; Marius Millot, *Lawrence Livermore National Laboratory* and June Wicks, *Johns Hopkins University*

Abstract: Magnesium oxide (MgO) is an important component of the Earth's mantle and is expected to make up on average by volume about 17 percent of the Earth's lower mantle. Even though it does not go through phase transitions under conditions found in our Earth's interior, the B1-B2 phase transition is expected to occur at 400-500 GPa, which are conditions achievable in Super-Earths. Super-Earths are terrestrial planets bigger than Earth found outside of our solar system. Magnesium oxide is thought to be found in the lower mantle of terrestrial bodies across different composition models (McDonough, 2016). In these planets, the B1-B2 transition at high pressure is suggested to have important effects on the viscosity of the mantle as a function of depth (Karato, 2011). Therefore, understanding the behavior of magnesium oxide at higher pressures and temperatures can lend insight into dynamics of Super-Earth interiors.

We report laser-driven decaying shock wave experiments on single crystal MgO [111] conducted on the OMEGA - EP laser facility at the Laboratory for Laser Energetics in Rochester, NY. Streaked optical pyrometry (SOP, Millot et al. 2015) measured the temperature of the shock Hugoniot, while velocity interferometry (VISAR, Celliers et al. 2004) was used to simultaneously measure pressure. We will report our results of this measurement and compare to previous work, discussing its implications on current challenges in temperature measurement at extreme conditions.

THU - 535 Phrephox: An *in-Situ* Approach to Metabolic State Quantification in the Open Ocean

Discipline: Geoscience
Subdiscipline: Other Geoscience

Solomon Chen*, *Woods Hole Oceanographic Institution*; Collin Ward, *Woods Hole Oceanographic Institution* and Matthew Long, *Woods Hole Oceanographic Institution*

Abstract: The quantification of the marine biogeochemical cycling is crucial for global carbon cycle modeling efforts. However, the magnitudes of marine fluxes are poorly constrained due to limited data collection and methods in marine environments. Of vital importance is the metabolic state of the open ocean, which remains unknown due to the large uncertainty in available estimates. The lack of marine metabolic state validations hinders the predictive understanding of how global biogeochemical cycles respond to stressors (e.g. ocean acidification, rising temperatures, hydrologic cycle changes). To bridge the gap, we built an *in-situ* prototype sensor package to measure Photosynthesis, Respiration, and Photo-Oxidation (PhRePhOx). The package is designed to collect data autonomously, using continuous measurements of oxygen and temperature within closed chambers. The package consists of a three-chamber incubator that flushes and pumps water into the 3 separate chambers producing dark, visible light, and ultraviolet (UV) + visible light incubations. During the incubation period, the oxygen content is monitored using oxygen optodes and temperature sensors. The package is equipped with UV LEDs to minimize biofouling, which can bias measurements by obstructing the light path for photosynthesis/photooxidation and by enhancing rates through biological growth on the chamber walls. This prototype is the first of its kind that is capable of continuous sampling at high frequency (~ 1hr) for constructing high-resolution time series of *in-situ* ecosystem processes. The future integration of this package on various vessels and platforms will greatly improve understanding of marine biogeochemical cycles.

THU - 536 Investigating the Submarine Volcanic System Near 9°50'N on the East Pacific Rise Using an Autonomous Submersible

Discipline: Geoscience
Subdiscipline: Other Geoscience

Klara Perkins*, *California Polytechnic State University* and Ross Parnell-Turner, *Scripps Institution of Oceanography at University of California, San Diego*

Abstract: The 9°50'N area of the East Pacific Rise (EPR), a mid-ocean ridge, hosts one of the most active submarine volcanoes on Earth. Major eruptions thought to occur here every ~15 years, the last being in 2006. Heat from this volcanic system drives vigorous hydrothermal vents, which support flourishing communities of extremophile fauna. Shortly after the 2006 eruption, near-bottom seafloor imagery was used to make a preliminary estimate of corresponding lava flow area and volume. However, these estimates are hampered by necessary assumptions, and questions remain about relationships between the geometry of the 2006 lava flow and the mechanics of the spreading center. A more accurate estimate of this flow volume and area is necessary to characterize and predict the properties of future submarine lava flows. Here, we estimate the geometry of the 2006 flow using 1 m resolution bathymetric data and 25 cm resolution sidescan sonar images, collected using the Autonomous Underwater Vehicle (AUV) *Sentry* in December 2018. We compare these new data with an earlier AUV dataset collected prior to the 2006 eruption, yielding new estimates for flow volume and distribution. The sidescan sonar images provide detailed insights about how individual lava flows were sourced and channelized, and how these processes relate to present-day vent ecosystems. Our results provide new constraints on the relationship between the morphology of the eruption and the along-axis characteristics at the EPR near 9°50'N, with implications for the extent and volume of the next eruption, which we anticipate may be as soon as 2021.

THU - 537 Simulating Low Density Parity Check Codes

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Elena Martinez*, *Loyola Marymount University* and Edward Mosteig, *Loyola Marymount University*

Abstract: All communication channels are subject to corruption. Corruption can have implications on how high performance technology transmits data. The need for efficient and accurate transmission has inspired new methods of protecting data. Low density parity check codes (LDPCs) connect message bits with a minimal amount of parity bits, forming parity checks that set off a rapid chain-reaction of simple operations. LDPCs ensure that message bits are protected without too much decoding complexity, and are therefore gaining popularity for implementation in modern systems. We seek to empirically show whether deterministic LDPC encoding schemes improve upon the efficiency and accuracy of current schemes that utilize levels of randomization. A binary erasure channel was programmed using Python 3 to simulate three classes of LDPCs: Gallager, MacKay Neal, and a unique method developed during the course of this research. A sizable amount of messages are simulated and run through the channel. We compare and report the accuracy of the three classes in recovering an original message from a corrupted message by using graphs produced in MATLAB. Results prove that it is worth exploring the production of deterministic LDPCS in comparison to LDPCs that contain a component of randomization.

THU - 538 Cyberbullying Classification: Semantic Analysis of Text in Shared Image Memes

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Jorge Garcia*, *Northeastern Illinois University*; Obsmara Ulloa, *Northeastern Illinois University*; Mirna Salem, *Northeastern Illinois University*; Christopher Gomez, *Northeastern Illinois University*; Rachel F. Adler, *Northeastern Illinois University*; Francisco Iacobelli, *Northeastern Illinois University* and Rachel Trana, *Northeastern Illinois University*

Abstract: The rise of online communication via social networks has facilitated an increase in the occurrence of cyberbullying incidents. Cyberbullying refers to the pervasive harassment of a victim through digital media, it has been shown that victims of cyberbullying can experience psychological distress. In this research, we examine the text found in image memes on social networking sites in order to build a machine-learning model that can adequately classify whether an image being shared contains

bullying text. Using optical character recognition (OCR) technology developed by Google via the Cloud Vision API we extract text from memes shared on social networks in order to examine their linguistic properties using a Bag of Words approach. Using a supervised classification model we will determine whether these texts contain bullying messages. Our model will be trained on a corpus of data consisting of user comments from sites such as *Instagram*, *Ask.fm,* and *Formspring,* alongside a database of commonly blacklisted words on social networks to aid in the classification*.* We will test and compare three main classifiers: Naïve Bayes, Random Forest, and Support Vector Machine. We will evaluate the performance of the classifiers first individually and then using a combination of classification algorithms to increase accuracy. Our goal in this research is to ultimately host a webpage that will allow the general public to upload image memes and have them be automatically screened for bullying messages, this tool could also be implemented by social networking sites.

THU - 539 Myosoft: A Machine Learning-Based Program to Automate Analysis of Muscle Fiber Morphometry and Type

Discipline: Computer & Information Sciences
Subdiscipline: Other Computer and Information Sciences

Lucas Encarnacion-Rivera*, *Emory University* and Hyojung Choo, *Emory University*

Abstract: Skeletal muscle comprises a heterogeneous arrangement of muscle fiber types: IIa, IIb, IIx, and I, which possess different metabolic strategies and contractile kinetics that ultimately determine their force output. Fiber size (e.g. cross-sectional area) and type are primary determinants of muscle function; thus, careful examination of these features provides functionally relevant information about muscle status. Importantly, fiber type composition responds to physiological changes like exercise and aging and is often altered in neuromuscular disease states. Analysis of fiber size and type in histological muscle preparations can be a useful method for quantifying key indicators of muscle function and for measuring responses to a variety of stimuli or stressors. However, despite the values of such analysis, it is often performed manually, which is both labor-intensive and time-consuming. To offset this obstacle, I developed Myosoft, a novel method to automate morphometric and fiber type analysis in immunofluorescently stained transverse muscle sections. Myosoft synergizes machine learning-based image segmentation with thresholding algorithms to extract morphometric features of muscle fibers (like cross-sectional area and mean ferret length) and their corresponding type for over 9,000 of fibers in under 16 minutes with >95% accuracy and minimal supervision from the investigator. Altogether, Myosoft is a a high-throughput, quick, accurate, and convenient solution to analyzing large sections of muscle tissue, capable of circumventing the error, bias, and labor incurred by manual annotation.

THU - 600 The Role of S1PR3 in Mechanosensation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Ifechukwu Okeke*, *University of California, Berkeley* and Diana Bautista, *University of California, Berkeley*

Abstract: Acute pain sensation or nociception is extremely important for alerting organisms to potential danger. Pain sensation is mediated through the somatosensory neurons of the peripheral nervous system called nociceptors that are fine-tuned to detect painful temperatures, chemicals, and/or mechanical forces. Previous work from our lab has established the signaling lipid sphingosine-1-phosphate (S1P) and one of its receptors S1P-receptor 3 (S1PR3), as important regulators of mechanical nociceptor excitability. S1PR3 is expressed in a subpopulation of nociceptors that are thought to be mechanonociceptors, and S1PR3 is required for normal sensitivity to noxious mechanical stimuli such as pinprick. However, whether S1PR3-expressing neurons are directly excited by mechanical stimuli remains untested. In my proposed research, I set out to test the hypothesis that S1PR3-expressing somatosensory neurons are mechanosensitive. To address this question, I cultured somatosensory neurons from mice that constitutively express mCherry in S1PR3-positive neurons on thin silicone membranes. I mechanically stimulated the cells by using a calibrated radial stretch system, while performing calcium imaging to observe whether they are activated by mechanical stimuli. My prediction is that a subset of S1PR3-expressing neurons are activated by the stretch stimulus, which would affirm their identity as mechanonociceptors. My work will advance our understanding of molecular mechanisms underlying pain sensation.

THU - 601 The Tetraspanin CD82 Regulates S1PR$_1$ mediated Hematopoietic Stem and Progenitor Cell Mobilization

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Magdalena Jiminez*, *University of New Mexico, Pathology*; Victoria Balise, *University of New Mexico, Pathology*; Chelsea Saito-Reis, *University of New Mexico, Pathology*; Erica Pascetti, *University of New Mexico, Pathology* and Jennifer Gillette, *University of New Mexico, Pathology*

Abstract: The mobilization of hematopoietic stem and progenitor cell (HSPCs) from the bone marrow into the blood occurs under normal physiological conditions and can be stimulated in the clinic to enable the isolation of HSPCs used for transplantation therapies. HSPC transplants are critical treatments for hematological diseases, and thus methods to improve HSPC isolation are of significant interest. Recent work from our laboratory identified the tetraspanin CD82 as a novel regulator of HSPC mobilization. Using a global CD82 knock out (CD82KO) mouse model, we measure enhanced mobilization of HSPCs within CD82KO mice following treatment with the mobilizing agent, AMD3100. Moreover, flow cytometry analysis indicates that CD82KO HSPCs have increased surface expression of sphingosine 1-phosphate receptor 1(S1PR$_1$), a G-coupled protein receptor that elicits downstream cellular activities such as migration, proliferation and cytoskeletal rearrangement. Additionally, we identified an increase in S1PR$_1$ gene expression in CD82KO HSPCs by qPCR analysis. In this study, we are testing the hypothesis that CD82 regulates S1PR$_1$ gene expression through activation of the transcription factor Signal Transducer and Activator of Transcription 3 (STAT3). Flow cytometry analysis demonstrates increased expression of phospho-STAT3(Tyr705) in CD82KO HSPCs when compared to WT HSPCs. Furthermore, pretreatment of CD82KO and WT animals with a STAT3 inhibitor reduces surface expression of S1PR$_1$, indicating enhanced STAT3 activation may promote surface expression of S1PR$_1$. Future studies will be directed at assessing the impact of STAT3 inhibition on CD82-mediated HSPC mobilization, which we predict will reduce the enhanced mobilization phenotype observed upon CD82KO.

THU - 602 Using Minipromoters to Optimize Differentiation Protocol of Dopaminergic Neurons

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Elizabeth Cervantes*, *University of Texas at San Antonio* and Christopher Navara, *University of Texas at San Antonio*

Abstract: Parkinson’s disease (PD) is a neurodegenerative disorder caused by the death of midbrain dopaminergic (mDA) neurons in the Substantia Nigra pars compacta (SNc). A promising therapy for PD is transplant of mDA neurons derived from induced pluripotent stem cells (iPSCs). A central hurdle to this therapy is determining which cells to transplant and how to most efficiently make those cells in culture. The purpose of our research is to optimize the differentiation protocol of mDA neurons of the appropriate type by creating a DNA construct to mark them accurately and intracellularly. Some markers such as Tyrosine hydroxylase (TH) are characteristic of mDA cells but also label non-mDA cells and label a population that is too mature to transplant. We are investigating MiniPromoters, of the genes encoding DAT and PITX3 to drive expressing of enhanced green fluorescent protein. MiniPromoters are human DNA sequences less than 4Kb for easy facilitation into integration sites. This construct will be inserted using CRISPR into the AAVS1 locus of iPSCs which will be differentiated into dopaminergic neurons. As a result, we will be able to count these neurons via microscopy or use flow cytometry to identify them without harming the cells enabling them to be used for further studies. It is expected that this study will aid in identifying dopaminergic neurons more efficiently and help with future treatments of PD.

THU - 603 Amelioration of SLC16A11 Expression and Stability By Altering Cell Culture Environment

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Michelle Mantilla*, *Broad Institute of MIT and Harvard* and Alina Ainbinder, *The Broad Institute of MIT and Harvard*

Abstract: Complications related to type 2 diabetes (T2D) are the leading cause of death in Mexico. Although environmental conditions, such as diet and exercise, lead to the development of T2D, there are also strong underlying genetic factors that contribute to risk of the condition. A genome wide association study recently identified a haplotype of genetic variants at the *SLC16A11* locus, common amongst individuals of Mexican and Latin American descent, that increases the risk of developing T2D. The T2D risk variants decrease the expression and function of SLC16A11, a proton-coupled monocarboxylate transporter that is predicted to play a key role in hepatic lipid metabolism. Therefore, individuals with T2D may benefit from the development of therapeutic approaches that increase hepatic SLC16A11 levels. SLC16A11 mRNA expression is not homogeneous amongst liver cells, with greater levels observed within pericentral (PC) hepatocytes surrounding the liver's central vein. This increase in mRNA expression can be modeled in vitro by changing cell culture conditions to reflect the pericentral environment (lower oxygen tension and less nutrient rich) and may lead to increased SLC16A11 protein levels. SLC16A11 protein has a short half-life; therefore, we are testing the effects of these PC-like conditions on SLC16A11 protein stability by western blotting at different times after treatment with cycloheximide. One way in which stability may be affected is through interactions with basigin, a protein that promotes cell-surface localization, and other SLC16A11 subunits. By understanding the mechanisms that increase SLC16A11 levels, this work will contribute to the effort to develop a treatment for T2D.

THU - 604 Utilizing Embryonic Stem Cells to Discover a Direct Correlation between the PGC7 Gene and X-Chromosome Inactivation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Alina Shahin*, *Pasadena City College* and Xiaochun Yu, *City of Hope*

Abstract: X-inactivation is a process by which one of the copies of the X chromosome present in female mammals is inactivated. Failure to choose and completely shut down one X chromosome often means immediate death for the developing embryo. If the X-chromosome is slightly or incorrectly inactivated, the female will survive, but will live with a variety of diseases, such as Rett syndrome or Duchenne's muscular dystrophy. PGC7 (also known as Stella or DPPA3), expressed in germ cells, is an important maternal factor for protecting DNA methylation, which is known to be essential for human X-chromosome inactivation. The purpose of this study is to demonstrate if the PGC7 gene plays a direct role in X-chromosome inactivation. Thus, embryonic stem cells (ES) were isolated from the PGC7 mutant mice. Genotyping was then performed to determine the PGC7 mutation in these cell lines. ES4 was identified as the PGC7-/-(knockout) cell line, meaning that the PGC7 gene was not present. Differentiation was then induced in ES4. After differentiation, Xist RNA FISH was performed in the ES4 cells to detect presence of X chromosome inactivation. The results showed that the mouse cells containing the PGC7 gene had X-chromosome inactivation while the PGC7 deficient cells did not. The hope is that this study can be repeated to determine if the PGC7 gene has the same function in humans as it does in mice. Understanding X-inactivation more fully, will allow for the prevention of inefficient X-chromosome inactivation, along with the negative effects that it has.

THU - 605 Edna Fallout: Analyzing Edna Concentration of Molluscs in the Marine Environment.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

David Calderon*, *California State University, Monterey Bay* and Emily Pierce, *California State University, Monterey Bay*

Abstract: Marine organisms release DNA into the surrounding aquatic environment, which is referred to as environmental DNA or eDNA. Sources of eDNA in the aquatic environment include, feces, mucus, carcasses, gametes, and other bioactive compounds from these organisms. We studied the persistence of eDNA in the environment, and how the prevalence of eDNA relates to the abundance of source organisms. Three different mollusc species were analyzed at two different densities of eDNA from small, medium, and large specimens of each species while comparing fed vs. unfed with kelp. Then the eDNA was placed under similar UV radiation from the sun and climate conditions to compare the effects of UV radiation similar to the sun and outside temperature on eDNA for each species. Three different mollusc species: the intertidal limpet (*Lottia digitalis*), the red abalone (*Haliotis rufescens*), and the California blue mussel (*Mytilus californianus*), were analyzed at two different population groups of eDNA from small, medium, and large specimens of species. We found more eDNA present and higher longevity when placed in UV in larger groups of each species both in size and quantity of each group. The data from this information was used to formulate rate of decay for each individual species. These methods could be adapted to help detect eDNA of endangered invertebrates, such as the owl limpet *Lottia gigantea*, black abalone *Haliotis cracherodii*, and the white abalone *H. sorenseni*. Identifying eDNA through molecular techniques could be an inexpensive monitoring tool that will expedite monitoring marine organisms.

THU - 606 The Role of Werner Protein in Responding to Oxidative Stress in *Drosophila Melanogaster*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Derek Epiney*, *Northeastern Illinois University* and Elyse Bolterstein, *Northeastern Illinois University*

Abstract: Oxidative stress, or the toxic buildup of free radicals, can cause DNA damage and interfere with DNA replication. One protein that responds to DNA damage is WRN, a RecQ helicase involved in maintaining genomic stability. Mutations in *WRN* cause Werner syndrome, a disease characterized by accelerated aging and an increased risk of cancer. The *Drosophila melanogaster*, WRN ortholog, WRNexo, only has a conserved exonuclease domain which allows us to focus on its unique exonuclease function separate from the helicase. A deletion in *WRNexo* (*WRNexo*$^{\Delta}$) results in deficiencies in DNA replication during the embryo and larval life stages. We investigated if *WRNexo* protects against DNA damage caused by oxidative stress during development by treating *WRNexo*$^{\Delta}$ larvae with paraquat, an herbicide that generates free radicals. Surprisingly, *WRNexo*$^{\Delta}$ larvae are not sensitive to paraquat as shown by similar relative survival between homozygous and heterozygous *WRNexo*$^{\Delta}$. Oxidative stress can also cause lipid peroxidation, leading to membrane damage and decreased body fat. Using larval buoyancy as a measure of body fat, we observed lower body fat in *WRNexo*$^{\Delta}$ compared wild type flies, which was partially rescued by feeding larvae antioxidants. Similarly, adult sensitivity to ethanol can be partially rescued by treating larvae with antioxidants. Our results suggest that *WRNexo* is involved in responding to oxidative stress but is not the primary mechanism in protecting against oxidative stress-induced damage. Understanding the interactions of WRNexo in responding to oxidative stress may allow us to develop better chemotherapy drugs and provide further insight on cancer and aging.

THU - 608 Investigating the Roles of Intestine Expressed Transcription Factors in *C. Elegans*.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Nicolai Apenes*, *University of Portland* and Erin Osborne Nishimura, *Colorado State University*

Abstract: *Caenorhabditis elegans* is a small transparent worm whose cell lineage is fully mapped, making it an ideal model organism to study organ development. The *C. elegans* intestine is a 20-cell organ that is specified early in development with a simple cell lineage. Previous work has identified a family of GATA transcription factors that work together to drive the early intestine gene regulatory network. However, transcription factors that work downstream of these GATA transcription factors are unknown.

Published intestine-specific transcriptome datasets were accessed to generate a list of 11 candidate transcription factors. These candidate transcription factors were investigated for their role in intestine development through RNA interference (RNAi) mediated knockdown. RNAi treated worms were imaged for gut granule formation and Nile Red stained lipid accumulation, which are two intestine specific features of *C. elegans*. Images of transcription factor knockdown worms were quantified for differences in fluorescence compared to untreated worms. This approach will help identify which candidate transcription factors play a role in intestine-specific functions.

THU - 609 Flight Performance of the Yellow Fever Mosquito in *Aedes Aegypti*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

John Billiot*, *New Mexico State University*; Xavier Jimenez, *New Mexico State University*; Yashoda Kandel, *New Mexico State University*; Charles Pelzman, *New Mexico State University* and Immo Hansen, *New Mexico State University*

Abstract: Novel mosquito control techniques like Wolbachia-based control, Population-Replacement (PR), and RIDL (release of insects carrying a dominant lethal) require releasing mass amounts of mosquitoes in the wild. Such Sterile Insect Technique (SIT) approaches rely on a male mosquito's ability to mate with wild female mosquitoes. Determining the fitness and flight ability of mosquitoes that are reared and raised in a laboratory environment is critical for planning a SIT field interventions.

Our hypothesis is that there are differences in flight performance between female and male mosquitoes, irradiated and non-irradiated male mosquitoes, and mosquitoes that were raised on bovine blood compared to mosquitoes raised on an artificial diet.

We used a flight mill setup to determine differences in flight performance between different experimental groups of mosquitoes. We measured distance traveled, time spent in flight, and velocity for individual mosquitoes from the *Aedes aegypti* UGAL strain.

We found that UGAL females fly significantly faster than males in average velocity and top speed measured in meters per second. Females also have stronger endurance than males due to their distance traveled being three times longer than a male's and their time in flight without stopping to be 12 minutes longer on average.

The flight mill is a useful tool for studying the flight behavior in order to assess fitness of *Aedes aegypti*. The results of this study will help to optimize the planning process for SIT interventions in populated areas.

THU - 610 JunB: A Potential Target for Treating Obesity Via Regulation of Thermogenic Gene Expression

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Aleyah Goins*, *University of New Mexico*; Xing Zhang, *University of New Mexico* and Meilian Liu, *University of New Mexico*

Abstract: Recent efforts to counteract obesity and its related diseases have come up short in producing suitable therapeutic drug targets. Previous attempts to induce weight loss by stimulating thermogenesis via β3-adrenoceptor agonists showed deleterious side effects and low efficacy in human clinical trials. Therefore, our research focuses on developing a novel therapeutic target — JunB, an AP-1 family transcriptional factor in the mTORC1 mechanistic pathway, which may mediate adipocyte thermogenesis via immune-nervous system crosstalk. We hypothesize that JunB is a key transcriptional regulator of thermogenesis and mediates the synergistic effects of IL-6 and β3-adrenoceptor agonists to induce thermogenic gene expression in brown adipocytes. To test this, we used adiponectin Cre in conjunction with JunB floxed mice to develop a new animal model with adipocyte-specific depletions of JunB. We confirmed genotyping by qPCR and western blot. Energy expenditure data was measured *in vivo* by a metabolic cage capturing oxygen consumption, water/food intake, activity, and weight, in baseline temperature (20°C) and cold-stress (4°C for 48 hours) conditions. Metabolic data indicates that JunB KO increases energy expenditure without significant difference in food/water intake or activity. Additionally, we checked thermogenic genes with qPCR and western blot. However, our current results suggest that JunB KO reveal decreased thermogenic gene expression under cold stress. In summary, JunB plays a negative role in energy expenditure. Further research is needed to clarify how JunB regulates energy expenditure independent of thermogenic gene expression, forming the basis of ongoing experiments.

THU - 611 Understanding Ire1 Dependent Decay in Mammalian Cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Haven Himmighoefer*, *University of Colorado, Denver*; Rachel Ancar, *University of Colorado, Anschutz Medical Campus* and Jay Hesselberth, *University of Colorado, Anschutz Medical Campus*

Abstract: The unfolded protein response (UPR) is a highly conserved response to endoplasmic reticulum (ER) stress caused by an accumulation of unfolded or misfolded proteins. Activation of the UPR resolves cell stress to proteostasis or apoptosis. Inositol requiring enzyme 1 (IRE1) is an essential ER transmembrane protein that activates the UPR through its RNase enzymatic activity resulting in its anomalous splicing of X-box protein 1 (XBP1) messenger ribonucleic acid (mRNA). IRE1 also functions in IRE1-dependent-decay (RIDD), where IRE1 cleaves ER associated mRNAs to maintain proteostasis. RNA fragments produced through RIDD have been suggested to cause inappropriate activation of retinoic acid inducible gene 1 (RIG-I), a pattern recognition receptor (PRR) of the innate immune system, initiating a type I interferon response. We propose to identify RNA fragments produced through RIDD, that may misactivate RIG-I, by identifying IRE1 downregulated mRNAs in XBP1-null cells. We are generating XBP1 knock-out cells using CRISPR-Cas9 technology, and have validated the ribonucleoprotein complex *in vitro*. In order to identify IRE1 specific cleavage of RNAs during RIDD, we are using a pharmacologic inhibitor, 4μ8C. When compared to WT and TG treated cells, 4μ8C inhibits IRE1 splicing activity by XBP1 splicing assay. Finally, we will use mRNA sequencing to identify RNAs that are specifically downregulated by IRE1 during RIDD. Identifying RNAs produced through RIDD is necessary to determine possible endogenous RIGI activators. This research will facilitate improved understanding of the role of RIG-I like receptors in the development of autoimmune disorders.

THU - 612 Isolation and Speciation of Intestinal Microbes from Tritonia Tetraquetra By Standard and Next-Generation Sequencing

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kanoa Redic*, *California State University East Bay* and Kenneth A. Curr, *California State University, East Bay*

Abstract: As climate change creates new environments for coastal organisms, animal populations that cannot adjust will decline, causing a domino effect that could result in habitat collapse. Delicate species, such as marine invertebrates, can act as an ecological marker that measure the health of local environments. As new conditions lead to different selective pressures, novel pathogens flourish due to changes in temperature, CO_2 and pH-levels. This research is concerned with the isolation and identification of bacterial species that reside within the intestinal tract of the marine nudibranch *Tritonia tetraquetra*. This marine sea invertebrate resides along the Pacific West Coast in areas that are populated with the sea pen, *Ptilosarcus gurnyei*, their primary food source. Due to the fact that the microbiota is a major factor in the organism's successful adaptation to novel environmental changes and is the greatest form of protection against enteric pathogens, it's of importance to understand the microbiome that inhabit this organism's intestinal tract.

This research uses standard microbial and molecular genetic techniques to isolate and culture a variety of bacterial populations within the slug's intestinal tract. Microbial genera and species are identified via DNA sequencing of the 16S rRNA gene and confirmed using standard bioinformatic and microbiological techniques. Identified genera are used as controls to ensure that the correct bacterial genera will be identified through Ion-Torrent Next-Generation Sequencing (Next-Gen). Next-Gen Sequencing will be used to create libraries to identify as many genera as

possible. Early results indicate *Pseudomonas*, *Aeromonas, Vibrio and Pseudoalteromonas* genera have been identified.

THU - 613 CRISPR-Induced Overexpression of Huntingtin As a Cellular Model of Huntington's Disease

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Dixie Blumenshine*, *Humboldt State University* and John Steele, *Humboldt State University*

Abstract: Huntington's disease (HD) is associated with CAG trinucleotide repeats in the *HTT* gene, which encodes the huntingtin protein. HD progressively damages patients' neurological function and causes eventual death earlier in each generation affected. Age of onset has been associated with the number of CAG repeats found in the *HTT* gene. Many attributes of the disease-associated mutant repeats in *HTT* are not yet understood, including how neurons are damaged and the role of normal and mutant huntingtin proteins in modifying neuronal viability. Our central hypothesis is that overexpression of normal huntingtin, with the eventual inhibition of cells' autophagy or other clearance pathway, will lead to a disease-like state. To address this hypothesis, we have developed a preliminary novel human cell model to allow us to assess how excess huntingtin is managed and/or cleared by cells, and how cell death occurs upon buildup of huntingtin. Overexpression of endogenous *HTT* gene products were induced using stably integrated inducible CRISPR transcriptional activator (dCas9-VP64 fusion) tools, allowing for transient and reversible transcriptional activation of the *HTT* gene. This model is our starting point to study the response of human cells following overexpression alone or with autophagy pathway modification to reveal how abnormal expression contributes to cell death. Incomplete findings are that cells overexpressing huntingtin occasionally have reduced viability, potentially dependent upon the differences between transcriptional activator guides. Here we report our generation and preliminary characterization of this novel model system for the study of HD, which will eventually be utilized in drug discovery applications.

THU - 615 Understanding Assembly of Vitelline Layer Proteins Perm-2 and Perm-4 in the *C. Elegans* eggshell at Fertilization

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Norani Abilo*, *Pomona College* and Sara Olson, *Pomona College*

Abstract: A key attribute of metazoan oocytes is a protective coat of extracellular matrix. Fertilization initiates remodeling of this coat to form a more permanent and protective barrier between a developing embryo and the environment. While this barrier goes by many different names, this coat is known as the vitelline layer in the nematode *Caenorhabditis elegans* and makes up the outermost layer of the nematode's impermeable eggshell. Analogous to the polymerizing zona pellucida glycoproteins of the vertebrate egg coat matrix, the vitelline layer requires the key proteins PERM-2 and PERM-4 to maintain eggshell integrity and keep embryos viable. Considering the functional similarity of the zona pellucida to the vitelline layer, we hope to explore polymerization of the two proteins as a possible strategy for building the oocyte vitelline layer and remodeling it after fertilization. We thus hypothesize that PERM-2 and PERM-4 self-polymerize or aggregate to form the matrix on the oocyte surface. To test this hypothesis, we are conducting biochemical polymerization assays on PERM-2 and PERM-4 isolated from control embryos and mutant embryos containing targeted deletions of amyloidogenic and aggregation-prone protein domains. I have successfully generated CRISPR/Cas9 targeting vectors that will delete two of these conserved domains in PERM-2 and will report on the phenotypic consequences of removing these domains. This approach will contribute to our understanding of how PERM-2 and PERM-4 contribute to the structural and functional properties of the vitelline layer at fertilization, as well as application to the zona pellucida and thus human health.

THU - 616 Characterization of MAD2L1BP Promoter

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Rabia Billoo*, *California State University, Northridge* and Cindy Malone, *California State University, Northridge*

Abstract:
Mitotic Arrest Deficient-like 1 Binding Protein gene encodes the MAD2L1-binding protein that is vital for proper cellular development and may be a component of the spindle-assembly checkpoint that prevents the initiation of anaphase until all chromosomes are correctly aligned during metaphase. Therefore, accurate regulation of MAD2L1BP gene expression is essential for proper cellular development. We hypothesize that the MAD2L1BP promoter will be isolated and characterized to identify the regulatory elements that drive transcription. The putative promoter region was isolated, PCR amplified, sub-cloned into a luciferase reporter vector, and verified by transient transfection for transcription activity. Sequential 5' deletions were constructed based on bioinformatics data identifying consensus transcription factor binding sites found within the MAD2L1BP promoter and transiently transfected into HEK293T cells, defining the proximal promoter region as the first 500 base pairs upstream of the transcription start site. Bioinformatics analysis via multiple sequence alignment programs determined conservation of sequences for C-Ets-1, SP-1, and XBP-1 consensus transcription factor binding sites across several species within the defined proximal promoter. The sequences will be individually deleted using PCR by exclusion to determine functional activity of these consensus sites. Chromatin immunoprecipitation assays will confirm the identity of transcription factors binding to functional consensus sites. Ultimately, characterization of the MAD2L1BP gene promoter region and the regulatory elements driving transcription will help us understand how MAD2L1BP gene expression is dysregulated in Mantle cell lymphoma and not expressed.

THU - 617 Isolation and Characterization of the UV Radiation Resistance Associated Gene Promoter Region

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Mary Antikyan*, *California State University, Northridge* and Cindy Malone, *California State University, Northridge*

Abstract: The UV Radiation Resistance Associated Gene (*UVRAG*), assists in autophagy and inhibits proliferation of human colon cancer cells by activating the Beclin1-Pl(3)KC3 complex. In a previous study, *UVRAG* was found to be expressed in normal B cells but not expressed in Mantle Cell Lymphoma against Small Lymphocytic Lymphoma found via suppression subtractive hybridization. In order to understand how this gene is turned on and off, the *UVRAG*'s putative promoter region was amplified and cloned into the pGC-Blue intermediate cloning vector, and subsequently sub-cloned into the luciferase expression vector, pGL3-Basic. Deletion constructs of the recombinant plasmid were engineered by site directed mutagenesis to define the proximal promoter region of *UVRAG*. A total of six deletion constructs were designed and used in transient transfections into Human Embryonic Kidney Cells. These data defined the maximal activity of the *UVRAG* promoter region, defining the proximal promoter of *UVRAG* to the -60bp position relative to the transcription start site. Multiple sequence alignment of orthologous *UVRAG* putative promoter sequences determined evolutionary conservation of the SP1 transcription factor-binding site in at least 8 different species. We hypothesize site-directed mutagenesis and transient transfections will determine the functional activity of this SP1 site. Chromatin immunoprecipitation assays will confirm the transcription factors that are binding to the conserved and functional site in the *UVRAG* promoter. Understanding how the *UVRAG* gene is regulated will allow for characterization of the dysregulated gene expression of UVRAG in mantle cell lymphoma.

THU - 618 Controlling the Localization of Cell-Fate Determinants Via Micropatterning Method

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Areli Jannes Javier*, *California State University San Marcos* and Carlos Luna Lopez, *California State University San Marcos*

Abstract: Stem-cells are non-specialized cells that are unique for their ability to differentiate into specialized cells. We are able to differentiate human adipose derived stem cells to several cell lineages and types, including osteoblasts and chondrocytes. However, the rate of differentiation remains a slow and inefficient process that limits our scale up capabilities. Thus, understanding how to precisely regulate cell fate remains a key goal in stem cell and musculoskeletal research.

A driving force of stem cell differentiation is the asymmetrical localization of cell-fate determinant factors. In our project we focused on the cell-fate determinant Numb, commonly known for inhibiting the Notch Signaling Pathway, responsible for regulating differentiation. We sought to regulate Numb localization by controlling cell morphology and spreading. To do this, we used a micropatterning method that can aid in controlling the regulation of stem cell morphology.

We approached this by plating cells on different micropatterned slides aimed to produce different shapes: circles, squares, and triangles. We cultured human adipose derived stem cells (HADSCs) for 3 days and used Fibronectin to promote cell adhesion.

As a result, the Numb was highly localized in areas of the cells that appear to be actively spreading. Numb localization depended more on the cell being actively spreading than in a specific morphology. Numb was localized in regions of the cell closer to the substrate rather than the top of the cell. These results indicate that Numb localization is a dynamic dependent process that depends on cell-substrate interactions.

THU - 619 Improving Diagnostics for the Lurking Pathogen*, Phytophthora Spp.*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Maribel Perez Espinal*, *Humboldt State University*; David S. Baston, *Humboldt State University*; Everett Hansen, *Oregon State University, College of Agricultural Sciences, Department of Botany and Plant Pathology*; Wendy Sutton, *Oregon State University, College of Agricultural Sciences, Department of Botany and Plant Pathology* and Paul Reeser, *Oregon State University, College of Agricultural Sciences, Department of Botany and Plant Pathology*

Abstract: *Phytophthora*, a member of the oomycete group, is a soil borne pathogen detrimental to trees and agricultural crops alike. We are focused on the *Phytophthora* spp. which target oak trees in California, specifically northern California coastal environments. Circa the mid-1990s many versions of the pathogen were inadvertently introduced in California. As an invasive species they caused significant damage to the survival of oak trees. Oak death has become a problem found in coastal areas and one of increasing concern toward action on habitat management. In an effort to monitor the spread of Sudden Oak Death a study was designed to develop an assay to identify 5 particular *Phytophthora* species: *tentaculata, ramorum, lateralis, cambivora,* and *cinnamomi*. Our aim is to identify these *Phytophthora* using Polymerase Chain Reaction (PCR) to categorize and build on distinguishing these closely related species through Single Nucleotide Polymorphism (SNP) genotyping. To start developing a complete assay several soil and/or tree samples were obtained in Humboldt County where our target species might be found. From these soil and tree samples we were able to bait, isolate, and extract DNA for PCR and sequencing identification.The PCR products from our PCR tests revealed bands that were then used to compare amplicon lengths of the five species to confirm the presence of that *Phytophthora*. This will allow for the development of probes, and the use of nanofluidics for the final assay which should reduce identification time from weeks to days.

THU - 620 Production and Purification of Virus like Particles (VLPs) Using MS2

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kaelyn Acothley*, *Northern Arizona University* and Naomi Lee, *Northern Arizona University*

Abstract: Neisseria gonorrhea (Ng) infections can originate as a mild or unnoticed infection but have the ability to evolve into harsher ailments such as infertility, ectopic pregnancy, or chronic pelvic pain. Fortunately, there are medications for Ng, but with the rise of antibiotic resistant Ng strains effective treatment options are gradually becoming scarce. The rise and emergence of using virus like particles (VLPs) to counteract antibiotic resistant bacterial strains while offering a low-cost vaccine is becoming more apparent that it could be an alternative pathway to combat the manifesting predicament of antibiotic resistant strains of bacteria. VLPs lack a viral genome but are able to mimic viral functions as if they were equipped with the machinery. Therefore, VLPs allow researchers to display antigens at a low dose, with a high antibody response because their viral structures have assembled into non-infectious particles. Two proteins on Ng, PorB and MtrE, were identified as key roles in pathogenesis due to the bacterial surface peptide loops. Using this information, an effective vaccine for Ng can be created to target PorB and MtrE surface peptides. To accomplish this, we used a plasmid, pDSP62, for genetic insertion of the desired antigens on the surface of the VLPs. Thus far, the one derivative of the VLPs were synthesized, lysed, and purified. In the future, the we will synthesize four additional VLP derivatives. The immunogenicity of the VLPs will be measured via ELISA assays in a murine model. In conclusion, VLP-based vaccines are potential candidates to conquering antibiotic resistance.

THU - 621 The Role of Insulin Signaling in Developmental Ethanol Toxicity

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Manae Matsubara*, *San Jose State University*; Rachel Vasquez, *San Jose State University* and Rachael French, *San Jose State University*

Abstract: Animal feeding behaviors are governed by conserved physiological mechanisms that promote sufficient feeding for developmental progression and survival. Developmental alcohol exposure (DAE) alters feeding behavior through multiple mechanisms, including suppressed feeding motivation and feeding abnormalities. These changes likely contribute to the detriment associated with fetal alcohol spectrum disorder (FASD). We have established *Drosophila* as a genetic and developmental model for FASD, and have demonstrated that DAE results in reduced feeding at every developmental stage in flies. The neuropeptide F (NPF/NPY) pathway regulates rewarding behaviors and is positively associated with increased feeding across all taxa. We have shown that in the presence of DAE, NPF signaling is increased in *Drosophila* larval brains indicating that NPF is necessary for larval survival. These data suggest that NPF is increased to compensate for reduced feeding caused by an as-yet-unidentified ethanol-dependent mechanism. Insulin negatively regulates NPF/NPY release, resulting in reduced feeding. We have previously demonstrated that insulin signaling is reduced by DAE, and we hypothesized that this reduction is a survival mechanism by which DAE-exposed larvae increase NPF release. We will present data in support of this hypothesis - mutations disrupting insulin signaling suppress ethanol-induced anorexia. Finally, both dopamine and octopamine signaling are regulated by insulin and enhance feeding. Both neurotransmitter receptors are reduced in DAE-exposed animals, and we hypothesize that one or both of these signals is the target for DAE-induced anorexia. We will perform genetic and molecular epistasis experiments to test the signaling relationships between insulin, NPF/NPY, octopamine, and dopamine.

THU - 623 Assessing the Role of *Hox3* during Segment Formation in the Leech *Helobdella Austinensis*.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Mariann Torres*, *University of California, Berkeley*; Christopher Winchell, *University of California, Berkeley*; Elizabeth Heath-Heckman, *University of California, Los Angeles* and David Weisblat, *University of California, Berkeley*

Abstract: Segmented worms (Phylum Annelida) elongate their body axis by adding new segments that develop from a posterior growth zone (PGZ). The molecular mechanisms responsible for establishing and maintaining the annelid PGZ are not well understood. However, expression of *Hox3* in the PGZ of several polychaete annelids suggests that this gene may play a conserved role in regulating posterior growth. Among annelids, the PGZ stem cells and the cellular basis of segment formation are characterized best in leech embryos. This knowledge can be leveraged to tailor experiments and interpret results concerning *Hox3* function. Our preliminary RNAseq results indicate that *Hox3* transcripts are most abundant during leech segment formation.

We are using *in situ* hybridization to test whether *Hox3* is expressed in teloblasts, the large and individually identifiable stem cells of the leech PGZ. In addition, we are using CRISPR-mediated mutagenesis to study the function of *Hox3*. We predict that *Hox3* is expressed in teloblasts as they generate primary blast cells, the cells giving rise to individual segments. Because teloblasts shutdown after generating the complement of only 32 segments in the leech embryo, we anticipate attenuation of *Hox3* expression once all primary blast cells are produced. In *Hox3* mutants, we expect to observe normal production of teloblats, but failure of primary blast cell production. Given that leeches are highly derived annelids with an abnormal (unclustered) arrangement of Hox genes within the genome, it is also possible that *Hox3* is regulated differently than in polychaetes, potentially leading to the evolution of novel functions.

THU - 624 The Role of ERK2 in Dendritic Cell Function

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Nawal Abdul-Baki*, *University of Texas at San Antonio*; Sean Jeffreys, *University of Texas at San Antonio*; Austin Negron, *University of Texas at San Antonio* and Thomas Forsthuber, *University of Texas at San Antonio*

Abstract: Dendritic cells (DCs) are an important link between the innate and adaptive immune systems, specifically by serving as key regulators of T cell-dependent (TD) immune responses. In DCs, several processes critical for initiating TD immune responses, such as migration, provision of costimulatory signals, and antigen uptake and presentation, utilize the mitogen-activated protein kinase (MAPK) signaling pathway. The dysregulation of these processes can result in the aberrant activation of autoreactive $CD4^+$ T cells, resulting in autoimmune disease. Extracellular signal-regulated kinases 1 and 2 (ERK1/2) are key effectors of the MAPK pathway, and while ERK1 has been shown to be a critical regulator of DC migration and TLR-induced IL-10 secretion, the function of ERK2 remains unknown. Our lab has developed a novel mouse model in which the inducible cre-mediated deletion of *Erk2* is accompanied by the expression of an eYFP reporter protein. This provides us the unique ability to circumvent the embryonic lethality of deleting *Erk2* in the germline while also allowing the detection of viable *Erk2*-deficient cells via flow cytometry. Preliminary data using this model has shown that *Erk2Δ* bone marrow-derived DCs (BMDCs), as well as *Erk2Δ* splenic DCs, exhibit altered expression of surface markers associated with T cell costimulation, antigen presentation, and migration compared with DCs from littermate controls. Taken together, this suggests that ERK2 plays a unique role in the regulation of several DC functions, potentially opening a new approach to treating $CD4^+$ T cell-mediated autoimmune diseases.

THU - 625 The Mechanism of Paternal Sex Ratio Chromosome in the Jewel Wasp *Nasonia Vitripennis*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Hoa Nguyen*, *University of California, San Diego* and Elena Benetta, *University of California, San Diego*

Abstract: The selfish B chromosome known as Paternal Sex Ratio (PSR) in the natural populations of Jewel Wasps, *Nasonia vitripennis,* induces the elimination of the paternal genome by forming a condensed mass called Paternal Chromatin Mass (PCM) by presumably altering histones modification. Since wasps' sex determination system is haplodiploidy, the elimination of the paternal genome by PSR results in fertilized eggs becoming PSR-carrying haploid males instead of females, leading to a male biased sex ratio. Recently, three genes highly associated with PSR were identified using pacBio technology and RNA sequencing. From this preliminary analysis, I hypothesized that each of these three genes play an important role in the elimination of the paternal chromosomes by PSR. By injecting PSR males with dsRNA designed specifically for each gene to reduce their expression in the testis, the effect of each gene on PSR were examined. Crosses between RNAi treated PSR males and wild-type virgin females were also conducted to determine the sex ratio. The preliminary data shows that the reduction of expression of one gene led to an increase in female sex ratio from around 0 to 0.6, suggesting that RNAi treated PSR males are able to produce females. On the other hand, the knockdown of the other two genes shows no significant difference on female sex ratio. These findings strongly suggest that only one of the three genes play a significant role in the process of histone modifications by PSR to eliminate the paternal genome that will be confirmed with further cytogenetics experiments.

THU - 626 Liver Expression of Prolactin Receptor Isoforms throughout the Murine Estrous Cycle

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Gillian Wright*, *University of California, Riverside* and Ameae Walker, *University of California, Riverside, School of Medicine*

Abstract: Like the human receptor, alternative splicing of the murine prolactin receptor (PRLR) pre-mRNA results in four isoforms: one long form (LF) and three short forms (SF1-3). While the LF PRLR promotes cell proliferation and survival, the SF PRLRs act as dominant negatives, promoting differentiation and apoptosis. The ratio of LF:SF PRLR is therefore important. Prolactin (PRL) plays an important protective role in the liver, resulting in female resistance to hepatocellular carcinoma and non-alcoholic fatty liver disease. Despite knowledge that PRL levels change with the estrous cycle and that PRL upregulates expression of its receptor in other tissues, expression of PRLRs in the murine liver has never been evaluated with respect to stage of the estrous cycle. After establishing consistent cycling, liver was collected and snap-frozen at proestrus, estrus, metestrus, and diestrus (n = 4-8 per stage), and RNA was extracted for real-time quantitative PCR for PRLR isoforms. Optimization produced PCR conditions resulting in similar efficiencies for all primer sets. All isoforms of the PRLR were detected in the liver at each stage of the estrous cycle and SF3 had the highest expression *versus* the housekeeping gene, Gapdh, at each stage. The only form of the receptor that changed with the cycle was the LF, which was significantly, but not greatly, upregulated in estrus, suggesting a positive effect of the proestrus surge of PRL. This would be anticipated to increase rather than decrease susceptibility to hepatocellular carcinoma, so it will be important to examine the LF:SF ratio in males *versus* females.

THU - 627 The Role of $G\alpha_o$-Coupled Neurotransmitter GPCRs in the *C. Elegans* Egg-Laying Circuit

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kimberly Wei*, *Yale University*; Robert Fernandez, *Yale University* and Michael Koelle, *Yale University*

Abstract: The nematode *C. elegans* is a well-studied model organism to investigate how neurons communicate to regulate behaviors. The location and function of every neuron is known and the mode of communication between neurons, chemicals called neurotransmitters that regulate behavior, has been mapped in every neuron. We are using these tools to study the *C. elegans* egg-laying circuit. The problem is that we do not know the location of the receptors the neurotransmitters act on to regulate egg-laying. To address this problem, we have previously mapped all 26 neurotransmitter G protein coupled receptor (GPCR) in the *C. elegans* egg-laying circuit. Using this map, we focused on a specific subset of GPCRs that couple to the G protein, Ga_O, in the egg-laying circuit. This G protein inhibits neurotransmitter release from the egg-laying circuit, which inhibits egg-laying events. If you inactivate Ga_O in this circuit, this leads to worms laying many eggs very quickly. We hypothesize that this egg-laying defect was through a neurotransmitter GPCR expressed in the egg-laying circuit, as these receptors act through G proteins to regulate behavior. We tested mutants that knock out or overexpress these receptors in egg-laying assays for the seven Ga_O-coupled neurotransmitter GPCRs found in this circuit. Manipulating the expression of these receptors resulted in egg-laying defects such as laying too many eggs or unable to lay eggs leading to retention of eggs inside the worm. Through our work, we hope to elucidate the functions of these receptors in their regulation of egg-laying behavior.

THU - 630 Inconsistencies in Type 1 Error Corrective Methods Used in Population Genetics Studies

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Ken Mey*, *California State University San Marcos* and Arun Sethuraman, *California State University San Marcos*

Abstract: Population Genetic studies commonly use multiple independent tests when making broad “family-wise” inferences about the current disposition of a population. However, when performing statistical tests across multiple independent pairs of genomic loci (or populations), the false positive rate grows at the Family-Wise Error Rate (FWER) of $1-(1-\alpha)^k$, where α is often set to a standardized value of $\alpha=0.05$, or a “less stringent” threshold value. As a result, the likelihood of obtaining False Discovery Rates (FDR) is inflated. Correction methods such as: Bonferroni, Sequential Bonferroni, and Benjamini and Hochberg (B-H method), etc. are commonly utilized to lessen inflation of FDR but vary on their level of stringency. We searched thousands of recent population genetics literature (2013-present) and retained 205 papers which assessed these population attributes: HWE, LD, and Fst, in order to test whether inconsistencies were present in the multiple testing correction methods used. A Fisher’s exact test of independence in correction methods used was performed between tests of HWE and differentiation and tests of LD and differentiation which indicated inconsistent usage of correction methods (p-value < 0.0001). A Chi-squared goodness of fit test was performed ($X^2= 40.85$, p-value $= 5.2e-6$) which indicated that less stringent corrections methods were largely being utilized over more stringent methods for retaining more “interesting” loci that were considered as Fst outliers. We show conclusively that editors and reviewers should necessitate authors to communicate their use of correction methods applied, and become aware of whether they are consciously, or unconsciously avoiding consistently applying them.

THU - 631 Contributions of KIN17 3_10 Helix Loop to Splice Site Choice

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Eimy Castellanos*, *University of California, Santa Cruz*; Jessie MNG Lopez, *University of California, Santa Cruz* and Alan Zahler, *University of California, Santa Cruz*

Abstract: The central dogma of biology describes the conversion of genetic information encoded in DNA into functional protein products; in eukaryotes, pre-mRNA is edited before it can code for a protein product. This editing includes excising regions on the pre-messenger RNA called introns and ligating together exons by a molecular machine called the spliceosome. There are cases in which the spliceosome edits the RNA transcript at different regions when compared to the wild-type transcript. It is important for the spliceosome to correctly splice the RNA transcript not only to avoid errors, which are associated with human disease, but to maintain all of the cells in our body. But how does the spliceosome determine the boundaries between the exon and intron (splice sites)? In a genetic screen by the Zahler lab, it was found that a methionine to isoleucine mutation in the loop on protein KIN17 can alter splice site choice in our model organism *C. elegans*. Surprisingly, according to the crystal structure of KIN17, this residue seems to point down into the globular body. We hypothesize that the mutation at methionine 107 repositions the loop, and three nearby highly conserved amino acids (two histidines and one tryptophan) are more directly mediating the change in splice site choice. By quantifying the splice site choice in both *C. elegans* KIN17 mutant and wild-type strains, we will evaluate the possible contributions of KIN17 in these highly conserved residues to splice site choice, and more broadly, the underlying mechanism(s) responsible for recognizing splice sites.

THU - 700 Comparison of Population Abundance, Distribution and Habitat Use of Western Pond Turtles on the Klamath and Trinity Rivers.

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Jade Haumann*, *Keuka College* and Matt Johnson, *Humboldt State University*

Abstract: The research objective is to compare abundance, distribution and habitat usage of the Western pond Turtles on the Klamath and Trinity Rivers. The project’s purpose is to provide data on Western Pond Turtle population on the Klamath River to be later compared with further research during and after dam removal. The expectation is that while habitat selected for basking by turtles will be similar between the rivers, differences in river conditions between the Klamath and Trinity will result in differences in turtle abundance and distribution. The methods follow similar protocol used on the Trinity River by Snover and Adams (2016). Four 5-mile survey reaches were surveyed with two oar-frame rafts on the Klamath river from mile 23.64 to mile 48.67. Each survey is conducted over a 4-day period and repeated 4 times. Data suggest that there are fewer turtles on the Klamath than on the Trinity. Results found that the Klamath River has adequate habitat suited for the Western Pond Turtle, although warmer water temperatures could be negatively impacting the population. The effect of dam removal on the river is unclear; however, data analysis suggests that decreasing the water temperature would be beneficial to the Western Pond Turtle. Observations suggest that jet boat traffic may disturb basking turtles and therefore have a greater impact on the Klamath Western Pond Turtle population. Further research on both the effect of jet boat traffic on basking turtles and the effect of dam removal on water temperatures would be beneficial for conservation strategies.

THU - 701 Analysis of Extremotolerant Tardigrade Genome for Potential Applications in Medical and Agricultural Fields

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Madison Granduke*, *Valencia College* and Dheeraj Verma, *Valencia college*

Abstract: Tardigrades are known for their extremotolerant abilities withstanding extreme temperatures, intense pressure, oxidative stress, and desiccation. Analysis of scaffolds of whole genome shotgun sequence revealed known stress-related genes including aquaporins, catalase, superoxide dismutase, and heat shock proteins(HSP). In humans, HSP’s play an important role in stress. The sequence query of tardigrade HSP against human sequence database did not give any hit to human HSP’s indicating tardigrade HSP’s are distinct with respect to their DNA sequence and protein structure. Although human HSP90 has been linked to neurodegenerative diseases, tardigrade HSP90 sequence was found to be significantly different from human HSP. However, tardigrade HSP has 64% identities, 81% similarities, and 1% gaps to tumor rejection antigen(which plays a role in cancer). Scaffold analysis also uncovered desiccation-related genes encoding for cytoplasmic abundant heat structure(CAHS) protein and secretory abundant heat soluble(SAHS) protein. The CAHS and SAHS sequence inquiry using the BLAST program resulted in no significant match to any of the available sequences in the NCBI database with closest identities being <30% indicating tardigrade-specificity. To determine the protein structure and possible functional mechanism, the protein models of CAHS8 and SAHS1 were created using DNASTAR-Nova applications and showed helices and several ligand binding sites. Additional exploration of remaining scaffolds could reveal more tardigrade-specific genes related to their extremotolerant abilities. This research has potential future applications in medical and agricultural fields. For example, CAHS and SAHS proteins could be used to store vaccines and other pharmaceuticals at room temperature, transport organs, and create drought-tolerant transgenic plants.

THU - 702 Therapeutic Effects of Phosphatidylglycerol (PG) on Neimann Pick Type-C Disease

Discipline: Life Sciences
Subdiscipline: Biology (general)

Miriam Waghalter*, *Rutgers University- New Brunswick*; Olga Ilynstka, *Rutgers University- New Brunswick*; Ran Li, *Rutgers University- New Brunswick* and Judith Storch, *Rutgers University- New Brunswick*

Abstract: Neimann Pick Type C (NPC) Disease is a rare lysosomal storage disorder in which one of the genes that code for NPC proteins (1 or 2) is mutated, resulting in absent or nonfunctional protein. Without either of these proteins, cells lose their ability to transport cholesterol through the endo-lysosomal compartment. The subsequent accumulation of cholesterol and secondary accumulation of other lipids in cells cause detrimental motor and neurological symptoms and ultimately death. Chevallier *et al (J.Biol.Chem 2008)* discovered that exogenous treatment of NPC1 cells with lysobisphosphatidic acid (LBPA) results in cholesterol clearance from late endosomes. We have recently shown that LBPA enrichment can occur by incubating cells with phosphatidylglycerol (PG), the precursor of LBPA. In this work, we induced the phenotype of NPC disease on apparently healthy human fibroblast cells using drug U18666A, which inhibits NPC1 from exporting cholesterol. We examined whether treating these cells with PG has an effect on clearance of cholesterol. We used three different concentrations of U18666A (0.5 μM, 1 μM, and 5μM) and treated the cells with PG over four different time points (48h, 40h, 34h, and 16h). Using flow cytometry and microscopy, we measured the cholesterol content in the cells after treatment and found that PG does reduce the amount of cholesterol within the U18666A-treated cells. These results on this isogenic model support our lab's previously obtained data on the therapeutic potential of exogenous PG/LBPA enrichment in cells with defects in NPC1.

THU - 703 **The Role of Type 2 Secretion System Protein Legp on *Legionella Pneumophila* growth**

Discipline: Life Sciences
Subdiscipline: Biology (general)

Patricia Del Rio*, *California Lutheran University* and Paloma Vargas, *California Lutheran University*

Abstract: *Legionella pneumophila* (Lpn) is a gram-negative bacterium that is found in fresh-water or in man-made water systems, such as cooling towers. Lpn is an opportunistic pathogen that targets immunocompromised people, causing severe pneumonia (Legionnaire's Disease), and a less severe form which is known as Pontiac fever. Lpn lives in environments ranging from 0°C to 60°C , but lives best between 37.5°C to 39°C (Konishi et al. 2006), which is the average temperature of the bacteria's perfect niche, the human body. Within the human host, *Legionella* has been shown to invade alveolar macrophages. Importantly, Lpn also colonizes freshwater amoeba. Previous studies (Cianciotto, 2008, Tyson et al. 2013) implicated the Type Two-Secretion System (T2SS) of Lpn in infection of both amoeba and human hosts. Moreover, the T2SS helps Lpn survive in low temperatures, and has been shown to be involved in biofilm production and intracellular infections of protozoans (Cianciotto et al. 2004). Subsequent studies identified that the T2SS secretes 25 effector proteins, including LegP, which aid in the survival of Lpn. T2SS proteins PlaC and LapA are known to play a role in the nutrient acquisition within the Legionella containing vacuole (White et al. 2018); however, the function of the other proteins, such as LegP, are unknown. In this study, LegP was tested to assess the effect of temperature in Lpn growth at 24°C and 37°C using spectrophotometry. At 24°C , LegP does not appear to play a role in Lpn growth, the role of LegP at additional temperatures will be assessed.

THU - 704 **Septic Extracellular Vesicles Accelerate Onset and Severity of Alzheimer's-like Pathology**

Discipline: Life Sciences
Subdiscipline: Biology (general)

Mya Vannoy*, *West Virginia University*; Divine Nwafor, *West Virginia University*; Allison Brichacek, *West Virginia University*; Ahmad Dakhlallah, *West Virginia University*; Emily Hoblitzell, *West Virginia University*; Catheryne Gambill, *West Virginia University*; Stanley Benkovic, *West Virginia University*; Clay Marsh, *West Virginia University*; Candice Brown, *West Virginia University* and Duaa Dakhallah, *West Virginia University*

Abstract: Sepsis is an incapacitating systemic inflammatory disease that is associated with infection etiology. Survival sepsis patients have a higher risk for developing chronic neurodegeneration and neuroinflammation, characteristics of Alzheimer's disease (AD) pathology. The mechanisms that link sepsis outcomes to chronic neurodegenerative conditions are poorly understood but could lead to possible therapeutic targets to delay the onset and progression of AD. Autophagy is the cellular process of degradation and critical to maintain immune homeostasis. In septic patients, autophagy can improve symptoms of multiple organ failure and defects in the pathway lead to the formation of pathological hallmarks of AD like amyloid plaques. In previous studies, human sepsis patients demonstrated that DNA methyltransferase (DNMTs) mRNAs are elevated in extracellular vesicles (EVs) and able to methylate essential autophagy genes in recipients of septic-EVs injection *invitro* and *invivo*. Using qRT-PCR with specific primers for genes involved with neuroprotection, DNA methylation and autophagy, we found elevated DNMTs mRNA expression in septic-EVs from plasma, brain, and liver, decrease autophagy mRNA expression, and detected increased DNA methylation of autophagy gene promoters using MSD method in septic murine models. Injection of septic-EVs in CVN-AD transgenic mice resulted in a septic phenotype with decreased brain autophagy expression. We hypothesize that the shedding of sepsis-EVs initiates the epigenetic silencing of autophagy resulting in acceleration of severity in AD-like pathology onset and cognitive impairment. Our long-term aim is to provide better understanding of septic-EVs' role in the progression of cognitive diseases and identify early diagnostic marker for sepsis and AD.

THU - 705 **Regional and Local Differences in Particulate Matter Pollution Revealed By the Use of Portable Air Sensors in Peru**

Discipline: Life Sciences
Subdiscipline: Biology (general)

Cynthia Amador*, *Mount Saint Mary's University*; Brigitte Solorzano, *Mount Saint Mary's University, Los Angeles* and Adriane Jones, *Mount St. Mary's University- Los Angeles*

Abstract: Air pollution including high levels of particulate matter is a known global health concern. Differences in particulate matter levels become apparent based on living conditions and practices among rural and urban communities' contribution to air pollution. The World Health Organization states that Lima Peru has some of the most polluted air in the world prompting us to ask the following questions 1) How does particulate matter pollution vary in rural compared to urban areas across Peru and 2) Could portable air sensors be a useful tool to assess day-to-day personal exposure. From July 31, 2018 to August 8, 2018, we collected data in urban and rural regions of Peru including Lima, Cusco, Quillabamba, and Santa Maria, by using the AirCasting Airbeam 2 portable air sensor to measure fine particulate matter (PM) in the sizes 10, 2.5 and 1 microns. We also conducted personal interviews in 2017 and 2018 with households and found that individuals residing in rural communities are more likely to cook with an open flame, and over 65% of the individuals surveyed in 2018 admitted to cooking with an open flame. We found that rural areas have low levels of PM in the ambient air ($\leq 20\ \mu g/m^3$ compared to urban levels $\geq 50\ \mu g/m^3$), but could be exposed to high PM levels while cooking with open-flame. Portable air sensors could be a useful tool to asses an individual's daily exposure as they move throughout their day and to empower citizens to advocate for their health.

THU - 706 **Evaluating Beta-Catenin and Formin-like 2 RNA As Microrna-29 Targets in Osteoclasts**

Discipline: Life Sciences
Subdiscipline: Biology (general)

Isaac Gandara*, *University of Texas at El Paso*; Henry Hrdlicka, *UConn Health* and Anne Delany, *UConn Health*

Abstract: Bone remodeling is a dynamic lifelong process, mediated by balanced bone resorption and formation. Osteoclasts are multinucleated monocytic cells that attach to, and resorb, bone matrix. Precursors treated with cytokines M-CSF and RANKL become motile, fuse, and form multinucleated osteoclasts. Excessive osteoclast function leads to common pathologies such as osteoporosis.

microRNAs (miRNAs) regulate osteoclast differentiation. Inhibition of the miR-29 family decreases osteoclast lineage commitment and cell motility. The E-cadherin complex regulates actin remodeling important for cell interactions needed for fusion and differentiation. Our lab has demonstrated that several mRNAs from the E-cadherin complex negatively correlate with miR-29a expression, including E-cadherin (Cdh1), beta-Catenin (Ctnnb1) and Formin-like 2 (Fmnl2). We experimentally verified one miR-29 binding site in the Cdh1 3'-UTR via site directed mutagenesis. Our goal is to validate potential miR-29 binding sites in Ctnnb1 and Fmnl2 using a similar strategy.

The miR-29 binding site of each transcript was removed via site directed mutagenesis PCR/overlap extension. These mutant UTRs were inserted into a luciferase reporter plasmid. The mutant UTR constructs will be transfected into a mouse monocytic cell line and treated with or without a miR-29 inhibitor; the wild type 3'-

UTR constructs will be used as positive controls. All cells will then be treated with RANKL to induce miR-29 expression, and luciferase activity will be measured. Failure of the miR-29 inhibitor to relieve repression of the mutant construct indicates that the miR-29 binding site was deleted. These studies will improve our understanding of the mechanisms by which miR-29 regulates osteoclast differentiation.

THU - 707 The First Assessment of Insecticide Resistance in *Aedes* mosquitoes in San Antonio, Texas Using the Centers for Disease Control Bottle Bioassays

Discipline: Life Sciences
Subdiscipline: Biology (general)

Tasheka Dillon*, *St. Philips College* and Megan Wise de Valdez, *Texas A&M University-San Antonio*

Abstract: Mosquito control and surveillance has become increasingly important due to transmission of Zika virus in Texas in 2016 and these activities are currently minimal in San Antonio. An important aspect of vector surveillance is conducting insecticide resistance assays to monitor the susceptibility of mosquitoes to different insecticides. We conducted Centers for Disease Control (CDC) bottle bioassays to assess the relative insecticide resistance of Aedes aegypti and Aedes albopictus mosquitoes in order to inform the local health district of San Antonio in their vector control efforts. We collected mosquito eggs by using 45 ovitraps in 9 residential areas across the city. We reared the eggs to adults in the laboratory, then identified and separated the adults based on species. We used a bottle bioassay kit provided by the CDC and conducted assays on each species using the insecticides Malathion (400ug/bottle), Naled (2.25ug/bottle), Permethrin (43ug/bottle), Chlorpyrifos (20ug/bottle), and Deltamethrin (0.75ug/bottle). We introduced 15-20 mosquitoes into each test bottle coated with insecticide and assessed the mortality rate over two hours. At least some form of resistance to insecticides is present if a portion of the test population survives the diagnostic dose at the diagnostic time. Preliminary data using Deltamethrin shows that Ae. aegypti and Ae. albopictus are susceptible to this insecticide, because mortality at the diagnostic time of 30 minutes was 100%. The remaining data to be gathered with this and other insecticides will provide a baseline so that we can compare data on insecticide resistance generated over time within San Antonio.

THU - 708 Regeneration of the Small Intestines Mediated By HIF2-Induced Wnt5a after Radiation Exposure

Discipline: Life Sciences
Subdiscipline: Biology (general)

Ariana C. Acevedo-Diaz*, *University of Puerto Rico, Bayamon Campus*; Carolina J. Garcia-Gracia, *The University of Texas MD Anderson Cancer Center UTHealth Graduate School of Biomedical Sciences-Department of Radiation Oncology, UT MD Anderson Cancer Center-Department of Experimental Radiation Oncology, UT MD Anderson Cancer Center*; Marimar De la Cruz Bonilla, *The University of Texas MD Anderson Cancer Center UTHealth Graduate School of Biomedical Science - Department of Experimental Radiation Oncology, UT MD Anderson Cancer Centers* and Cullen M. Taniguchi, *Department of Radiation Oncology, UT MD Anderson Cancer Center-Department of Experimental Radiation Oncology, UT MD Anderson Cancer Center*

Abstract: Radiation-induced gastrointestinal syndrome (RIGS) occurs after irreparable radiation damage to the small intestinal crypts, which disrupts self-renewal and leads to villi shortening and malabsorption, fluid loss, and electrolyte imbalances. There is currently no treatment that can protect or mitigate the intestines from RIGS, but we showed recently that hypoxia-inducible factor 2 (HIF2) radioprotects the intestinal epithelium. To understand the mechanism of this effect, we performed RNA-seq on intestinal organoids harvested from mice that carry a nondegradable Hif2α allele, and found 65 upregulated target genes, including several with roles in intestine homeostasis and damage response. Wnt5a, a non-canonical Wnt ligand that has been shown to be necessary for colonic crypt regeneration, was upregulated. Therefore, we hypothesized that HIF2 induces Wnt5a to protect the intestine against radiation injury. We confirmed that HIF2 induces Wnt5a expression by RT-qPCR. To evaluate if Wnt5a is a radioprotector, we performed spheroid formation assays (SFA) using a Click Beetle Red Luciferase reporter organoid line pre-treated with recombinant Wnt5a (rWnt5a) before radiation. We found that rWnt5a administered before (0, 2, 4, 8) radiation exposure, enhanced spheroid formation in compared to the control. Then we conditionally knocked-out (KO) Wnt5a in $Wnt5a^{fl/fl}$ intestinal organoids and performed SFAs to assess crypt regeneration. After 6 Gy of radiation, spheroids could not regenerate when Wnt5a was KO. In addition, we observed that HIF2 activates the Wnt5a promoter by a dual luciferase assay. Taken together, our preliminary results suggest that Wnt5a plays a role in radioprotection and is induced by HIF2 in the intestine.

THU - 709 The Impact of Seasonality and Social Jetlag on Academic Performance

Discipline: Life Sciences
Subdiscipline: Biology (general)

Michael Vujnovich*, *Northeastern Illinois University*; Annick Laure Ishami, *Northeastern Illinois University*; Aaron Schirmer, *Northeastern Illinois University* and Benjamin Smarr, *University of California at Berkeley*

Abstract: Human circadian rythms are 24-hour oscillations in an individual's behavior and physiology that are synchronized by light signals over the 24-hour day. Changes in the duration and intensity of these light signals (for example seasonal fluctuations in day length or jetlag) or the imposition of one's social schedule, termed social jetlag (SJL), can cause a misalignment between these rhythms and the environment. Such misalignments have been shown to have severe consequences to behavior and physiology. Previous studies have shown that increased average SJL strongly correlates with decreased academic performance; however, individual seasonal changes in SJL have not been evaluated. Online records of daily logins from the Northeastern Illinois University learning management system Desire2Learn (D2L) were used to study the interactions between circadian rythms, seasonality, SJL, and academic performance. Data from over 3 million login events were analyzed in the R 3.5.0 statistical package to identify seasonal patterns of SJL across individual students. SJL was calculated in three-week bins for all students by subtracting the median phase of non-class days from class days. These data were assessed for seasonal changes in SJL by applying a linear model to each student and extracting the slope, x- and y-intercept, and r^2 values. Preliminary results show that average SJL is significantly higher in the fall compared to the spring, and that patterns of login activity and SJL vary across semesters. These data will provide knowledge for students, educators, and universities to optimize schedules, minimize social jetlag, and increase overall academic performance.

THU - 710 Determining How TLR4 Knockouts in Townes Mice Limits Inflammation in Sickle Cell Disease

Discipline: Life Sciences
Subdiscipline: Biology (general)

Dormarie Rivera Rodriguez*, *University of Puerto Rico in Ponce*; Rachel Kirchner, *The Ohio State University*; John Belcher, *University of Minnesota Medical School* and Gregory Vercellotti, *University of Minnesota Medical School*

Abstract: Sickle cell disease (SCD) is a devastating disorder that affects millions worldwide. This disorder occurs due to a point mutation in the β-globin gene of hemoglobin (Hb) producing hemoglobin-S (HbS). HbS polymerizes when deoxygenated causing sickle-shaped red blood cells (RBC). Heme, a damage-associated molecular pattern (DAMP), is released from sickle RBC and interacts with the innate immune toll-like receptor 4 (TLR4) on vascular cells and activates cell signaling. This activates the pro-inflammatory transcription factor NF-kB leading to production of cytokines and adhesion molecules that promote inflammation, coagulation, and vaso-occlusion (VO). Previous studies in our lab have demonstrated that TLR4-/- mice reduces stasis in the blood vessels after being infused with hemin. We hypothesize that TLR4 deficiency will limit inflammation, coagulation, and VO in SCD. We tested our hypothesis in transgenic Townes SCD mice that express human α-globin and β^S-globin (HbS). These mice were bred with Tlr4-/- and Tlr4+/+ mice and backcrossed 10 generations to produce Tlr4-/- and Tlr4+/+ mice expressing human HbS. After 19 weeks of age, liver and kidneys from Tlr4-/- and Tlr4+/+ mice were collected. Relative mRNA expression for pro-inflammatory genes was quantified by RT-qPCR and the mean differences in gene expression were

calculated using GAPDH as a housekeeping gene. We found no significant differences between these 2 groups at baseline. Additional studies are underway to measure the response of pro-inflammatory genes in these mice after a challenge with hemin.

THU - 711 Fire Ecology: Using Seed Dispersers to Restore Native Species in Burn Areas

Discipline: Life Sciences
Subdiscipline: Biology (general)

Minerva Rivera*, *Santa Barbara City College* and Mario Pesendorfer, *Cornell Lab of Ornithology*

Abstract: One of the key goals summarized in the 2018 Strategic Fire Plan for California is “to implement needed assessments and action for post-fire protection and recovery.” Our changing landscape and increase in fire intensity and occurrence in California create a need for new and innovative ways to accelerate burn scar recovery after fires. Seed dispersal can be crucial mechanism of recovery as animals move seeds away from the parent plant into the impacted areas. We tested the hypothesis that providing seeds in targeted areas impacted by fire can result in increased seedling recruitment, thus accelerating habitat recovery. To do so, we provided *Aphelocoma insularis*, the Island Scrub-Jay endemic to Santa Cruz Island, with acorns presented on feeding platforms which were placed into the scar of a recent 1-ha fire. We recorded over 300 acorn GPS points of seed caching locations, which provide us with information on dispersal distance and arrival habitat. Later this spring, we will monitor the target area for oak seedlings and compare the observed density of seedlings to control areas where no feeders were placed. We predict that we will detect an increase in seedling density. In future work, we plan to develop a more expansive set of strategies aimed at using ecosystem processes to restore habitat impacted by fire.

THU - 712 Using *in Situ H*ybridization to Investigate the Expression of *vgll1* in Zebrafish Embryo

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Stephanie Perez*, *California State University Dominguez Hills*; Melissa Guardado, *Cal State Dominguez Hills*; Maricruz De La Torre, *Cal State Dominguez Hills* and Fang Wang, *California State University, Dominguez Hills*

Abstract: The skin is the largest organ of the body and acts as a protective layer from the environment. Using RNA-Seq we were able to identify many genes that are highly expressed in the skin cells. Through its development the skin interacts with other cells such as touch-sensing neurons that detect touch stimuli. The goal of our research is to better understand the biology of skin cells and their development, which provides potential molecular mechanisms for better diagnosis and treatments of skin diseases. We are studying a transcription factor gene expressed in the skin during early development in zebrafish: *Vestigal Like Family Member 1 (vgll1).* Using in situ hybridization we were able to detect gene expression patterns at different developmental stages. In situ hybridization is a powerful tool used to visualize and obtain temporal and spatial information about gene expression. Our results show that among the three development stages – 20 somite-stage (20ss), 52 hours post fertilization (hpf) and 72 hpf, we have examined, the highest expression level of vgll1 appear at 20ss. Currently, we are investigating the expression of *vgll1* gene at additional developmental stages, including 2-cell stage, 4-cell stage, 8-cell stage, high stage, 50% epiboly and 30 hpf. Our preliminary data showed that *vgll1* is at least highly expressed at 50% epiboly. More *in situ* hybridization experiments are required to determine the expression window of *vgll1* gene.

THU - 713 The Role of Tubulin Beta-III in Neural Crest Cell Fate Determination

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Jose Chacon*, *California State University, Northridge* and Crystal D. Rogers, *California State University*

Abstract: Neural crest cells are a transient stem-like cell population that forms in the dorsal neural tube of amniote embryos and then migrates to various locations to differentiate into diverse derivatives such as craniofacial bone and cartilage and the enteric and peripheral nervous systems. The current dogma of neural crest cell development suggests that there is a specific gene regulatory network (GRN) that controls the induction, specification, and differentiation of these cells at specific developmental times. Our lab has recently discovered the expression of a marker of differentiated neurons, Tubulin Beta-III (TUBB3), in newly specified premigratory neural crest cells. TUBB3 has previously been identified as a major constituent of microtubules and is required for the proper guidance and maintenance of axons during embryonic development. Using the model organism, *Gallus gallus*, we have characterized TUBB3 determined that it appears to be expressed in some, but not all definitive neural crest cells, suggesting that it is expressed only in a subset for a reason. In our early gain and loss of function assays, we have that loss of TUBB3 results in a reduction of NC cells and an expansion of the neural progenitor cells, which invade the area normally occupied by neural crest cells. These observations have given us a new perspective on the role TUBB3 might have in neural crest cell fate determination. We believe TUBB3 might have roles in neural crest domain maintenance, migration, and neuron specification.

THU - 714 The Role of MUSA1 during Somitogenesis in *Xenopus Laevis*

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Juan Carlos Velázquez Matos*, *University of Puerto Rico at Humacao* and Edwin Traverso Avilés, *University of Puerto Rico at Humacao*

Abstract: The segmented vertebrate body plan is derived from transient structures called somites, which give rise to muscle, bone and cartilage. The differentiation of muscle fibers within somites is tightly regulated by several processes, including protein ubiquitination. MUSA1 is a F-box protein, subunit of the SCF ubiquitin ligase, which binds proteins to induce their degradation through ubiquitination. In mice, MUSA1 works as negative regulator in the maintenance of muscle mass in the adult. However, the role of MUSA1 during embryogenesis is unknown. Preliminary data shows that *X. laevis* MUSA1 transcript is maternally expressed, decreases at gastrulation, and is detected in significant levels in the somites during organogenesis. We injected embryos with MUSA1 morpholinos to determine the effect of knocking down MUSA1 during somitogenesis. Our data showed that depletion of MUSA1 leads to changes in somite morphology. In order to study the MUSA1 protein directly by immunostaining and Western Blotting, we designed four different antibodies against different MUSA1 peptides that are present in the N-terminal, C-terminal or the inner part of the protein sequence. By performing immunostaining with these antibodies, we localized the MUSA1 protein in the nuclei of somitic and epidermal cells. To complement these analyses, we are testing our four antibodies in Western Blotting, with lysates from embryos at different development stages. This will allow us to establish the temporal profile for MUSA1 protein abundance during embryogenesis. We believe that the ubiquitination mediated by MUSA1 plays an essential role at the generation of the first muscle fibers of the organism.

THU - 715 Investigating the Relationship between mRNA Localization and Fertility in *Drosophila*

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Sara Shatela*, *California State University, Northridge*; Matthew Niepielko, *Princeton University*; Caroline Doherty, *Princeton University* and Elizabeth Gavis, *Princeton University*

Abstract: RNA localization is a highly conserved strategy used to generate polarized cell function in a variety of cell types. In the *Drosophila* embryo, *nanos (nos)* and *polar granule component (pgc)* mRNAs localize to the germ plasm, a highly specialized cytoplasm at the embryo posterior that is both necessary and sufficient to induce the formation of primordial germ cells. During the localization process, *nos* and *pgc* incorporate into higher order structures called germ granules. Within these granules, these RNAs organize into spatially distinct clusters, called homotypic clusters, each containing multiple copies of the same RNA. Although the complete loss of *nos* localization is associated with *Drosophila* female sterility, the relationship between the sizes of homotypic clusters and fertility robustness remains unclear.

Using single molecule Fluorescence In Situ Hybridization (smFISH) to determine cluster size and genetic techniques to reduce the sizes of *nos* and *pgc* homotypic clusters, we investigated the role homotypic clustering has in fertility. Our data demonstrate that reducing *pgc* cluster size increases primordial germ cell number and the number of eggs laid while reducing *nos* cluster size had little effect. Our future studies will focus on reducing *nos* homotypic cluster size further to determine if there is a clustering threshold that can confer robust egg laying. In addition, we will investigate the mechanisms by which *pgc* reduction generates more primordial germ cells.

THU - 717 Analysis of BMP Type II Receptor Functions in Early Embryonic Axial Patterning

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Jira White*, *Claflin University*; Benjamin Tajer, *University of Pennsylvania* and Mary Mullins, *University of Pennsylvania*

Abstract: Bone Morphogenetic Protein (BMP) signaling patterns the dorsal-ventral axis during early embryonic development. The dimeric BMP ligand brings together two type I and two type II receptors to signal. The type II receptors then phosphorylate the type I receptors, which in turn phosphorylate and activate Smad transcription factors. Recent studies have shown that dorsal-ventral patterning requires a complex containing two different type I receptors, Acvr1 and Bmpr1, yet the roles of the Acvr2 type II receptors in this complex remain uncharacterized. Murine gastrulation requires Acvr2, but this process involves Nodal and BMP ligands both of which bind Acvr2, confounding the role of Acvr2 receptors in early development. Zebrafish phenotypes for Nodal and BMP deficiencies are distinct, allowing us to separate the role of Acvr2 in these pathways. To explore these roles, we have developed mutants for each of the four zebrafish Acvr2 receptors. Though all Acvr2 single mutants present with a wild-type phenotype, combining these mutants through crosses reveals a variety of loss of function phenotypes. Acvr2ba and Acvr2bb play the largest roles, with zygotic acvr2ba;acvr2bb double mutants having a mildly dorsalized phenotype. While acvr2aa;acvr2ab double mutants have no phenotype, they do contribute to dorsoventral patterning, as the quadruple mutants are severely dorsalized. We have also observed some variability between embryos of the same zygotic genotype, which may be due to maternal contribution. We aim to further characterize the maternal and zygotic contributions of each Acvr2 receptor through further crosses, morpholino knockdowns, and RNA rescue experiments.

THU - 718 Identifying Natural Killer Cell Ly49 Subset Development in Vitro

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Jeremy Libang*, *University of California, Merced, School of Natural Sciences*; Alberto Millan-Hernandez, *University of California, Merced, School of Natural Sciences* and Jennifer Manilay, *University of California, Merced, School of Natural Sciences*

Abstract: As part of the innate immune system, Natural Killer (NK) cells recognize and terminate virally infected and cancerous cells. Evidence shows Ly49 receptors play an important role in target cell recognition, but how NK cells acquire Ly49 receptors is incompletely understood. Ly49 activating and inhibitory receptors are membrane bound glycoproteins encoded by genes in murine NK cells, thought to be expressed stochastically. We suggest an alternative hypothesis: Ly49 receptor expression is tightly regulated and sequentially forms unique NK cell subsets over time. We developed an assay in which we stimulated immature NK cells (CD27+CD11b-) in vitro to identify 16 possible combinations (clusters) of activating Ly49D and Ly49H, and inhibitory Ly49I and Ly49G2 receptors over time using flow cytometry. Our data identifies four novel clusters that significantly differ in frequencies over a period of six days in culture. We predict from frequencies a sequential cluster pathway that may originate from “Cluster 11” (Ly49H+Ly49D-Ly49G2-Ly49I+) which develops into “Cluster 14” by downregulating Ly49H, and then develops into “Cluster 8” (Ly49H-Ly49D-Ly49G2-Ly49I-) by downregulating all four receptors. We then predict “Cluster 8” to upregulate Ly49D and Ly49G2 to develop into “Cluster 6” (Ly49H-Ly49D+Ly49G2+Ly49I-). To test our predictions, we will sort and culture these clusters to determine the trajectory of development for each cluster over time. These data provide evidence of controlled regulation of Ly49 receptor expression on NK cells, which may indicate Ly49 receptor expression is not stochastic. Such analysis could provide insights into novel biological parameters to increase NK cell killing efficiency for immunotherapies.

THU - 719 A Genetic Screen to Identify New FGFR Signaling Components in *C. Elegans*

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Victoria Puccini*, *Northeastern Illinois University*; Jessica Palalay, *Northeastern Illinois University*; Xenia Alava, *Northeastern Illinois University*; Omar Payan Parra, *Northeastern Illinois University*; Mariya Stefinko, *Northeastern Illinois University*; Cindy Voisine, *Northeastern Illinois University*; Te-Wen Lo, *Ithaca College* and Michael Stern, *Northeastern Illinois University*

Abstract: Fibroblast growth factor receptors (FGFRs) are cell-surface receptor tyrosine-kinases (RTKs) that phosphorylate specific intracellular tyrosine residues to trigger downstream responses such as cell proliferation, migration, and differentiation. The study of the EGL-15 FGFR in the nematode *C. elegans* has long been used to understand principles of RTK signaling, since defects in the processes mediated by EGL-15 result in striking phenotypes that provide powerful genetic tools. One such process is the regulation of fluid homeostasis. Hyperactivation of EGL-15 causes excessive accumulation of clear fluid inside the worm’s body (the Clr phenotype). The isolation of **S**uppressor **O**f **C**lr (*soc*) mutants has led to the identification of many of the core components of EGL-15 signaling, such as the Grb2/SEM-5 adaptor protein that links RTK signaling to the RAS/MAPK pathway. Although SEM-5 is required for EGL-15 signaling, the *egl-15(n1457)* mutation, that truncates the carboxy-terminal domain of EGL-15 (ΔCTD) and eliminates its known SEM-5 binding sites, does not confer a Soc phenotype. These data suggest the existence of an alternate pathway that links EGL-15 to SEM-5/Grb2. To identify components of this alternate pathway, we repeated the screen for Soc mutants in an *n1457* (ΔCTD) background. Interestingly, many of the enhancer mutations show only partial Soc phenotypes on their own, and are enhanced by the *n1457* (ΔCTD) mutation. Preliminary characterization of these enhancer alleles indicates that they define up to three new *soc* genes. Genetic analysis and whole-genome sequencing will be used to determine the molecular identities of these potential new FGFR signaling genes.

THU - 720 Dietary Preference of Meso-Predators in the Wake of an Herbivore Outbreak

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Cheyenne Jarman*, *University of California, Santa Cruz*; Joshua Smith, *University of California, Santa Cruz* and Mark Carr, *University of California, Santa Cruz*

Abstract: Higher level predators have a well-known impact on herbivore populations within their ecosystem, but little is known about the contribution of middle level predators (i.e., meso-predators) to trophic dynamics. This study aims to evaluate the effects of meso-predator prey preference on the stability and resilience of kelp forest ecosystems in the wake of an ongoing sea urchin outbreak along the central coast of California. Intensive grazing by herbivorous sea urchins have modified underwater landscape of kelp forests resulting in isolated patches of forests and barrens. These patches impact the conditions (i.e., gonad condition) of urchins in the area. In this study I examine the prey preferences of leather sea stars (*Dermasterias imbricata*) and red rock crabs (*Cancer spp.*) on purple sea urchins (*Strongylocentrotus purpuratus*). Predators were given a choice between a gravid urchin and a non-gravid urchin and interactions were documented using video surveillance. Videos are being analyzed for three different interactions from the predator: touch, pass, and attack. Preliminary analysis on first attack by leather stars has shown that these predators prefer gravid urchins, which may indirectly impact urchin population in other forest patches. I am currently in the process of assessing the remaining work. Results from this experiment will help us get a deeper understanding of the interactions occurring in kelp forest ecosystems.

THU - 721 A Tale of Two Songs: A Comparison of Song Dialect between African and Southern Californian Populations of the Pin-Tailed Whydah (*Vidua macroura*)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Sydnee R. Dunn*, *California State University, Fullerton* and William Hoese, *California State University, Fullerton*

Abstract: The pin-tailed whydah (*Vidua macroura*) is a passerine songbird, native to Africa, that has recently established a breeding population in southern California. The pin-tailed whydah is an obligate brood parasite and lays its eggs in the nests of other species. Songbirds typically learn their song from conspecific males, though other brood parasites in the Viduidae family often mimic their host. Song is culturally transmitted and varies over time and space. Thus a newly established population of pin-tailed whydahs is likely to differ from its source population. We hypothesized that pin-tailed whydahs in southern California would sing different songs compared with individuals in their native African range. We recorded songs from males in Southern California and compared them to recordings of songs from males in Africa. We measured song length, total number of syllables per song, total number of different syllables per song, as well as maximum, minimum, and peak frequencies of the third syllable of each song and the entire song to characterize dialectical differences. Preliminary results based on a subset of three songs per male from six southern Californian and nine African males suggest that there is no significant difference in song dialect between the populations. Therefore, these birds may be highly tuned into recognizing and learning the songs of their own species. Investigating song in newly established populations of the pin-tailed whydah may provide insight into the persistence of this species in its new habitat.

THU - 722 West Coast Tide Pool Copepods Response to Environmental Change

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Estrella Organiz Altamirano*, *California State University Channel Islands*; Benjamin Van Allen, *University of California San DIego* and Jonathan Shurin, *University of California San Diego*

Abstract: Predicting the responses organisms have after being introduced to environmental change is crucial for conservation efforts. Copepods are small crustaceans that inhabit tidal pools which require them to adapt to harsh conditions in terms of sporadic periods of nutrient deficiencies. To measure the effects of resource availability and environmental change in *Tigriopus californicus*, 48 populations were created and monitored for a period of 20 weeks. The populations were divided into six sections with different combinations of food levels of powdered *spirulina* and maintained in 60 ml of salt water in high sterile plastic containers. The food levels were divided into four sections, very low, low, medium and high and ranged from 2.5 mg/ml to 15 mg/ml. The populations were kept in the laboratory at room temperature next to a large window where sunlight was available. The population size and body size of female copepods from each population were measured every five weeks. The experiment demonstrated that the populations in low feeding levels had a higher survival rate in low resource environments than the populations that began at a high feeding levels. However, the populations that began in a nutrient rich environment and continued at high feeding level were twice as large as other populations. Two populations ended in extinction due to the lack of resources and adaptability. This research can be applied to other populations facing dramatic and drastic environmental change caused by global climate change.

THU - 723 Biogeography of Shell Morphology in over-Exploited Shellfish Suggests Adaptation on Human Inhabited Islands and Incipient Lineage Bifurcation

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Ashley Hamilton*, *Texas A&M University -- Corpus Christi*; Rebecca Hamner, *Texas A&M University -- Corpus Christi*; Jason Selwyn, *Texas A&M University -- Corpus Christi* and Christopher Bird, *Texas A&M University -- Corpus Christi*

Abstract: Opposing selective pressures caused by anthropogenic activities can drive adaptive tradeoffs in phenotype. Limpets have conical shells, experience lengthy exposures to solar irradiation, and commonly experience a selective tradeoff where flatter shells are more resistant to predation but more susceptible to overheating. Flatter shells are more difficult to crush or dislodge but dissipate less heat from solar irradiation, which leads to higher body temperature. In contrast, taller shells have a greater surface area to dissipate heat but are easier to crush or dislodge. Shell coloration can also impact body temperature where lighter shells absorb less solar irradiation than darker shells. We conducted a range-wide survey to test for biogeographic patterns in shell morphology in the endemic, over-harvested Hawaiian limpet, *Cellana exarata*. The higher latitude islands (25.0-23.1N) are unpopulated by humans, whereas the islands at lower latitudes (21.9-19.5N) were colonized 1500-2000 years ago and remain densely populated. On the uninhabited islands, shells are taller with decreasing latitude. However, on the human-populated islands, which are also the hottest in the archipelago, shells are less variable, darker, and substantially flatter than even those from the northern-most island in the range. We propose this decrease in shell height, and thus surface area and volume, is a recent selective tradeoff driven by increased predation pressure due to humans, leading to a shift toward a more predator-resistant shell shape and cryptic shell coloration. Overall, the data are consistent with the colonization of the Hawaiian Islands by humans driving incipient lineage bifurcation in *C. exarata*.

THU - 725 Factors Limiting Denitrification Rates in a Hyper-Eutrophic Midwestern Reservoir at the Sediment-Water Interface

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Ashley Mickens*, *Miami University*; Tanner Williamson, *Miami University* and Michael Vanni, *Miami University*

Abstract: Anthropogenic activities have dramatically altered nitrogen cycling at the global scale, greatly increasing the amount of bioreactive nitrogen in our environment. Excess bioreactive nitrogen contributes to eutrophication and dead zones, with profound ecological, social, and economic consequences. Denitrification, the conversion of nitrate to dinitrogen gas, is an important ecosystem service that removes bioreactive nitrogen from ecosystems. Denitrification rates in Acton Lake, a hyper-eutrophic reservoir in southwestern Ohio, are relatively high in spring and decrease through summer and early fall. Nitrate drawdown likely limits denitrification rates, but we know little about what modulates denitrification rates. Determining these will allow us to better understand nitrogen cycling in eutrophic lakes. Our objective was to assess whether denitrification rates were limited by nitrate or algal carbon at sites near the inflow and outflow of the lake. We added nitrate and algal carbon separately and in combination to lake sediment cores, which were then incubated in flow-through chambers. We found that denitrification rates in the inflow of Acton were significantly higher than in the outflow, likely due to temperature differences. Denitrification rates were nitrate limited at both sites, and carbon additions did not increase denitrification rates. Our findings contribute much understanding to the processes that govern this valuable ecosystem service.

THU - 726 Differences in Terrestrial Invertebrate Communities Along Perennial and Ephemeral Streams in the Chiricahua Mountains, AZ

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Rezwana Islam*, *University of Arizona*; Earyn Nycole McGee, *University of Arizona* and Michael Bogan, *University of Arizona*

Abstract: Invertebrates play important roles in most food webs because they consume basal resources and in turn are consumed by larger species. Southeastern Arizona has a high level of invertebrate diversity, especially in riparian areas along streams. However, terrestrial invertebrate communities may differ between perennial (i.e., wet) and ephemeral (i.e., dry) stream beds due to differing levels of moisture, resource availability, and habitat complexity. We surveyed riparian invertebrates along three perennial and three ephemeral 100-meter stream reaches in the Chiricahua Mountains of southeast Arizona. In each of the six reaches, we used beating sheets to collect terrestrial invertebrates from leaf litter and riparian vegetation in 5 x 5 meter grids at 25, 50 and 75 meters, as well as three lateral distances (5, 10 and 15 meters) away from the streams. We predicted that: 1) a greater abundance and variety of invertebrates would be found along perennial streams compared to ephemeral streams and 2) a greater abundance and diversity of invertebrates would be found closer to the stream bed than further away laterally. Data analyses shows some support for our predictions. At both perennial and ephemeral sites, the richness of invertebrate orders and total abundance of invertebrates generally were higher closer to the streambed as opposed to farther away. Overall abundance of invertebrates was marginally higher in perennial streams compared to ephemeral streams. We hope our results will help predict how riparian invertebrate communities might change if drought and water withdrawals cause perennial streams to become ephemeral.

THU - 727 Initial Impacts of Hurricanes Irma and Maria on Migratory Bird Diversity on Punta Cucharas Natural Reserve, Ponce, Puerto Rico

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Ian Luis Maldonado Ortiz*, *University of Puerto Rico- Ponce*; Eduardo M. Llegus Santiago, *University of Puerto Rico, Medical Sciences Campus*; Gilmarie Rivera Castellar, *Para La Naturaleza* and Jose G. Rodriguez Ramirez, *University of Puerto Rico- Ponce*

Abstract: Birds all over the world migrate to Puerto Rico during winter season looking for food resources and breeding sites. Migratory birds have an important role as bioindicators of environmental conditions, pollination, seed dispersal and the trophic structure of Punta Cucharas Natural Reserve, yet habitat loss threatens their population. Punta Cucharas has an area of 35 hectares that includes mangroves, xerophytic forest, lagoons, salty plains, and sandy beach.The reserve provides habitat and stopover sites for over 80 endemic and migratory species birds, endemic and migratory. In September 20, 2017, Hurricane Maria's compelling winds and rainfall defoliated trees and flooded the breeding grounds of Punta Cucharas. We wanted to compare the estimated population size of bird species before and after Hurricane Maria. We conducted 10-minute bird counts in six different habitats from September to December during years 2016 and 2017 to assess the conditions in the habitats before and after the hurricane. We performed the Krustal-Wallis test ($\alpha=0.05$) to compare bird species diversity between habitats and years. We determined there was a significant difference in diversity of bird species ($P=0.01$, $dF=1$) between both years, and forest/mangrove habitats. Bird individuals declined in 52% from population after the impact from María. This assessment provides an initial information that will help to identify where post-Hurricane recovery efforts must be focused within Punta Cucharas. Our surveys inform us about changes in search for food supplies and habitat use by migratory birds, as well may serve as a post-hurricane baseline to monitor avian population responses over time.

THU - 728 The Cellular Process behind Unisexual Flower Development in *Cylindropuntia Wolfii*

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Amy Orduño-Baez*, *San Diego State University*; Niveditha Ramadoss, *San Diego State University* and Lluvia Flores-Renteria, *San Diego State University*

Abstract: Although most plants are hermaphrodites, unisexuality has evolved independently multiple times in evolutionary history as a preventative measure to selfing. There are two major pathways that drive unisexuality in plants, 1) Sterility and 2) Inception. It has been found that sterility can be attributed to Programmed Cell Death (PCD), a process of cell suicide known to control the developmental process in flowering plants. As the family of Cactaceae has wide polymorphism in sexual systems, this was considered an ideal model to study sexual reproduction in plants. *Cylindropuntia wolfii* has been reported as gynodioecious meaning having populations with female and hermaphrodite plants. However, in 2017 we identified some individuals with aborted ovules, leading to more unanswered questions about *C. wolfii's* sexual system. Our main goal is to accurately identify the sexual system of *C. wolfii* and understand the cellular mechanisms leading to that system. We predict that *C. wolfii* will be functionally dioecious driven by PCD. We have used histological approaches to confirm the sexual development and have found individuals with functional male and individuals with functional female flowers, suggesting *C. wolfii* has a functional dioecious system. TUNEL assay will be conducted to detect DNA fragmentation in male and female ovules and anthers to evaluate the role of PCD as the mechanism driving unisexuality in *C. wolfii.* By analyzing the cellular mechanism that determines sexual separation in *C. wolfii* we will have a greater understanding of the evolution of unisexuality and can apply it to the conservation of this endemic cactus.

THU - 729 Investigating the Potential of Soil Microbiomes from Fallow Agricultural Fields to Improve the Pest Resistance of Crops

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Christian Munoz*, *Cornell University*; Mia Howard, *Cornell University* and Andre Kessler, *Cornell University*

Abstract: Crop species are known to be susceptible to herbivore attack, reducing agricultural yields. The soil microbiome has been known to affect complex plant phenotypes, including resistance to insect pests. We previously found that the resistance of a native plant, *Solidago altissima*, against herbivores increased when it was inoculated with soil microbiomes from late old field (fallow) ecological succession. In this study, we sought to assess an agricultural application of this finding by examining whether fallow fields cultivate soil microbial communities with an increased potential to improve the resistance of crop plants to insect pests. We inoculated four crop species (maize, cucumber, lettuce, and tomato) with soil microbiomes from conventional maize fields and three stages of old field succession (fallow for 1, 3, and 16 years), and compared their growth and herbivore resistance. In order to assess the resistance of the plants to herbivores, we compared the feeding preference of two different species of common crop pests, *Trichoplusia ni* and *Spodoptera frugiperda*, for plants treated with the different soil microbiomes. Our preliminary results indicate that the successional age of microbiomes can influence the growth of lettuce plants and that the herbivores were less likely to eat cucumber plants inoculated with agricultural microbiomes than the other respective successional years. Manipulating crop microbiomes is increasingly looked at as a tool for sustainably improving agricultural production, and this research will help us learn more about the interactions between soil microbiomes, herbivory, and the plants we consume.

THU - 730 Do Phage-Resistant *Pseudomonas Syringae* Revert Back to Sensitivity in the Absence of Phage?

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Nina De Luna*, *The Pennsylvania State University*; Reena Debray, *University of California, Berkeley* and Britt Koskella, *University of California, Berkeley*

Abstract: *Pseudomonas syringae* is a bacterial pathogen that infects economically important crop species. Bacterial viruses called bacteriophages (phages) are capable of infecting and killing *P. syringae;* however, strains of *P. syringae* may develop resistance to bacteriophages. Resistance may be accompanied by costs or trade-offs between phage-resistance and other traits that influence bacterial fitness. The costs of resistance may manifest through a slower growth rate, decreased virulence and ability to compete within the microbial community, or enhanced susceptibility to other phages. Given that costs may accompany resistance, we seek to understand whether phage-resistant *P. syringae* revert back to sensitivity when experimentally evolved in the absence of phage. Prior to this experiment, replicate lines of *P. syringae* were evolved in either the presence or absence of the focal phage, FRS. Our preliminary findings demonstrate that initially phage-resistant *P. syringae* exhibit a slower growth rate than their sensitive counterparts, but after multiple passages, the growth rates of the resistant lines catch-up to the those of the sensitive lines. Resistance assays were also performed using phages in addition to FRS. We found that resistance to FRS seemed to be linked to greater resistance to distinct phages.

Growth rate, susceptibility to distinct phages, virulence, and competitive ability will be tested at different time points throughout the experiment to determine the costs of resistance, and understand how they contribute to the maintenance of resistance. Ultimately, understanding the costs of phage-resistance and how resistance is affected in the absence of phage can help shape better phage therapy treatments.

THU - 731 Relationship between Settlement and Resultant Recruitment, Size, and Mortality of the Olympia Oyster, *Ostrea Lurida*, across Two Bays in Southern California

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jesus Torres*, *California State University, Fullerton*; Danielle Zacherl, *California State University, Fullerton*; Rick Torres, *Cal State University of Fullerton*; Bryce Perog, *Cal State University of Fullerton* and Salvador Gutierrez Gutierrez, *California State University Fullerton*

Abstract: Urban development, disease, pollution, and overharvesting have had drastic effects on marine species within California estuaries, including the Olympia oyster, *Ostrea lurida*, which is now considered functionally extinct throughout its range. Oysters are a foundation species that help sustain biodiversity, prevent erosion, and act as biofilters that improve water quality in marine habitats and are therefore common targets of restoration in southern California. Ideal restoration sites would support high densities of oysters able to grow to their maximum size range but these may not be sites that receive maximal oyster settlement due to possible density dependent recruitment. We investigated the correlation between *O. lurida* settlement, recruitment, resultant size, and mortality rates by deploying and collecting ceramic tiles at 0 m and + 2 m MLLW from May to September, 2018 at E Street and Grand Caribe in San Diego Bay and Coney Island and 15th Street in Newport Bay, CA. We hypothesized that sites with greater settlement will experience greater recruitment and mortality, but recruitment will plateau at a threshold, average and maximum size will plateau at a lower threshold, and the sites with highest recruitment will experience the highest mortality rates. Preliminary results from retrieved tiles so far show that recruitment was greatest at 0 m MLLW across all sites, and among sites was greatest at Grand Caribe and lowest at Coney Island. Identifying ideal sites and tidal elevations that maximize recruitment and oyster growth can enhance future oyster restoration efforts.

THU - 732 Salinity Responses of the Desert Shrubs *Isocoma Acradenia* and *Larrea Tridentata*

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jennifer N. Ibarra*, *California State University, Fullerton*; Kevin S. Whittemore A.A., *California State University, Fullerton*; Abigail Cho, *California State University, Fullerton*; Taylor E. Naquin, *California State University, Fullerton*; Mayra A. Silva, *California State University, Fullerton*; Julia B. Teeple, *California State University, Fullerton*; Kerri Mocko, *California State University, Fullerton*; Jochen H. Schenk, *California State University, Fullerton*; Jennifer L. Burnaford, *California State University, Fullerton* and William J. Hoese, *California State University, Fullerton*

Abstract: Desert organisms are great for studying adaptive responses to high-stress environments. For example, desert plants must cope with limited water availability and high exposure to solar radiation and in many desert environments also with the accumulation of salts into their soils. Saline soils inhibit or even prohibit the growth of plants via ion toxicity and osmotic stress. We investigated the salinity responses of two desert shrubs, *Isocoma acradenia* and *Larrea tridentata*, on a slope adjacent to Soda Dry Lake in the Mojave Desert, California, hypothesizing that ion concentrations in these shrubs would be related to the salinity of the surrounding soil. We collected predawn plant and soil samples in 30-40 meter intervals along a belt transect from the dry lakebed up the slope and measured soil conductance and ion concentration in xylem sap and leaves. Conductance was higher in soil associated with *Isocoma* (mean ± SE: 5447.50 ± 5038.75 μS/cm) than with *Larrea* (mean ± SE: 90.63 ± 23.13 μS/cm). *Isocoma* leaves contained about 4× more sodium (mean ± SE: 549.19 ± 19.94 mmol/kg) than potassium (mean ± SE: 133.73 ± 18.75 mmol/kg), and *Larrea* leaves maintained a 1:1 ratio. Trends were similar in xylem sap, with *Isocoma* having higher levels of both ions than *Larrea*. *Isocoma* may concentrate sodium in leaves or excrete it. It's notable that plants sharing similar distributions have such different ion concentrations. There are no previously described salt-excreting members of *Asteraceae*, and if *Isocoma* can be confirmed as such, it will be a new discovery.

THU - 733 Recovery in Midrib Vein Embolism of Two Diverse Species Exposed to Different Levels of Drought and Rehydration Time

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Monserrat Orozco*, *California State University, Los Angeles* and Christine Scoffoni, *California State University, Los Angeles*

Abstract: Climate change is generating an increase in drought severity and frequency throughout different regions in the globe. Extended drought cycles play an important role in land degradation processes and affect geographical areas. It is crucial to investigate how plant species respond to drought and how/if they can recover. During a drought, air bubbles can seed into the leaf xylem, which transports water throughout the leaf, causing the xylem conduit to embolize and could lead to plant death. It is still unclear whether plants can easily recovery from these embolism events. In this study, we investigated the differences in recovery in embolism across two diverse species, Magnolia grandiflora and Lantana camara, dehydrated to different drought levels and rehydrated for different times. Our results showed that for both species, the percent recovery from embolism significantly varied with rehydration time treatments (the longer the rehydration time, the higher the recovery), but the level of dehydration to which samples were previously exposed to prior to rehydration did not impact the percent recovery in embolism. Samples recovered in similar amounts when exposed to similar rehydration times, regardless of whether they had previously been dehydrated to wilting point, or exposed to stronger drought. Notably, while both species did not significantly differ in the amount they recovered after 5min and 1h, Lantana camara recovered completely from embolism after 12h rehydration, while Magnolia grandiflora only recovered partially. These results suggest that at the leaf level, recovery from embolism is a lengthy process, and unlikely to occur in nature.

THU - 734 Species Delimitation and Distribution of the Tropical Tree *Protium Subserratum* using Morphometric Methods and Digital Soil Maps

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Austin Betancourt*, *San José State University*; Tracey Simmons, *San José State University*; Benjamin Carter, *San José State University* and Tracy Misiewicz, *University of Oklahoma*

Abstract: The lowland Amazon rainforest is a biodiversity hotspot with more tree species per unit area than any other forest on earth. In spite of this diversity few studies address questions about speciation and natural selection in the tropics. The Amazon tree *Protium subserratum,* is an ideal system to study how natural selection in different habitats can lead to the formation of new species. *P. subserratum* is a common, tropical tree and its range extends across the entire lowland Amazon basin. In the Western Amazon it is known to have distinct populations adapted to different soil types. Populations found on clay, brown sand and white-sand soils in Peru exhibit morphological and genetic variation that corresponds with habitat type and are thought to represent recently formed species. Yet variation in morphology across the entire range remains unquantified and it is unclear how many undescribed species may actually exist under the current classification of *P. subserratum*. Leaf morphology data will be collected from over 300 specimens of *P. subserratum* from across its range. These data will be analyzed using normal mixture models (NMM), a novel method for species delimitation based on morphology which, unlike traditionally used statistical methods, does not require an *apriori* hypothesis of species assignments. Individuals assigned as putative species will then be mapped with soil data to determine whether geographic or edaphic affinities exist. This work will inform our knowledge of speciation and taxonomic classification in Amazon trees.

THU - 735 Functional Analysis of Three TIR-NBS-LRR Genes in the Regulation in Leaf Senescence in *Arabidopsis thaliana*

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Lillian Wang*, *California State University, Long Beach* and Judy Brusslan, *California State University of Long Beach*

Abstract: Leaf senescence is the final stage in leaf development when the plant relocates its nutrients from aging leaves to developing tissues such as seeds. The molecular events of leaf senescence can be studied by isolating mutants in potential regulatory genes and then quantifying leaf senescence in these lines. The TIR-NBS-LRR (TNL) gene family encodes disease resistance cytoplasmic signaling proteins with an estimation of 149 TNL genes in the *Arabidopsis thaliana* genome. The expression level of two TNL genes from the H family, AT4G14370, and AT4G11170, are up-regulated during leaf senescence and AT1G63860 maintains a constant level of expression. These signaling proteins may play a role in regulating leaf senescence. T-DNA insertion mutants that disrupt each of the three genes were isolated. The single mutants display no obvious changes in senescence. We hypothesize that the TNL-H genes compensate for one another and that a triple mutant may show altered leaf senescence. An experiment to quantify senescence-associated gene expression by real-time qPCR and chlorophyll loss will determine if there is a significant difference in leaf senescence among single, double, and triple mutants. Triple mutants have been isolated and senescence phenotypes are being measured for each line. Determining whether TNL proteins contribute to the regulation of leaf senescence can help decipher the complex pathways that signal leaf senescence in *Arabidopsis thaliana* and may lead to increased efficiency in nitrogen recycling, which can reduce the need for fertilizers in commercial agriculture.

THU - 736 Molecular Tools May Help with Early Detection of Invasive Plant Species: A Case Study with *Typha Domingensis*

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Gloria Rios*, *Northeastern Illinois University*; Samantha Garcia, *Northeastern Illinois University* and Pamela Geddes, *Northeastern Illinois University*

Abstract: There are three *Typha* species (cattails) in the midwestern U.S.: native *Typha latifolia*, invasive *Typha angustifolia*, and an aggressive hybrid between the two, *Typha x glauca*. First-time sightings of southern cattail, *T. domingensis*, were reported in Wisconsin and Ohio way beyond its native range. This northward expansion may promote hybridization between *T. domingensis* and the midwestern species creating aggressive hybrids that decrease native plant biodiversity as has been documented for *Typha x glauca*. Additionally, since these four *Typha* species are morphologically very similar, it is difficult to identify them visually. Recent studies suggest that molecular analysis can accurately identify *Typha* species. Therefore, we hypothesized that molecular markers (microsatellites) would provide a genetic signature unique to *T. domingensis* allowing its differentiation from the midwestern cattails. We genetically tested 11 *T. domingensis* samples collected from its native range in Florida using 6 microsatellite markers that have been diagnostic for the midwestern cattails. However, results from those markers were inconclusive. Therefore, other previously-developed markers from *T. angustifolia*, *T. latifolia*, and *T. minima* were tested on the FL samples. Four of the 11 *T. angustifolia* markers showed they may be reliable indicators of *T. domingensis*. We are currently testing 7 primers from *T. latifolia* and 17 from *T. minima* to expand the number of diagnostic markers. Finding a genetic signature unique to *T. domingensis* is a priority so that we can continue to monitor its invasion and possible hybridization, and act before areas become dominated by it.

THU - 737 Analysis of Taxonomy and Function of Tonga Trench Microbes Using Metagenomic Analysis

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Joshua Sakai*, *Willamette University* and Rosa León-Zayas, *Willamette University*

Abstract: The Tonga Trench, located in the South Pacific, is the second deepest trench in the world, with a maximum depth of 10,882m. To our knowledge the samples taken during the Microbial Oceanography of the Tonga Trench (MOTT) Expedition at 400m, 3000m, 5000m, 9000m, and sediment are the deepest metagenomes analyzed to date, allowing for an unprecedented look of an understudied section of our planet. Using Next-Gen sequencing and metagenomics analysis organisms have been identified to the best of our ability through taxonomic and functional metabolic analysis. This has allowed for a more detailed assessment of the role specific Archaea and Bacteria classes across the Tonga Trench water column and sediments. Specifically, determination of taxonomy and function in deep sea microbial communities was used to compare abundance of traits across the depths of the column. One of the notable trends was a high degree of motility across all depths with phyla such as proteobacteria or Euryarchaeota throughout the column. However, bins of Thaumarcheota were found throughout many deeper parts of the column. This implies that while hadal biospheres are largely inhospitable to most life, some phyla either can move between the environments or possess novel metabolisms that make them competitive enough in either environment. Similarly, certain traits such as urea and chitin degradation appear to strengthen as depth increases potentially linking depth to selection for certain traits among microbial communities. This supports the idea that prokaryotes in deep sea biospheres trend towards specialization, novel fixation pathways, and novel metabolisms.

THU - 738 Effects of Human Secondary Metabolites in Cancer

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Delmarie Rivera Rodriguez*, *University of Puerto Rico at Bayamon*; Taotao Ling, *St. Jude Children's Research Hospital*; Walter Lang, *St. Jude Children's Research Hospital*; Michelle Martinez, *Univerisdad Central del Caribe-School of Medicine* and Fatima Rivas, *St. Jude Children's Research Hospital*

Abstract: Cholesterol represents close to 30% of the total lipid content of the cell membrane and is a critical component in maintaining cell homeostasis. Cholesterol serves mainly in cell membrane and lipid raft infrastructure, but some of its roles remain unclear. Upon cellular insult or a high-stress state, lipid peroxidation processes occur and one of the resultant peroxide metabolites is an oxidized cholesterol metabolite (CP). CP is a member of the sterol family of natural products, and displays a higher oxidized state. While natural endoperoxides products display a broad range of biological activities (i.e. anti-cancer, anti-fungal, anti-malaria, etc.), little is known about the biological properties of CP. Thus, the main objective of this study is to investigate the biological effects of CP against solid cancer models, particularly against colorectal cell lines (HCT116, HCT116 -/- p53, and RKO). We hypothesize that CP might act as a trojan horse, entering the cell via receptor-mediated endocytosis, and then inducing cell death by releasing its peroxide payload. To test this hypothesis, we use the following molecular biology methods during the study: a) mammalian cell culture protocols, b) cytotoxicity assays, c) cell cycle and cell death modalities assays, and d) western blotting to study mode of action. Our results indicate that CP inhibits cell proliferation, induces cell death in a dose-dependent manner and cell-cycle arrest. In conclusion, our studies will show for the first time that CP is a potential early-lead compound against cancer cell models.

THU - 800 Computational Exploration of the Chebyshev Bias

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Alayt Abraham Issak*, *THE COLLEGE OF WOOSTER*; Ghaith Hiary, *The Ohio State University* and Dhir Patel, *The Ohio State University*

Abstract: In 1853, the Russian mathematician Pafnuty Chebyshev observed an unexpected bias in the otherwise seemingly random distribution of prime numbers. For primes less than a given number , he stated that there were “many more” primes of the form 4m+3, denoted by Π(;4,3), than of the form 4m+1, denoted by Π(;4,1). This arithmetic bias in the distribution of primes is referred to as the Chebyshev bias. In this research, we define a function delta (δ) by the formula δ( ) =Π(;4,3) - Π(;4,1), which, according to the Chebychev bias, should be positive. Our preliminary computation shows that δ( ) is positive more than 99.9% of the time over selected ranges of ≤ 3×10^{7}. On the other hand, Rubinstein and Sarnak pointed out, and Kaczorowski proved that if the Generalized Riemann Hypothesis (GRH) is true, as is widely expected, then the natural density should not exist. Hence, for instance, the 99.9% figure would not be stable for large . We aim to find novel numerical evidence for this GRH prediction. We compute a natural density rescaled in accordance with the GRH, i.e. δ( )√ /Π( ), for large values and ranges of , as was initiated by Shanks and later by Brent in the analogous case of the Π( ) and li( ) race. Therefore, our work will (1) extend the range of previous computations, (2) implement an efficient algorithm for computing δ( ), and (3) consider reasons why the natural density would not exist and modifications to the usual definition of natural density.

THU - 801 Sum-Difference Numbers in the Ring of Integers Modulo N

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Joshua Crouch*, *Southern Nazarene University* and Nicholas Zoller, *Southern Nazarene University*

Abstract: In a 2010 paper, Shi fully characterized all sum-difference numbers in the positive integers. In this paper, a positive integer *n* is a sum-difference number if *n = xy = wz* and *x - y = w + z* where x, y, w, and z are positive integers. For example, 6 is a sum-difference number because 6 = 6*1 = 3*2 and 6 - 1 = 3 + 2. In order to expand on this interesting classification, this research focused on fully characterizing sum-difference numbers (congruence classes) in the ring of integers modulo *n* (*Z/nZ*). We hypothesized that a number in *Z/nZ* is a sum-difference number if and only if it corresponds to a positive integer that is a sum-difference number. However, this is not true. While every sum-difference number in the positive integers corresponds to a sum-difference number in *Z/nZ*, the converse is false. When *n* is prime, we primarily used the Law of Quadratic Reciprocity to characterize the sum-difference numbers in *Z/nZ*. For these cases, every element of *Z/nZ* is a sum-difference number unless *n* = 3 or 5. When *n* is composite, an element in *Z/nZ* is a sum-difference number if and only if it is a sum-difference number in *Z/fZ* where *f* is a factor of *n* with the exception of *n* = 4.

THU - 802 On (t,r) Broadcast Domination in Paths and Other Graphs

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Alexandro Vasquez*, *Manhattan College*; Sean Hays, *University of South Florida*; Pamela Harris, *Williams College*; Marissa Loving, *University of Illinois, Urbana-Champaign*; Gordon Rojas Kirby, *University of California, Santa Barbara*; Robert Rennie, *University at Illinois at Urbana-Champaign* and Natasha Crepeau, *Harvey Mudd College*

Abstract: If G=(V(G), E(G)) is a connected graph, then a subset D of V(G) is dominating if every vertex of V-D has at least one neighbor in D. A generalization of this concept is (t,r) broadcast domination. In this setting certain vertices are designated as towers of signal strength t, which send out signal to neighboring vertices decaying linearly as the signal traverses the edges of the graph. We let T be the set of all towers and we define the signal received by a vertex v in V(G) as f(v)= the sum of the max(0,t-d(v,w)), where w is a tower and d(v,w) denotes the distance between v and w. Blessing, Insko, Johnson, Mauretour (2004) defined a (t,r) broadcast dominating set, or a (t,r) broadcast, on G as a set T of V(G) such that f(v) greater than or equal to r for all v in V(G). The minimal cardinality of a (t, r) broadcast on G is called the (t, r) broadcast domination number of G.

In this poster, we present our research on the (t,r) broadcast domination number for graphs including paths and certain families of trees.

THU - 803 Predicting Dissolved Oxygen Levels in Loko ‘Ia (Hawaiian Fishpond) Using ODE

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Tanner Johnson*, *University of Hawaii - West Oahu* and Esther Widiasih, *University of Hawaii - West Oahu*

Abstract: In aquaculture and marine life in general, a factor that plays a significant role in maintaining a healthy ecosystem is the level of dissolved oxygen in the water. When oxygen levels drop below 5 ppm, most fish and wildlife experience stress or come at risk of death. This occurred twice in 2009-2010 at the He’eia fishpond in Oahu, where a combination of high temperature, low winds, and low tide caused spikes in fish deaths. These water quality variables are monitored in real time with observation nodes at several fishponds across Hawaii, including the Mokauea fishpond located off the southern coast of Oahu. An Ordinary Differential Equation (ODE) model developed by Xu, Zhen and Xu, Y. Jun (2016) combines water temperature, wind speed, chlorophyll-a level, as well as solar radiance to model dissolved oxygen level.

We hypothesize that this ODE model can be used to forecast dissolved oxygen levels at Mokauea fishpond to predict future fish kill events. Early results in our experiments using the Xu & Xu (2016) model show that a weakening of wind speed and increase in temperature could cause the dissolved oxygen level to fall below a safe range. Identifying a more specific parameter range in the model would be useful for the loko ’ia cultural practitioners in avoiding a potential fish kill scenario.

THU - 804 Development of Stable Approximations for the Vibration Control of Piezoelectric Devices

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Emma Moore*, *Western Kentucky University* and Ahmet Ozkan Ozer, *Western Kentucky University*

Abstract: Piezoelectric devices are elastic laminates with multiple active and passive bonded elastic layers. Active layers could be chosen as piezoelectric materials, a smart material to develop electric displacement that is directly proportional to an applied mechanical stress, and vice versa. Vibrations on these devices can be insulated by the active piezoelectric components, which can dampen vibrations by their actuation and sensing capabilities.

This project develops reliable computational tools to simulate the vibration control on a single piezoelectric layer, described by a novel “Partial Differential Equation” (PDE) model. Our computational tools are developed by emerging stable approximation techniques: “filtered” semi- or fully-discrete Finite Difference and Finite Element-based methods, proved to provide fast and reliable computation. These methods are simply based on filtering spurious high-frequency vibrations, as they provide a false stability result; that is, the approximate models do not mimic the behavior of the PDE models at all without filtering. Our numerical results will be compared to each other side by side and to the experimentally collected data as well. We plan to analyze each approximation by the discrete non-harmonic Fourier series and multipliers techniques to back up the simulations. Next, we apply the same approximation technique for controlling the vibrations on a three-layer piezoelectric device for which the existing literature lacks rigorous results.

Our computational tools are essential to provide new insights into the active controlling of piezoelectric devices, such as cardiac pacemakers, NASA/commercially-operated inflatable space antennas, etc.

THU - 805 Smart Assistance - a Machine Learning Project

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Vinh Bui*, *Bakersfield College*; Gabriel Diaz, *Bakersfield College* and Jonathan Brown, *Bakersfield College*

Abstract: Writing is essential for students' academic success. However, manual grading is a time consuming process, so it costs a lot of money to read and evaluate essays. Therefore, a tireless helper could share the burden with professors is needed. The project's goal is to create an automated assistant that can give grades to essays based on what she learns and justify her grades by providing evidence. In the first phase of the project we use a publicly available dataset to refine our approach. In a Latent Semantic Space we find by experimentation which variant of n-closest predicts grades best by different methods such as voting, mean, and median. We then use this as an input, along with more standard natural language algorithms, to produce our final Bayesian Decision Tree learner. In phase two we train our agent against our original datasets that we collected Bakersfield College professors. The models produced will be cross validated and then used by Bakersfield College Philosophy and English departments. By design, the models will provide graders with recommendations and allow the users to see the reasoning.

THU - 806 Mathematically Modeling the Financial and Social Effects from the Health and Sustainability Issues Occurring in the Migration Detention Centers at the U.S. - Mexico Border

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Ariel Ramos*, *Central Washington University* and Brandy Wiegers, *Central Washington University*

Abstract: As of July 2019, the United States government has reported a 66% increase in migrant children held in immigration processing detention centers. The increase of migration without evidence based policy is causing problems like overcrowding, unsanitary conditions, poor living environments, and decreases in the mental and physical health of the detainees in migration holdings. We are interested in the financial, social, and health effects that occur in the conditions these children are in. Our work will be centered around creating SEIR (Susceptible- Exposed- Infectious- Recovered) and SEIRS (Susceptible- Exposed- Infected- Recovered- Susceptible) models based around the diseases that enter these centers to determine how a disease would spread. The limited space the children are in would increase the chances of infection spreading much more. We are also interested in the negative social effects that stem from the children remaining in these holdings for long periods of time. The financial costs and benefits of maintaining and caring for the immigrant children within the centers will also be compared to other prospects we have found. Our models are made to explore the options that may help alleviate the issues present in these establishments with the goal of providing recommendations for the future policy within the Unites States to sustainability handle the influx of migrant children in these centers.

THU - 807 Solving Partial Differential Equations Using the Least Square Regression Method

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Luis Monje Maldonado*, *University of California, Merced*; Maxime Theillard, *University of California, Merced* and Arnold Kim, *University of California, Merced*

Abstract: Least-squares regression (LSQR) has been used extensively for modeling data. For that problem, we seek to approximate a polynomial that best fits a data set by minimizing the misfit of the model to the data. We review this method and apply it to model several examples of stock prices. Then we present our new LSQR based numerical method for solving boundary values problems for differential equations. Compared to traditional discretization techniques this new method offers the following advantages: (a) the implementation is straightforward (b) adaptive grids are easily handled (c) high order discretizations can be easily constructed. This new approach opens up the possibility of developing simple, efficient, and novel computational methods to simulate real-world phenomena with high accuracy at a minimal implementation cost.

THU - 808 Surface Tension Induced Folding- a Simplified Model

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Erica Ward*, *California State University, Fullerton*; Nicholas Brubaker, *California State University, Fullerton* and Jasmine Camero, *California State University, Fullerton*

Abstract: Optimization problems frequently appear in everyday life and in most physical situations there is a limiting constraint involved. In this study, we have built a mathematical model that will accurately predict when a paper structure will fold onto itself after a drop of water has started to evaporate from within it. By scaling down to a two-dimensional cross-section, we've analyzed the relationship between the angles with respect their vertical axes and constructed a model to measure the energy that is emitted from the changing positions. By using a combination of the method of the Lagrange Multipliers and creating a matrix of second derivatives of our model, we have composed a modified eigenvalue problem. Through further analysis, we have been able to determine the minimum amount of energy required to move the structure into its desired state. For our future work, we hope to continue analyzing this model with varied parameters to further understand the physical implications of this structure.

THU - 809 Spatial Dynamics of Myeloid-Tumor Cell Interactions Druing Early Non-Small Adenocarcinoma Development

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Peter Manosalvas*, *Eastern Washington University*; Arie Gurin, *Western Washington University*; Luis Perez, *California Lutheran University* and Henry Secaira, *Yachay Tech University*

Abstract: Lung cancer yields the greatest mortality rate of all cancers in the United States. Among the types of lung cancer, non-small cell adenocarcinoma occurs most commonly in non-smokers. The immune system is the body's first response to abnormal cell behavior. However, tumor progression often evades the immune system's response and grows uncontrollably. This is a result of both tumor selfdefense mechanisms inhibiting the maturation of myeloid cells in the environment, and/or natural spatial barriers of clumped tumor mass. We use a stochastic Cellular Automaton (CA) model to study the spatial dynamics of the immune cells (myeloid cells and T-cells) in response to tumor progression. This research explores how local effects of tumor defense mechanisms affect the spatial dynamics of tumor growth in terms of myeloid cell maturation and tumor proliferation. The mathematical analysis includes a mean-field approximation (MF) through a system of ordinary differential equations. The MF model is a non-spatial approximation to the spatially explicit Cellular Automaton model. We use numerical simulations to explore the control and growth of tumor progression. The results suggest that it is insufficient for mature myeloid cell quantities to surpass tumor cell quantities in order to eradicate tumor cells or vice versa.

THU - 810 Disease-Driven Dynamics of Evolutionary Rescue from a Game Theoretic Perspective

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Ana Kilgore*, *Colorado College* and Nina Fefferman, *University of Tennessee, Knoxville*

Abstract: Changing habitat ranges and shifting environmental conditions are altering the disease landscapes for hosts, vectors, and pathogens. Epidemiological modeling is an integral aspect of mathematical biology and has greatly furthered research and assessment of at-risk populations, attempting to holistically capture the impacts of pathogens upon a host population. Accurately portraying these epidemiological patterns requires an understanding of the host's behavioral and evolutionary patterns, especially when attempting to capture the dynamics of a population experiencing pressures that impact their shifting environments. Evolutionary game theory has been used previously to analyze the payoffs associated with and predict the results of completing strategies. As one of the first steps in an ongoing project to model the impacts of a shifting climate on the coevolution of vector-borne avian malaria in the Hawaiian Honeycreeper population, we integrated game theoretical breeding dynamics into a diseased population model undergoing environmental changes, representing real-life pressures such as habitat loss and climate change.

Our preliminary model explores the evolutionary dynamics of a host population facing selective pressures, focusing in particularly on evolutionary rescue. Evolutionary rescue may be defined as rapid adaptation of a species to avoid extinction due to an environmental change. Our goal is to explore and produce population dynamics resembling evolutionary rescue and identify factors that create this phenomenon within the host population. Our preliminary results demonstrate that a robust mutant type population less susceptible to infection grows more successfully than the more susceptible wild type population under the pressure of disease with a high transmission rate.

THU - 811 Quantum Metrics on the Diagonal of the Quantum Podleś Sphere

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Olga Bustamante*, *Arizona State University* and Konrad Aguilar, *Arizona State University*

Abstract: If a real-valued function is differentiable with bounded derivative, then its maximum slope can be calculated using standard calculus, which provides vital information about a given function. When a continuous function is not differentiable, it may be the case that this function has a maximum slope but this requires much more advanced methods to calculate. One method to approach this is to use the Lipschitz seminorm, but this does not come from a process like derivation and can be quite difficult to calculate. Another method comes from the work of M. A. Rieffel, which provides a more algebraic method for calculating a new version of maximum slope using the notion of a quantum metric space and Lip-norms. K. Aguilar and J. Kaad were able to produce a quantum metric on certain continuous functions that have no derivative that are taken from the diagonal of the quantum Podleś sphere. Our work thus far has translated the constructions presented by Aguilar and Kaad into explicit formulas on certain types of the functions they work with. This not only has allowed us to study this quantum metric in more detail, but also has provided comparisons between this new version of maximum slope with the classical version provided by the Lipschitz seminorm. Thus, our research has solved some of the mystery of the analytical behavior of these continuous functions of the Podleś sphere by studying and comparing both the classical notion of maximum slope and the quantum metric maximum slope.

THU - 813 Spatial Variation in Infantile Hypertrophic Pyloric Stenosis in Iowa, 2001-2015

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Jacob Oleson, *University of Iowa*; Paul Romitti, *The University of Iowa*; Amy Hahn, *The University of Iowa*; Lino Yoshikawa*, *University of Hawaii at Hilo*; Eliezer Santos, *University of Puerto Rico-Medical Sciences Campus* and Lianne Novak, *Michigan Technological University*

Abstract: Previous studies suggest that infantile hypertrophic pyloric stenosis (IHPS) has a multifactorial etiology that includes both genetic and environmental (broadly defined) factors. Beyond genetic predisposition, numerous environmental factors have been suggested, but only a few factors have been replicated. To expand the search for environmental risk factors for IHPS, we examined spatial variation in the occurrence of this birth defect using data for a 15-year cohort of IHPS cases (2001-1015) obtained from the Iowa Registry for Congenital and Inherited Disorders (IRCID) and compared these data to all Iowa live births during the same time period. We analyzed the geocoded coordinates of maternal residential address at birth to detect geographic clusters of IHPS using generalized additive models. We also estimated odds ratios using simple logistic regression models for selected variables, including child sex and birth year and maternal age, race/ethnicity, and gravidity to include as covariates in our spatial models. Findings generated from our spatial models will be used to identify “hot spots” of IHPS occurrence for further interrogation of environmental factors.

THU - 814 Peg Solitaire in Three Colors on Double Star Graphs

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Alexxis De Lamere*, *Hawaii Pacific University* and Tara Davis, *Hawaii Pacific University*

Abstract: Peg solitaire is a one-person game that has been played on various types of boards for over 300 years. In this poster we follow the work of Beeler and Hoilman by playing on mathematical graphs instead of on traditional game boards. We generalize their work by allowing for multicolored pegs; an innovation that produced different results from previous work done in only two colors. The main problem that we consider is determining the solvability of the peg solitaire game on double star graphs in three colors. Our hypothesis was that the addition of a third color would lead to a greater number of possible game moves, and therefore, more double star graphs being classified as freely solvable. We prove that for R>2, the double star graph DS(L,R) is freely solvable if L=R; it is solvable if L=R+2; and it is solvable but not freely solvable for L=R+1. In the L=R case, we produce an algorithm to win any possible game. In the L=R+1 and L=R+2 cases, we provide the necessary examples of winning and losing games. Each of our theorems was discovered by extensively playing games using a combination of educated repetitive guessing and trial and error. We will also shed light on open questions that may be answered with the techniques we developed, as well as future directions for this research program.

THU - 815 Estimation of Hidden Ancestry Substructure Using a Least Squares Mixture Model with Summary Genotype Frequency Data

Discipline: Mathematics
Subdiscipline: Statistics

Ian Arriaga-MacKenzie*, *University of Colorado Denver*; Alexandria Ronco, *University of Colorado Denver*; Gregory Matesi, *University of Colorado Denver*; Ryan Scherenberg, *University of Colorado Denver*; Yinfei Wu, *University of Colorado Denver*; James Vance, *University of Colorado Denver*; Jordan Hall, *University of Colorado Denver*; Christopher Gignoux, *University of Colorado, Anschutz*; Megan Null, *University of Colorado Denver* and Audrey Hendricks, *University of Colorado Denver*

Abstract: Recent advancements have resulted in large publicly available genetic databases that are invaluable resources in the genetics of health and disease. Over 80% of large-scale genetic research has been in cohorts of European ancestry, limiting the understanding of this research overall and specifically in non-European ancestries. These publicly available databases contain non-European ancestries and could be used to increase diversity in genetic research. However, summary level genetic data can mask ancestry information, limiting the ability to associate ancestry with genetic conditions.

We develop a probabilistic mixture model that uses a reference dataset of ancestries to estimate the proportion of each ancestry in genetic databases. We then extend this method to identify ancestries not in the reference dataset. To do this, we identify an exponential relationship between the percentage of ancestry not present in our reference data and the mean square error of our model, and use this relationship to estimate a range for the proportion of hidden ancestry.

We evaluate our method in hundreds of simulation scenarios using combinations from a reference ancestry dataset of five broad ancestry groups (non-Finnish European, South Asian, East Asian, African, and Native American). Our method is easily expanded to other reference ancestries. We then apply our method to the African and Latino ancestry datasets in the Genome Aggregation Database and estimate the proportion of both known and unknown ancestries. Our method will allow for accurate interpretation of the proportions of ancestry in these and other genetic databases for use in large-scale genetic studies.

THU - 818 A Computational and Experimental Investigation of Relationships between Magnetic Resonance Diffusion Tensor Imaging Fractional Anisotropy and Applied Mechanical Strain

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Ouniol Aklilu*, *Pennsylvania State University* and Reuben Kraft, *Pennsylvania State University*

Abstract: Traumatic brain injury (TBI) and related disability affects more than 2% of the U.S. population. Diffuse axonal injury (DAI) is a common pathology associated with TBI in which deformation of axonal cells leads to rupture and axonal degeneration. DAI can be observed in white matter tissue in the brain, which consists largely of bundles of aligned, myelin-sheathed axons. State-of-the-art imaging techniques (magnetic resonance diffusion tensor imaging, or MR-DTI) can be used to visualize these fibrous structures. However, sensitive measures of structural changes due to injury that can be detected with MR-DTI, notably fractional anisotropy (FA), show conflicting trends in how FA changes in response to injury. FA values can be obtained through analyzing the MR-DTI using applicable software such as FMRIB Software Library (FSL). In this work, we provide a detailed examination of the correlation between MR-DTI changes and mechanical strain using an experimental and computational investigation approach. The research is classified into a three step process which consists of 1) pre-imaging the sample of interest to obtain undamaged MR-DTI data of the sample, including FA measures 2) impose mechanical strain on the sample to cause deformation and rupture of the fibers in the sample and 3) obtain a post MR-DTI image of the sample to observe changes in FA. This presentation will focus on the MR-DTI data, mechanical testing and finite element simulation that have been conducted to correlate mechanical strain with changes in fractional anisotropy. In the future, the research will be expanded using high-quality MR-DTI phantoms.

THU - 819 Comparing Thromboelastography (TEG) and Turbidity to Monitor Bovine and Human Fibrin Clot Formation at Increasing Thrombin Concentrations

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Mahussi Fagnon*, *Indiana University - Purdue University Indianapolis*; Ziqian Zeng, *Purdue University* and Nathan Alves, *Indiana University School of Medicine*

Abstract: Monitoring clot formation and digestion dynamics under different conditions is important in determining a patient's hemostatic state. For this study, turbidity and thromboelastography were used to monitor clot formation in a simplified fibrinogen/thrombin clot model to compare these different clot interrogation tools. Turbidity is a common laboratory method used by researchers to monitor clot formation by taking optical measurements via a microplate reader. Turbidity measurements were tracked over time at 405 nm in 96-well plates at room temperature. Alternatively, thromboelastography is a direct viscoelastic measurement of clot strength that utilizes a specialized TEG5000 instrument and is primarily a clinical diagnostic tool. While TEG has many experimental outputs, the maximum clot strength (MA) and time to reach MA (TMA) were utilized for this study to compare to the maximum turbidity (MT) and time to reach MT (TMT) via turbidity analysis. For both techniques, fibrin clots were formed by adding either human or bovine fibrinogen (3 mg/mL) to increasing concentrations of human or bovine thrombin (0.1 to 10 U/mL). Results demonstrate that in both human and bovine, increasing thrombin concentrations increases the maximum clot strength (MA=5.1 to 35.6 mm and 15.6 to 22.8 mm, respectively) but decreases the maximum turbidity (MT=0.79 to 0.26 and 1.42 to 0.18, respectively) with no significant differences observed in clot formation time. These results demonstrate that TEG and turbidity may be interchangeable for tracking clot formation time but TEG is necessary to determine clot strength as clot strength and turbidity are inversely proportional.

THU - 820 Multilayer Stackable Tissue Culture Platform for 3D Co-Culture

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Rishabh Hirday*, *Rutgers, The State University of New Jersey*; Ileana Marrero-Berrios, *Rutgers, The State University of New Jersey*; Rene Schloss, *Rutgers, The State University of New Jersey* and Martin L. Yarmush, *Rutgers, The State University of New Jersey*

Abstract: In vitro cell culture and the study of single cell populations allow for the study of simplified versions of complex cell systems. However, as we try to simplify the cellular environment, the physiological relevance of observed results may come into question due to the lack of microenvironmental factors that help determine cell behavior. Currently, the standard method to study paracrine interactions between cells in co-culture includes the use of permeable supports with porous membranes, commonly known as transwells. These transwells are limited to one per well, meaning the interactions between a maximum number of two cell cultures can be studied; this is inadequate for more complex systems. We have created a stackable device that allows for any number of cell cultures to be cultured within the same well, limited only by the height of the well itself. The device consists of a permeable membrane attached to an acrylic support by chemical adhesion. The membrane is treated to increase hydrophilicity and cell attachment and is ready to use within hours after creation. So far, initial testing has indicated that these devices have similar levels of cell attachment and viability as commercially available transwells. Current testing is focused on studying cell viability and cell secretion when greater than two cell cultures are incubated in the same well. Perfecting this device to allow for the culture of multiple cell types in vitro will help future studies build more accurate models of physiological research and open doors into the research of complex cell systems.

THU - 821 Evaluation of Antimicrobial Activity of Alzheimer's Amyloid-ß Peptide

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Chris Hunter*, *University of New Mexico*; Adeline Fanni, *University of New Mexico* and Eva Chi, *University of New Mexico*

Abstract: Alzheimer's Disease (AD) affects thirty million people worldwide and a primary hallmark of the disease is plaques composed of amyloid-ß (Aß) fibrils. The cause is unknown, yet observations of abnormal microbiota and the co-localization of viral DNA and inflammation with AD pathology have led to a novel hypothesis that Aß expression and deposition may be central to its function as an antimicrobial peptide (AMP).

Our research seeks to elucidate how Aß functions as an AMP by investigating its toxicity toward bacteria using a live/dead assay via flow cytometry and a metabolic assay of viability. Flow cytometry has shown a deleterious effect of monomeric Aß on *E. coli* viability in the stationary phase of growth, where coincubation with concentrations of 50 µg/ml and 100 µg/ml for three hours has resulted in 34% and 48% increases in nonviable cells, respectively.

To investigate the mechanism of Aß's antimicrobial activity, we are studying interactions between Aß and bacterial and mammalian cell mimic membranes. We measured the insertion of Aß into anionic (bacterial mimic) and zwitterionic (mammalian mimic) lipid monolayers at the air-water interface in a Langmuir trough. Our results show that Aß spontaneously inserted into anionic DMPG and DMPC/LPS membranes, disrupting membrane morphology, yet didn't insert into zwitterionic DMPC monolayers. This suggests Aß favorably and selectively interacts with bacterial membranes, possibly contributing to its selective antimicrobial activity. Understanding Aß's antimicrobial activity can shed light on the role of infection in AD, with the potential to lead to better detection and treatments for the disease.

THU - 822 Dual Encapsulation of Neurotrophic Factors for Targeted Drug Delivery

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Elisheva Strauss*, *Rutgers, The State University of New Jersey*; Xiomara I. Perez, *Rutgers, The State University of New Jersey*; Mollie Davis, *Rutgers, The State University of New Jersey*; Rene S. Schloss, *Rutgers, The State University of New Jersey* and Martin L. Yarmush, *Rutgers, The State University of New Jersey*

Abstract: Traumatic brain injury (TBI) leads to a cascade of neurodegenerative events. As a result of primary injury, neuronal axons are physically damaged, leading to secondary injury, including inflammation. To aid in functional recovery of neurons, a multimodal therapy which can promote neuro-regeneration is required. Although current therapies aim to treat the associated symptoms, the addition of positional control of therapeutics allows for directed and sustained delivery to the injury site. Therefore, our group is encapsulating neurotrophic factors (NFs) in nanoparticles (NPs) constructed from lipid or a polymer, and further encapsulating these NPs in a hydrogel. Encapsulating NFs, which aid in survival and regeneration of neurons, within NPs will assist in drug delivery; while further encapsulating the biomolecule-loaded NPs in alginate enables localization and sustained release. The purpose of this study is to optimize the ideal material necessary to synthesize NPs that can be used to ensure adequate encapsulation as well as sustained release. The lipid NPs were synthesized using a dehydration-rehydration protocol whereas the polymeric NP were constructed using a double emulsion protocol. In order to perform diffusion studies using a trans-well system, 0.5 ug/mL of albumin, a model protein, was encapsulated in the NPs. The diffusion values over time were obtained using an enzyme linked immunosorbent assay. Future work includes optimizing the proper concentration of protein to be encapsulated to enable release over a specified interval.

THU - 825 Using Organic Photo-Voltaics to Regulate Photobioreactor Temperatures and Improve Algae Growth

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Larry Moore*, *Dine College* and Don Robinson, *Dine' College*

Abstract: Concerns of Uranium and Arsenic groundwater contamination linger on the Navajo Nation. Current nano-filtration models remove these toxic substances from water and address broader southwestern water scarcity concerns. Nanofiltration, however, produces a concentrated toxic brine. Using micro algae to uptake heavy metals, a process called phytoremediation, offers a potential cost-effective management strategy. Phytoremediation in southwestern climates requires an algae species tolerant of heat and able to uptake metals, justifying the use of *Chlorella sorokiniana*. Despite its tolerance, excessive heat reduces its growth rate and thus the efficiency of phytoremediation. This research attempts to maintain optimal growing temperature within outdoor photobioreactors (PBRs). To simultaneously reduce heat and optimize photosynthesis, the PBRs are lined with organic photovoltaic solar panels (OPVs). This allows wavelengths optimal for photosynthesis (523nm to 625nm) to penetrate the system while utilizing the remaining wavelengths to generate energy. The hypothesis holds that OPVs will maintain temperatures below 40ºC leading to greater maximum concentration of algal biomass. The study will test four PBRs; two lined with OPVs and two without. Daily samples will be taken to determine the biomass concentration in each photobioreactor. Optical density will be measured daily by taking the absorbance of a 1mL sample at 750nm. Biomass concentration (g/mL) will be determined through optical density and ash free dry weight. An analysis of the data will indicate the maximum growth rate and biomass productivity. This will establish the efficacy of using OPVs to reduce heat buildup and improve algal growth and ultimately the efficiency of phytoremediation.

THU - 826 Evaluating the Mucoadhesive Properties of Functionalized Hydrogels to Treat Irritable Bowel Disease

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Ashley Santana*, *University of Central Florida*; Bradley Willenberg, *University of Central Florida*; Justine Tigno-Aranjuez, *University of Central Florida*; Edward Ross, *University of Central Florida* and Kaitlyn Crawford, *University of Central Florida*

Abstract: Irritable Bowel Disease (IBD) is a chronic gastrointestinal (GI) disease that comprises up to 50% of global GI related diagnoses annually. It is associated with motor dysfunction and somatovisceral sensitivity of the large intestine. Prescription drugs for IBD only provide short term remedies, as there is no long-term cure available. Topical treatments directed at reducing inflammation and improving drug absorption may provide viable routes to long term management of IBD. This current work evaluates the long-term effects of functionalized hydrogels and their ability to adhere to the intestinal wall as a therapeutic structure. The hydrogel being tested is a modification of the natural polysaccharide chitosan. Literature has shown that modified chitosan has the ability to bind to the mucosal layer and serve as a medium for mucosal drug delivery and relieve chronic inflammation. The goal of this study is to determine the mucoadhesive abilities of functionalized chitosan derivatives and its effect on the integrity of the mucosal layer. Functionalized chitosan as a bioadhesive for the large intestine has the potential to counter the motor and somatovisceral sensitivities of individuals with IBD. The mucoadhesive strength of the material is evaluated through three characterization tests. 180-degree tensile testing, rotating disk investigations, and roll off tests are the primary procedures conducted. Positive initial results have shown functionalized chitosan adhesion times greater than three weeks on the mucosal layer. Future work will analyze drug delivery rates in the presence of a functionalized chitosan bioadhesive. Presented are preliminary data for each characterization test.

THU - 827 Development of an Analytical Method to Measure Surfactant Concentrations in Samples from Surfactant EOR

Discipline: Engineering
Subdiscipline: Chemical Engineering

Romesha Abimbola*, *University of Kansas* and Karen Peltier, *University of Kansas*

Abstract: Surfactants are widely used in the oil and gas industrial for increased oil production with Chemically Enhanced Oil Recovery (EOR). The concentration and detection method at which these surfactants are tested has been a critical issue for oil producers. The objective of this research was to observe and developed an analytical method to measure surfactant concentrations in samples from Surfactant EOR. A series of experiments were performed using the High-Performance Liquid Chromatography Method to analyze the volume at which each concentration was detected. Two different surfactants, Petrostep S2 and A6 were tested at six diluted solutions of 0, 0.1, 0.02, 0.04, 0.06, and 0.08 percent. I developed concentration/calibration profiles to observe and determining the dynamic range and concentration limit of detection of both surfactants. The Student-t Test was used to determine the reproducibility for each surfactant at the various concentrations and uncertainty in the amounts detected. Surfactant A6 was prepared as heated and unheated to observe and compare different sample preparation techniques and to analyze concentration versus amount detected relationship change. In conclusion, the concentrations of surfactant A6 is detected accurately when heated before testing. The profile correlation between concentrations and volume detected showed as linear, where the minimal concentration detected is 0.02%. The detection range maximum is unknown, as the current peak area and height data collected follows a linear trend with no significant deviation from the trend. Therefore, more experiments using higher diluted concentrations are needed to identify the maximum concentration for the dynamic range for both surfactants.

THU - 829 Development of a Microfluidic Flow Cytometer: Reducing Excitation Light Noise with Optical Filtering

Discipline: Engineering
Subdiscipline: Chemical Engineering

Moses Begaye*, *New Mexico State University* and Jessica Houston, *New Mexico State University*

Abstract: Flow cytometers are instruments that analyze single cells and provide phenotypic, genetic, or morphological information at a very high throughput. These systems can sample cells at rates of thousands-per-second and are therefore essential for diagnoses of diseases such as cancer and immunological disorders. Cytometers operate by flowing cells in a fluid suspension through the path of a focused laser beam. As cells pass through the excitation source, fluorescence is emitted and detected if the cell is labeled with fluorescent markers. In this research we present the design of a new flow cytometer that utilizes acoustics to move cells through a microfluidic channel, which eliminates problematic pressure-driven flow (hydrodynamics). Part of our design considerations are to optimize the amount of fluorescence detectable when cells are excited by the laser. Yet, bright laser light is scattered by cells and results in a large background, or “noise,” signal. Since the background signal impedes our ability to detect the dimmer fluorescence, we hypothesized that a unique combination of spatial and fluorescence filtering will improve the overall signal-to-noise ratio. To test this hypothesis, we optimized the optical pathway using optomechanics on aluminum breadboards, translation stages, 30-mm alignment cages, dichroic beamsplitters, and holographic notch band-rejection and bandpass filters. We evaluate signal to noise by measuring photon flux. We calculated 10^{21} photons/second prior to the optimization and were able to reduce it to 10^{13} photons/second after the re-design. Our results are significant for this cytometer, which will be used for cancer research and other important biomedical applications.

THU - 830 Investigating Web Shear Development in Post-Tensioned Box Girders

Discipline: Engineering

Subdiscipline: Civil Engineering

Emmanuel Vazquez Arreola*, *University of California, Davis*; Sashi Kunnath, *University of California, Davis* and John Bolander, *University of California, Davis*

Abstract: Design of post-tensioned (PT) box-girder bridges is governed by the national AASHTO LRFD Bridge Design Specifications which requires a reduction (25% of the grouted duct diameter) of the effective girder width to calculate nominal shear resistance. Caltrans amended this provision allowing the full girder width be used assuming the conservatism in the code-based estimation of concrete shear resistance accommodates this concern of reduced shear strength in the presence of ducts. The AASHTO provisions recognize that PT-ducts alter the shear-flow in box-girders, based primarily on panel tests that represent an inclined compressive-strut formed during shear loading. However, no full-scale tests on PT-girders have been conducted in the United States. This research project investigates the development of shear-flow and the resistance provided by concrete, in the presence of a PT-ducts, by testing two full-scale box-girder specimens. The 5’-tall and 32’-long simply-supported specimen, with 6” soffit and 7.625” deck, will be loaded on the bottom flange to simulate the negative moment region adjacent to the column-support of a continuous bridge. The specimen is designed with an 8.5’X5’ critical-section where loading will expectedly result in shear failure, characterized by diagonal cracking in the web, initiating at the bottom corner near the loading and extending upwards. Findings from the testing will verify if the shear resistance of the girder is adequate to affirm Caltrans’ assumption that conservatism in concrete shear resistance estimate accounts for altered shear-flow in box-girders and allow Caltrans to continue current practice in neglecting web-width reduction in shear design of PT girders.

THU - 831 Investigating the Biogeochemistry of Phosphate Mobilization in Anaerobic Sediments Containing Iron and Sulfate in Experimental Wild Rice Mesocosms

Discipline: Engineering
Subdiscipline: Civil Engineering

Victoria Thrash*, *The University of Iowa* and Sophie LaFond-Hudson, *The University of Minnesota Duluth*

Abstract: Wild rice (*Zizania palustris)* or manoomin, in Anishinaabe, is a culturally significant food source for the Ojibwe people in the Great Lakes region and serves as a foundational ecological resource. Concerns over increased anthropogenic sulfate pollution have provoked examination to determine an appropriate sulfate standard for the state of Minnesota to protect the vitality of wild rice. In this study, we investigated how sulfate and iron in an experimental system interact to produce mobilized phosphate, a limiting nutrient for algae, in soil porewater. Sulfate reduces to sulfide in anoxic sediment, where naturally occurring iron (II) preferentially binds to sulfide, liberating phosphate anions contributing to algal blooms in experimental mesocosm tanks. We hypothesized that sulfate is directly related to algal productivity and tanks with more available iron reduce algal productivity. We collected surface and pore water using passive diffusion samplers placed in 32 mesocosms, 8 replicates of 4 treatments, containing controls, sulfate amendments, iron amendments, and tanks containing both sulfate and iron. Ion chromatography and spectrophotometry were used to quantify sulfide, iron, and phosphate concentrations in these samples and a multiparameter sonde was employed to quantify chlorophyll a concentrations in the surface water of each tank. It was observed that sulfate amended mesocosms contained more algal abundance suggesting that sulfate is directly related to liberated phosphate and eutrophication. These experiments emulate the natural geochemical processes of wild rice beds and help us understand the potential for algae to outcompete wild rice for light and nutrients due to increased sulfate pollution.

THU - 832 Comparing Untargeted Metabolomic VOC Analyses on Different Gas Chromatography Mass Analyzers: Single Quadrupole (MS) Vs Quadrupole Time-of-Flight (QTOF)

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Paula Angarita Rivera*, *Indiana University-Purdue University of Indianapolis*; Mangilal Agarwal, *Indiana University-Purdue University of Indianapolis*; Mark Woollam, *Indiana University-Purdue University of Indianapolis*; Meghana Teli, *Indiana University-Purdue University of Indianapolis*; Amanda Siegel, *Indiana University-Purdue University of Indianapolis* and Ali Daneshkhah, *Indiana University-Purdue University of Indianapolis*

Abstract: One in eight women will likely test positive for breast cancer in their lifetime. Therefore, it is important to diagnose potential patients before cancer metastasizes. Screening test are the primary method used by physicians to detect breast cancer in patients before a biopsy is performed. However, from the biopsy only 20% of those patients have breast cancer. The current screening method is not very efficient and there is no other method that accurately determines if a patient has breast cancer or not. Volatile organic compounds (VOCs) are metabolites that can serve as biomarkers for different types of diseases. An effective method to analyze these VOCs is using gas chromatography-mass spectrometry. There are two common mass analyzers which differentiate ions by their mass to charge ratio: single-quadrupole (GC-MS) and quadrupole time-of-flight (GC-QTOF). The goal is to demonstrate that these mass analyzers can identify the same statistically significant biomarkers that can distinguish between localized and delocalized breast cancer. Eight urine samples were collected from mice with cancer in the mammary pad and ten from mice with cancer metastasized to the bone. Multivariate analysis such as Principal Component Analysis (PCA), Linear Discriminant Analysis (LDA) and Leave One Out Cross Validation (LOOCV) were used to identify the statistically significant biomarkers present in breast cancer. The results demonstrate that 7 biomarkers are present in both data sets (95% accuracy). Furthermore, these biomarkers, if confirmed in human studies, could be used to design a resistive based sensor to detected breast cancer non-invasively in human urine.

THU - 834 Investing in Sustainability: 3D Printed Metal Gyroids

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Kennard Johnston*, *Morgan State University*; Douglas Hart, *Massachusetts Institute of Technology* and Matthew Pearlson, *Massachusetts Institute of Technology*

Abstract: 3D printed metal gyroids provide a promising ultra-strong, lightweight, and sustainably produced trajectory for investment-cast structures of all kinds. Gyroids are 3D assemblies of graphene, one of the stiffest and strongest materials. With their unique triply periodic, minimal surface area, and material-independent strength qualities, gyroids offer an improved alternative to traditional lattice structures. While these structures have the potential to be highly useful, current additive and subtractive manufacturing techniques inhibit them from being produced and used in the real world. This work explores proprietary methods to overcome this by combining computer aided design (CAD) produced software models that are then 3D printed via vat photopolymerization, and then investment-cast. To create metal gyroids, the structure is first fabricated using Autodesk Nettfabb Ultimate 2018, software “sliced”, printed on a stereolithography (SLA) apparatus (i.e. FormLabs 2) using cast-able resin that can “burnout”, invested, fired in a pre-programmed burn out oven, and cast with metal alloys such as aluminum. Cast parts’ strength, mass, and complexity are thus appropriately and specifically optimized with this combination of SLA technology, topological optimization software, and 3D printer enabled rapid prototyping. Increase of design and product flexibility makes the casting process less wasteful in material and more useful in real-world engineering applications; specifically structures. The production of these gyroids using existing and available resources highlights that the incorporation of them into the world is feasible and has potential to make cast metal gyroids a reality. Future work in this field includes mechanical testing, heterogenous configurations, and finer features.

THU - 835 Characterization of Electron Emission and Field Ionization Using Gated Silicon Nanotip Arrays

Discipline: Engineering
Subdiscipline: Electrical Engineering

Alvaro Sahagun*, *University of Illinois at Chicago*; Girish Rughoobur, *Massachusetts Institute of Technology*; Nedeljko Karaulac, *Massachusetts Institute of Technology* and Akintunde Akinwande, *Massachusetts Institute of Technology*

Abstract: The process of ionizing gases and emitting electrons from the surface of a solid is widely used in fundamental science and industry, such as in mass spectrometry, x-ray sources, electron microscopes, e-beam lithography, and more. However, the current methods used are bulky, costly, and inefficient. In this work, we explore the approach of using strong electrostatic fields to facilitate gas ionization and electron emission, also known as field ionization and field emission. We report gated silicon nanotip arrays with tip radii <10 nm that have demonstrated high-output current density (~100 A/cm^2), long lifetime under continuous use (>100 hours), and the ability to operate at low voltages (<30 V). These advantages are promising for high-scalability, low-power, compact, and inexpensive applications for emerging and existing technologies within the field. Despite these potentials, the non-uniform radii, low breakdown voltages, and the need for an ultra-high vacuum environment have limited the current use of nanotip arrays to research applications; however, we aim to change that. In this work, we characterize the electrical properties of large arrays of nanotips (>100×100 nanotips) for both electron emission and field ionization to design devices with enhanced performance. In electron emission, we investigate the current scalability, Joule heating effects, electric-field enhancement, array utilization efficiency, and the potential for operating in ambient environments using a graphene membrane to create poor-vacuum. In addition, we study the generation of ions from argon, deuterium, and helium using the strong electric field around the nanotip, which enables a stronger ion flux at low voltages.

THU - 836 Particle Internet of Things Air Monitoring System to Investigate the Relationship between Particulate (PM2.5) and Carbon Dioxide Concentration in Urban Locations

Discipline: Engineering
Subdiscipline: Engineering (general)

Margaret McCormick*, *Los Angeles City College* and Jayesh Bhakta, *Los Angeles Community College District*

Abstract: Monitoring air quality is increasingly vital given the current need for environmental protection around polluted cities. Using the hypothesis that vehicles are a significant source of outdoor particulate concentration (PM$_{2.5}$), it is expected there may be a correlation between outdoor particulate concentration and local CO$_2$ concentrations in urban locations. A Particle Internet of Things network creates an environmental monitoring system for exactly this purpose. An Internet of Things connects everyday objects and devices, allowing them to be remotely monitored and controlled. Using the platform Particle, the Internet of Things monitors PM$_{2.5}$, CO$_2$, temperature, humidity and location using GPS. The aggregate data collected is presented via a spatial data display using ArcGIS software. Previous testing using a single sensor did not find a correlation between outdoor particulate concentration (PM$_{2.5}$) and local CO$_2$ concentrations, but it is expected that expanding the range of the monitoring system will provide evidence of a correlation. The design of the sensor network and the results of the statistical analysis of the collected data will be presented.

THU - 837 Remediation of Soil and Water at Legacy Mining Sites

Discipline: Engineering
Subdiscipline: Other Engineering

Esai Lopez*, *New Mexico State University*; Catherine Brewer, *New Mexico State University - Department of Chemical and Materials Engineering* and April Ulery, *New Mexico State University*

Abstract: Legacy uranium mines in New Mexico are environmental and health hazards. Leaching from spent ore piles and mine tailings have concentrated radionuclides in the soil and water near mines. The hypothesis of the research is phytoremediation can be used to remove radionuclides in a cost-effective way from legacy mining sites in northwestern New Mexico. Radium will be more readily up taken compared to uranium. A greenhouse study was used to test ten species of plants for growth and uptake: five are native to New Mexico and five are non-native oil-seed producing species. Soil pH and electrical conductivity were analyzed using the saturated paste method. To measure the concentration of uranium-238, radium-226, and other elements, soil and biomass samples were ashed, concentrated using ion chromatography exchange, and analyzed using inductively coupled plasma optical emission spectroscopy (ICP-OES) and high resolution ICP mass spectroscopy (MS). Soil collected from one of the sites (#29) for initial characterization had a pH of 8.0, electrical conductivity of 0.5 ds·m-1. Preliminary soil analysis by ICP MS showed the concentrations of uranium, calcium, sodium, and magnesium to be 0.775 mg·L-1, 5.85 meq·L-1, 1.47 meq·L-1, and 1.82 meq·L-1 respectively. Soil collected from site 29 is not saline and may be suitable for plant growth following the greenhouse study. Future work includes completion of the first season greenhouse study and characterizing the soil and biomass. Data from ICP OES analysis will be coupled with mass balances to determine the partitioning of the radionuclides within the biomass.

THU - 838 Predictability of Biomethane Potential from Anaerobic Co-Digestion of Food Waste.

Discipline: Engineering
Subdiscipline: Other Engineering

Aranza Barreda*, *University of Kansas* and Belinda Sturm, *University of Kansas*

Abstract: Biogas, which is primarily methane along with carbon dioxide, is produced through a variety of natural processes, including anaerobic digestion, where micro-organisms break down organic material in the absence of oxygen. The objective of this project was to create an empirical relationship that would predict the percentage of biomethane produced from the co-digestion of food waste where the protein concentration was variable and incorporated into the equation that predicts biomethane potential. The hypothesis was the co-digestion of food with the equal amounts of carbohydrates and protein in the organic matter will have a greatest biomethane yield. The next highest biomethane yield was hypothesized to be co-digestion of food with a greater carbohydrates to protein ratio. Triplicates tests measuring the volume of biomethane as a function of time were performed for three varying protein compositions studied. The next steps would be to further characterize the remaining wet solid to be used a nutrient-rich fertilizer.

THU - 840 Chemically Reduced Pt Nanoparticles for Ammonia Oxidation Electrocatalyst

Discipline: Materials Research
Subdiscipline: Materials Research

Andrés D. Rivera-Ruiz*, *Universidad Ana G. Méndez*; Namir A. Huertas, *Universidad Ana G. Mendez* and Ileana Gonzalez-Gonzalez, *Universidad Ana G. Mendez*

Abstract: The interest in metal nanoparticles, like platinum, has increased due to their unique properties for applications as catalysts. In this work, we synthesized Pt particles by chemical reduction methods using different precursors (K_2PtCl_6 or $H_2Pt(OH)_6$) in order to compare their electrocatalytic activities for ammonia oxidation. Platinum particles are typically synthesized by the reduction of a platinum precursor in solution with a capping agent and a reduction agent to form colloidal nanoparticles. Platinum precursors were reduced with $NaBH_4$ and particle size was controlled with tartaric acid as capping agent. After precipitation of Pt particles, capping agent was removed by a washing method with acetone and electrochemical cleaning. These particles were then mixed with Nafion and used to paint a disk glassy carbon electrode to do an electrochemical characterization of the synthesized platinum particles in acid solution. Following the electrochemical characterization of Pt particles, cyclic voltammetry was used to measure their electrocatalyst potential for ammonia oxidation. Apparently, there is no difference in the electrocatalytic activity for the ammonia oxidation reaction based on the metal precursor. Until now, the highest current density was achieved by particles synthesized from the $H_2Pt(OH)_6$ precursor, with a value of 8.94×10^{-3} mA/cm^2. We are currently exploring different post-synthesis cleaning protocols to have a more accurate comparison of the synthesized particles. Recognizing the cost challenge that platinum arises, our aim is to incorporate non-noble materials (metal oxides) into the catalyst to assist the water activation process.

THU - 841 Inducing Fluidity in Short-Chain, Amphiphilic Block Copolymer Bilayer Membranes Via Polymer Functionality

Discipline: Materials Research
Subdiscipline: Materials Research

Harrison Reid*, *Northern Arizona University* and Gabriel Montano, *Northern Arizona University*

Abstract: Amphiphilic block copolymers (ABC) can self-assemble into bilayer or monolayer membranes on surfaces. Relatively low molecular weight ABC bio-inspired membranes have previously been reported to be fluid as monolayers but immobile as bilayer membranes. (Goertz et. al.) As such, polymer membranes exhibit potential as biomimetic membrane materials however the lack of bilayer fluidity to-date limits their potential application space. In this study, we investigated low molecular weight polybutadiene-b-polyacrylic acid (pBD-b-pAA) and polybutadiene-b-polyethylene oxide (pBD-b-pEO) bilayer fluidity as a function of environmental conditions such as pH and buffer capacity. pBD-b-pAA demonstrated the ability to generate fluid bilayers at all tested pH values while pBD-b-pEO bilayers remained immobile as previously reported. Diffusion rates within the pBD-b-pAA bilayer were observed to exhibit pH and buffer dependence providing evidence as to the nature of polymer membrane fluidity. Fluorescence recovery after photobleaching (FRAP) and in-situ Atomic Force Microscopy (AFM) were used to characterize the membrane composites and their functional properties. Our findings report the potential for generating mobile polymer membranes that closely mimic fluid bilayers similar to those found in biological lipid systems.

Reference:

Goertz, M.P., Marks, L.E. & Montaño, G.A. (2012) *Biomimetic Monolayer and Bilayer Membranes Made From Amphiphilic Block Copolymer Micelles.* ACS Nano: 6(2):1532-40.

THU - 842 Maturation and Localizatin of Vacuoles in *Pombe*

Discipline: Materials Research
Subdiscipline: Materials Research

Maura De Jesus*, *San Francisco State University* and Mark Chan, *San Francisco State University*

Abstract: *Schizosaccharomyces Pombe,* commonly known as fission yeast, is an important organism in studying the cellular responses to DNA damage and the process of DNA replication. Organelles are key compartments found in all eukaryotic cells and are essential for all cells. Vacuoles are organelles that degrade and store proteins in the cell. Previous research has shown that the yeast vacuole is equivalent to the mammalian lysosome. With many parallels found in mammalian lysosomes it is critical to know how vacuoles move with respect to its stage in the cell cycle as time progresses. The study of how the maturation and localization differs as it proceeds through medial fission will aid clarity to a better undertanding of the cell cycle. Using two Lipophilic dyes, FM4-64 and MDY-64, the vacuoles will be visualized. FM4-64 enters vacuoles via the endocytotic pathway and flouresces red and MDY-64 flouresces green. Both dyes are used as markers in a wild type strain SP-175. With the use of a confocal spinning disk time series data sets are collected to further analyze using ImageJ. With further analysis I expect to find vacuoles arising first around the nucleus and being pushed outwards towards the tips as newer vacuoles. My results may have implications in studies related to several lysosomal storage disorders such as Gaucher disease, Tay Sachs disease. Overall, through experimentation it is expected to find that vacuoles will move with respect to the arisal of newer vacoles as it undergoes cell division.

THU - 843 Confinement Heteroepitaxy and Electrochemical Properties of 2D Metals

Discipline: Materials Research
Subdiscipline: Materials Research

Ana De La Fuente Duran*, *The Pennsylvania State University*; Natalie Briggs, *The Pennsylvania State University*; Riccardo Torsi, *The Pennsylvania State University*; Derrick Butler, *The Pennsylvania State University* and Joshua Robinson, *The Pennsylvania State University*

Abstract: Developing efficient photosynthetic systems that can economically convert solar energy into chemical energy on a large scale is crucial for the realization of a sustainable economy. The production of hydrogen gas by reducing water is a promising solar energy conversion technique, and it has been extensively researched in semiconductor-based photoelectrochemical devices. However, the role that plasmon-induced charge separation (PICS) can play in enhancing the photocatalytic performance of semiconductors has been relatively limited. Here, we explore how the plasmonic properties of the 2D allotropes of 3D metals can enhance the catalytic performance of MoS_2 in the hydrogen evolution reaction.

Air-stable, crystalline, atomically-thin metals can be realized at the epitaxial graphene/silicon carbide interface through a method termed confinement heteroepitaxy (CHet). For this intercalation method, graphene defects created through exposure to O_2 plasma serve as entry points for a metal that is vaporized at high temperatures (>700°C). X-ray photoelectron spectroscopy confirms the presence of Ga/In metal in all samples, and transmission electron microscopy shows 2-5 atomic layers of metal beneath graphene layers. Subsequent growth of MoS_2 on the 2D sample surface was achieved through powder vaporization (<650°C) in a tube furnace. Raman spectroscopy confirmed the presence of MoS_2 on resulting samples. In order to gauge the photocatalytic performance, a laser is utilized in conjunction with a three-electrode system in an electrochemical cell. Electrochemical impedance spectroscopy, cyclic voltammetry, and linear sweep voltammetry measurements are completed with and without light to elucidate the role that PICS can play in catalyzing reactions that yield carbon-neutral fuels.

THU - 844 Simulating the Signaling and Target Binding of SERS Substrates

Discipline: Materials Research
Subdiscipline: Other Materials Research

Devanshu Kumar*, *University of California, Meced* and Tao Ye, *University of California, Merced*

Abstract: SERS (Surface enhanced Raman Spectroscopy) is an ultrasensitive detection technique capable of detecting various analytes at extremely low concentration. The SERS enhancement factor (EF) is proportional to the fourth power of local electromagnetic (EM) field. Plasmonic nanostructure are promising SERS substrates because they amplify EM fields near their surfaces and in gap junctions drastically. Currently, EF's are qualitatively examined using simulated EM distribution maps and there is no quantitative analysis of EF around plasmonic structures in literature. Here, we developed a program using MATLAB to quantitatively examine the EF around the plasmonic structure. We analyzed trimeric substrates of a 10nm gold nanoparticle (AuNP) situated between two large AuNPs. The EM distribution maps of our trimeric substrates were obtained using Finite-Difference Time Domain (FDTD) simulations displaying hot spots near the central 10nm AuNP. We extracted the EF values around the plasmonic structures by calculating the mesh size and setting an appropriate threshold around individual AuNPs. Two cases were simulated: analytes preferentially binding to the surface of 10nm nanoparticle and random binding on the trimeric substrates. Both cases were simulated 100,000 times with a sample size of 100 analytes. The average EF for both cases suggests that analytes preferentially binding to the 10nm gold nanoparticle are three orders of magnitude greater than that of random binding. Our quantitative analyses provide insightful information on EF around plasmonic nanostructure and demonstrate that maximum signal enhancements can be achieved by localizing analytes near hot spots. Moreover, this program can facilitate future designs of SERS substrates.

THU - 845 Modulation of Micrornas By Epigallocatechin 3-Gallate in Cancer Biology Using Computational Study

Discipline: Other
Subdiscipline: Other Professional Fields

Ndeye Bakhoum*, *HOSTOS COMMUNITY COLLEGE* and Yoel Rodriguez, *HOSTOS COMMUNITY COLLEGE*

Abstract: MicroRNAs (miRNAs) are singled-stranded small non-coding RNAs 22-nucleotides long. They intervene in post-transcriptional regulation of gene expression1. miRNAs are involved in cell proliferation and apoptosis, and have been shown

to be deregulated in cancer cells2. Hence, modulation of miRNA activity could make them promising therapeutic targets.Epigallocatechin-3-gallate (EGCG) is a main component of green tea, and evidence suggests it has anti-carcinogenic effects that might be mediated by miRNAs. Our collaborator Dr. Delgado-Cruzata's group at CUNY's John Jay College has identified changes in levels of miR-1246, miR-494 and miR-579 after exposure to 50uM EGCG for 72hrs. We hypothesized that miRNA-EGCG recognition might lead to changes in miRNA levels. Thus, here we use computational methods to predict the dynamics of this interaction by 1) determining whether EGCG binds directly to miRNAs, and 2) if so, determining which miRNA sequence EGCG prefers. Towards this end, we usecombined computational biophysics approaches and experimental biology assays. Specifically, we conductedsecondary structure prediction calculations to obtain the 2D and 3D structures of miRNAs by using the RNAFold and RNAstructure as well as SimRNAweb and iFoldRNA Ver2.0 webservers, respectively. We also applied structure-based molecular docking to predict the binding mode of EGCG to specific miRNAs using rDock program3. SF5 scoring functionwas used to rank EGCG binding affinity towards miRNAs. Theresults of this study can shed light into the mechanism of miRNA regulation by EGCG and help understand the potential of using EGCG as a therapeutic in breast cancer.

THU - 846 In Search of Nutraceuticals in Yellow *Capsicum* Species

Discipline: Other
Subdiscipline: Other Professional Fields

Krystal Vargas*, *New Mexico State University* and Ivette Guzman, *New Mexico State University*

Abstract: Over 700 different carotenoids exist in nature. They are the yellow, red, and orange pigments typically found in fruits and vegetables. Xanthophylls are yellow compounds and make up one of the two carotenoid groups. One xanthophyll, lutein, has been shown to improve cognitive health and decrease risks of macular degeneration. Lutein accumulates on the retinal nerve in the eye and assists in absorption of blue light that the eyes are subjected to daily. Chile peppers, *Capsicum* species fruits are one of the few fruits and vegetables that may accumulate xanthophylls such as lutein. For this reason, 36 genetically diverse yellow chile peppers from New Mexico State University's Chile Pepper Institute plots were harvested for lutein, beta-carotene, and total carotenoid analysis. The hypothesis was that there are high amounts of lutein in yellow chile peppers and low amounts of beta-carotene, an orange carotenoid. Peppers were cut up, frozen in liquid nitrogen, lyophilized, ground up and extracted for carotenoids. After extraction, peppers were saponified for quantitative analysis using a high performance liquid chromatography (HPLC) method. Carotenoid standards were used to identify and quantify amounts of beta-carotene and lutein. These results indicated that only six of the 33 yellow peppers were found to have lutein as the major carotenoid, while the other 33 peppers contained a mixture of at least five carotenoids. This was the first time that multiple yellow peppers were screened for lutein amounts. In order to understand the health benefits, bioavailability of lutein from yellow peppers will be assayed.

THU - 847 ROS As a Secondary Messenger Mediating Free Fatty Acids in Signaling Macrophages

Discipline: Other
Subdiscipline: Other Professional Fields

Blake McBeth*, *University of Chicago* and Lev Becker, *The University of Chicago*

Abstract: Obesity is an ongoing epidemic in the United States with more than 10% of the population diagnosed as type 2 diabetics. Unfortunately, women with type 2 diabetes (T2D) also have an increased risk for triple negative breast cancer (TNBC) though the mechanism of this association is poorly understood. A promising connection between T2D and TNBC is the low levels of chronic inflammation that is a hallmark of T2D. A major source of this inflammation are infiltrating adipose tissue macrophages (ATMs). Macrophages often infiltrate stressed tissue in an attempt to maintain homeostasis and these proinflammatory macrophages have often been classified as "classically" activated (M1) which are crucial in fighting infectious disease. However, we have shown that obese ATMs, while inflamed, adopt a phenotype distinct from classical activation. This new metabolic activation (MMe) is driven by free fatty acids rather than bacterial products. We have shown MMe macrophages promote both insulin-resistance and tumor "stemness". However, the signaling pathway that drives this new phenotype is unknown. Our data shows antioxidants inhibit MMe polarization, suggesting a reactive oxygen species (ROS) dependent mechanism. Here we aim to functionally confirm ROS as a key player in both the insulin resistance and tumor stemness functions of MMe by Akt phosphorylation and tumorsphere assay respectively. Understanding this new pathway provides potential targets for reducing obesity-driven inflammation while leaving classical host defense in tact.

THU - 848 Prescription Burn Effects on Miin (blueberry) Growth.

Discipline: Other
Subdiscipline: Other Professional Fields

anita cloud*, *Leech Lake Tribal College* and Melinda Neville, *leech lake tribal college*

Abstract: Miinan, the Ojibwemowin word for blueberries (*Vaccinium angustifolium* and *V. myrtilloides* (lowbush blueberry and velvet-leaf blueberry), can be found growing in acidic barrens, bogs and clearings throughout its range, which includes much of the U.S. and Canada. Miinan are historically and culturally significant to the Ojibwe people. Not only are these wild berries low in calories and high in nutrients, they also have more anti-oxidants than other fruits and can help maintain brain function and improve memory. However, widespread clear cutting followed by fire suppression and vegetation shifts throughout the 19th & 20th century have inhibited blueberry plant growth and berry production in northern Minnesota. To better understand management techniques that can increase blueberry abundance and production, the Leech Lake Band of Ojibwe Division of Resource Management and USDA Forest Service initiated a project within the Chippewa National Forest to observe the effects of a prescribed burn on blueberry plant abundance in the Sunken Lake old growth pine woodlands located northeast of Lake Winnibigoshish. This project will determine if the miinan respond to the fire prescription by repopulating the burned area or if the burn will hinder blueberry production in that area.

THU - 849 New Mexico's Superfood: Chile Peppers

Discipline: Other
Subdiscipline: Other Professional Fields

Francisco Chacon*, *New Mexico State University* and Ivette Guzman, *New Mexico State University*

Abstract: Phenolic compounds are antioxidants that hold nutritional value in protection against infectious diseases, inflammation, and certain types of cancers. Peppers are consumed worldwide and are a common culinary ingredient. Thirty-four varieties of peppers were extracted and analyzed for total phenolics and compared to a phenolic-rich superfood, blueberries. Since phenolic compounds contribute to color in plants, we hypothesized that 34 genetically diverse peppers (Capsicum species) contained the same amount of total phenolics due to their yellow color. The peppers were harvested from the New Mexico State University Chile Pepper Institute Teaching Garden located in Las Cruces, New Mexico, and freeze-dried. Phenolics were extracted from freeze-dried tissue with 2% methanolic acetic acid and quantified using the Folin-Ciocalteu assay. A spectrophotometer detected phenolics at 765 nm. Utilizing a gallic acid standard, a standard curve was made to quantify total phenolics in the pepper samples. The 34 Capsicum species varied in total phenolics. A Yellow Chiltepin had the lowest amount with 1.45 mg/g of dry weight (DW). Two Capsicums, Fatali, and a Mulato x Permagreen hybrid contained higher amounts of phenolics with 4.64 and 4.54 mg/g DW, respectively. While blueberries, a nationally recognized superfood, contained 3.91 mg/g DW of total phenolics. The results indicate that select Capsicum species should also be considered a superfood with high nutritional value. Also, peppers contain low amounts of sugars, unlike blueberries, providing a healthier substitution. In conclusion, peppers are an untapped source to beneficial antioxidants and should be considered as a superfood.

THU - 900 Hydrophobic Coatings on Paper Substrates to Analyze Hydrophilic Compounds Using Paper Spray Mass

Discipline: Chemistry

Subdiscipline: Analytical Chemistry

Iyunade Adebowale*, *Indiana University- Purdue University Indianapolis*; Chrisitine Skaggs, *Indiana University- Purdue University Indianapolis*; Sarah Dowling, *Indiana University- Purdue University Indianapolis* and Nicholas Manicke, *Indiana University- Purdue University Indianapolis*

Abstract: Paper spray ionization mass spectrometry (PSI-MS) is a technique used to analyze a variety of sample types cheaply, quickly, and reproducibly. PSI-MS works by spotting a drop of biofluid onto a triangular shaped paper substrate followed by the addition of an extraction solvent. A voltage is applied producing charged droplets that will enter the inlet of the mass spectrometer. Hydrophilic molecules are difficult to analyze via PSI-MS due to the strong binding interactions that these molecules have to the paper. Because of this, detection limits are higher, analytes typically have poor recovery, and there is greater ion suppression. Due to the aforementioned limitation, various paper coating methods were developed in this research to aid in the extraction of hydrophilic analytes off the paper substrate. The different coating methods includes polystyrene coated paper, carbon sputtered and Silanol coated paper. The Whatman 31ET paper serves as the control. After optimizing the solvent parameters for each coating type, we analyzed different hydrophobic coatings for our hydrophilic molecules to determine which would most greatly impact the extraction of these molecules. Experiments were performed on a Thermo LTQ XL mass spectrometer (San Jose, CA). Preliminary data indicates that the carbon sputtered paper will not only have a higher AUC for our analyte but will also have a higher signal-to-blank.

THU - 901 Optimization of the Colorimetric Detection of Nicotine from Third-Hand Smoke Residue

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Catrin Law*, *San Diego State University*; Arrion Smith, *San Diego State University* and Christopher Harrison, *San Diego State University*

Abstract: Third-Hand Smoke (THS), is a complex and harmful mixture of chemicals from tobacco smoke that remains on surfaces in environments, such as a car or a home for weeks to months after the cessation of smoking. These chemicals tend to persist even after treatment with harsh house-hold cleaning supplies. A detection method for THS residue is necessary due to the toxicity of the chemicals and their persistence in environments such as rental housing, where past smoking behaviors may not be apparent to new tenants. Though THS analysis can be done with laboratory equipment, such resources are inaccessible to most individuals. We aim to create a simple testing device, akin to a home pregnancy test available for consumers to use to test their homes to obtain semi-quantitative data about THS contamination. The detection method we are exploring are colorimetric complexation reactions between nicotine (the most abundant molecule in THS) and a dye such as methyl orange or Brilliant Blue G. The identification of the presence of nicotine is accomplished by the selective partitioning of the nicotine-dye complex into chloroform. This poster will present our work investigating different types of buffers and the influence of pH on the formation and extraction of the nicotine-dye complex. This optimization aims to reduce the potential for false positives, while increasing the sensitivity for the means of detection.

THU - 902 Efficacy of Direct on-Column Injection & Multivariate Analysis for Detecting Short Chain Poly-/per- Flourinated Alkyl Contaminants in El Paso County, Colorado Drinking Water

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Karina Grande*, *Colorado College*; Eli Fahrenkrug, *Colorado College* and Nicole Chavarria, *Colorado College*

Abstract: Per- and poly-flourinated alkyl substances (PFAS) are a class of 4,000 chemical compounds with widespread commercial application in non-stick cookware, foams, and other cosmetic products (e.g. teflon and GoreTex™). Extended exposure to these compounds have been linked to liver damage, cancer, and complications in pregnancy. In 2016, the New York Times Magazine described high levels of PFAS in the Widefield aquifer in El Paso County, Colorado that supplies drinking water to 70,000 residents. Subsequent reports indicated the contamination source was linked to fire-fighting drills carried out at neighboring Peterson Air Force Base since the early 1970s. The Fountain Valley Water Project was formed in response as a citizen-science advocacy group to evaluate the full extent of the PFAS contamination and its effects. This presentation will start by broadly outlining the scientific, educational, and translational aims of the group with a focus on the organization principles required to initiate and sustain a community-based water monitoring project. The specific theme of the presentation will elaborate on the challenges with our current analytical methodology as it pertains to short-chain PFAS compound retention along with our progress towards adopting a more applicable direct on-column injection process using high performance liquid chromatography and tandem mass spectrometry. This work will directly compare results obtained from the traditional EPA Method 537.1 with newly adopted direct-injection process. Finally, this work will comment on multivariate statistical analyses of the community groundwater data as a means to extract meaningful fate and transport parameters.

THU - 903 Removal of Chromium(VI) from Aqueous Solution Using ZnO Nanoparticles an Investigation in to the Effect Light and Dark Conditions on the Binding.

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Daniel Ramirez*, *University of Texas Rio Grande Valley* and Jason Parsons, *University of Texas Rio Grande Valley*

Abstract: Chromium(VI) is known as a carcinogenic compound, which needs to be removed from drinking water. Nanoparticles of metal oxides have the potential to act as adsorbents for dissolved metal ions. In the current investigation, ZnO nanoparticles were synthesized through a precipitation method. The Nanoparticles were characterized using a combination of SEM and powder X-ray diffraction. Batch studies were performed to investigate the potential binding of Cr(VI) and Cr(III)to ZnO nanoparticles under light and dark conditions. ZnO is a photoactive material which has the potential to transfer electrons to compounds bound onto the surface of the compound. The effects of pH, time, and temperature were investigated were investigated under batch experimentation conditions. In addition, the effect of light on the binding and potential reduction of Cr(VI) to Cr(III) in solution was investigated. The determination of Cr(VI) concentration was performed using the diphenylcarbizide method. In addition, isotherm studies were performed to determine the maximum binding capacity of Cr(VI) and Cr(III) to the ZnO nanoparticles. The effects of potential interferences on the binding were also investigated hard cation were investigated for Cr(III) binding. For the binding of Cr(VI) common anions were studied for the potential interferences on binding. The optimal pH for binding was determined to be pH 3, the binding capacities for Cr(VI) were determined were 8.35mg/g, 2.90mg/g and 41.67mg/g, at temperatures of 4, 25, and 45 degrees Celsius.

THU - 904 Optimizing and Data Analysis of *Turnera Diffusa* (damiana) Tea Leaves

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Vanessa Quevedo*, *Williams College* and Nathan Cook, *Williams College*

Abstract: Traditional medicines remain widely used as remedies for a range of ailments from stomach discomfort to impotence. The leaves of the plant *Turnera diffusa* (colloquially known as damiana) are purported to treat many of these such, but few studies have definitively identified active medicinal compounds. Our investigation is the first to report antibiotic potential in aqueous leaf extracts, which parallels the ways in which the plant is most often consumed, as a tea. Additionally, we have combined disc diffusion assays, optical scattering plate assays, and high resolution LC-MS to further isolate and identify the active components in these leaves. The first part of this experiment has focused on optimizing the extraction and purification of the active ingredients from its leaves. Our current efforts are focused on data analysis to investigate the effectiveness and mode of action of the currently unidentified antibiotic compounds.

THU - 905 Omega-3 Fatty Acids in Native American Traditional Food

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Karlee Cooper*, *Northwest Indian College* and John Rombold, *Northwest Indian College*

Abstract: The Northwest Native American population has depended on local plants and animals for sustenance since time immemorial. In having a traditional type of diet, we have obtained nutrients such as omega-3 fatty acids that may have supported our health and reduced the risk of diseases. Consuming fatty acids through eating Native American traditional foods may help eliminate plaque buildup on teeth as well as in arteries. These essential fatty acids will strengthen tooth enamel, which helps reduce the risk of periodontal disease. Omega-3 fatty acids are hypothesized to have anti-inflammatory properties and aid in slowing down and may even stop the growth of bacteria that cause oral diseases. By improving oral health of the Native American population, we reduce the risk of acquiring other diseases. The Northwest traditional diet has beneficial effects that are linked with fatty acids such as reduced strokes, lower insulin resistance, and reduced prevalence of autoimmune diseases; all of which are major health issues within modern Native American communities. We hypothesize that Northwest traditional foods will accommodate more than the recommended intake of omega-3 fatty acids. We will examine the accuracy of our hypothesis by extracting fatty acids from traditional foods that were harvested by the Northwest Indigenous people and analyzing our samples with the assistance of the University of Oregon. Projected results include evidence that elk, bear, geoduck, deer, seal, herring eggs, mallard duck, longfin smelt, and others will contain more than the adequate intake of omega-3 fatty acids in a suggested serving.

THU - 906 Synthesis and Characterization of Prussian Blue Nanoparticles (PBNP)

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Merlin Sosa Olivares*, *Los Angeles City College*; Uzma Tanveer, *California State University, Los Angeles.* and Yixian Wang, *California State University, Los Angeles.*

Abstract: Detection of hydrogen peroxide, H_2O_2, is of great importance in different fields, such as the manufacturing industry as it is used in aseptic packaging, where limitations of H_2O_2 present in food by the Food and Drugs Administration are set to very low tolerances. It is important for living organisms to catalyze H_2O_2 at the cellular level to protect from oxidative damage due to reactive oxygen species resulting from the decomposition of H_2O_2 (Zhang et al.). Prussian blue, Iron(III) hexacyanoferrate(II), has proven to be a good electrochemical sensor to detect H_2O_2 at increasingly low concentrations (Cinti et al.). The final goal is to improve the detection of H_2O_2 using Prussian Blue Nanoparticles (PBNP) in hopes of better understanding the formation of free radicals at a cellular level and cellular death, as well as protein decomposition due to hydration. Characterization of PBNP was performed using Atomic Force Microscopy. Synthesis of PBNP was performed using potassium ferrocyanide and iron(III) chloride in the presence of hydrochloric acid as described (Ahmadalinezhad, Kafi, and Chen). The performed characterizations of the PBNP showed that the crystal structures are present but need a better deposition method to allow for a thicker layering of PBNP that will potentially increase sensitivity of the molecules towards H_2O_2, which will be confirmed through cyclic voltammetry analysis and sharper imaging methods.

THU - 907 TCNE Attachment to Iron Dinitrosyl Complexes Containing Bis(Diphenylphosphine) Derivatives: Potential As Anti-Tumor Agents

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Diego Velarde*, *California State University Long Beach* and Lijuan Li, *California State University Long Beach*

Abstract: Biological versatility of metal nitrosyl complexes has stimulated increased interest in their synthesis and application. Previous research has revealed metal complexes containing nitric oxide and phosphine derivatives to possess *in* vitro anti-tumor properties. Furthermore, tailoring function of these ligands can prove critical for enabling targeting in specific biological environments. Although ruthenium, copper and gold complexes containing bis(diphenylphosphine) derivatives have been prepared and tested for anti-tumor properties an iron center has not. Contributing to this bank of compounds, synthesis of three new complexes $[Fe(NO)_2(DPPX)(TCNE)]$, {DPPX= 1,2 –Bis(diphenylphosphino)ethane, 1,4 –Bis(diphenylphosphino)butane, and 1,6 –Bis(diphenylphosphino)hexane} has been carried out in an inert environment and characterized by FT-IR, NMR, UV–Vis, and CV. A two-step synthesis first produced a stable intermediate of the mono-substituted products. FT-IR data confirmed the substitution of a carbonyl group by the disappearance of one of the carbonyls stretching frequencies and red shifting nitrosyl frequencies in the intermediate. Subsequent addition of TCNE (tetracyanoethylene) to these monosubstituted products generated the final products by replacing the second carbonyl ligand. Further insight into the characteristic nature of these compounds will allow for future development in associated research anticipating effective combatants of cancerous tumor cells.

THU - 908 Syntheses, Characterization, and Anticancer Activity of Arsenoplatin-4

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Matthew Martin*, *Northeastern Illinois University*; Wenan Qiang, *Center for Developmental Therapeutics at the Chemistry of Life Processes Institute, Northwestern University*; Annie Fritz, *Northeastern Illinois University*; Denana Miodragovic, *Chemistry of Life Processes Institute, Northwestern University* and Thomas O'Halloran, *Chemistry of Life Processes Institute, Northwestern University*

Abstract: Cisplatin is one of the most widely used drugs to treat cancer, currently included in nearly half of all chemotherapeutic protocols. The only additional FDA approved inorganic anticancer drug, arsenic trioxide (As_2O_3), is limited to the treatment of acute promyelocytic leukemia and some blood cancers including multiple myeloma. As_2O_3 is highly effective, but due to its rapid renal clearance, it has been ineffective in the treatment of solid cancers. Cisplatin and arsenic trioxide trigger cell apoptosis but through different mechanisms. A new class of very potent anticancer agents, arsenoplatins, have been synthesized, containing arsenic and platinum moieties of both drugs. A variation of this Pt-As core complex, named arsenoplatin-2, was obtained through the reaction of $K_2[PtCl_4]$ with As_2O_3 in the presence of propionitrile. A very high Pearson correlation coefficient (r = 0.96) is obtained while comparing anticancer activity of arsenoplatin-2 to As_2O_3 in the NCI-60 screen, suggesting that two compounds act in a similar manner. This project aims to synthesize, characterize, and test the anticancer activity of an iodide analog of arsenoplatin-2, named arsenoplatin-4. NMR and elemental analysis have been completed to determine the structure and purity of this new compound, and cytotoxicity has been assessed by MTS assay. Interactions with biologically important ligands with thiol groups to determine possible cellular resistance will be presented. Based on current results, AP-2 and AP-4 may act as a delivery vehicle for As_2O_3, overcoming one of the primary limitations of As_2O_3 as a drug for solid cancers.

THU - 909 Redox Active Ligands for Separation of Lanthanides from Nuclear Waste

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Kyle Covington*, *Cypress College* and Chantal Stieber, *Cal Poly Pomona*

Abstract: During nuclear fission of uranium, various elements including lanthanides and actinides are created through a cascading transfer of neutrons. Processes have been developed to separate actinides from nuclear waste for their continued use, which are useful for extending the lifespan of a nuclear power plant. However, a good process for separating the lanthanides has not yet been developed. Lanthanides are detrimental to the lifespan of the fuel, but have a variety of commercial uses such as magnets in electronics, lenses, and as catalysts. Ideally, a relatively inexpensive bench-top process could be developed to separate lanthanides from nuclear waste. Redox-active ligands

are a potential solution because they could allow for differences in electronic properties to be tailored for separations. Catecholates of gadolinium made in a basic solution are known, but were synthesized air-free. In the current work, redox active ligands including catechol and toluene-3,4-dithiol were reacted with neodymium to test air-free and bench top syntheses. This will help determine whether these ligands are suitable candidates for separations, and crystals were grown to compare structural properties. Initial findings indicate that benchtop reactions produce different products than under argon and efforts are underway to fully characterize these products.

THU - 910 Contaminated Deionized Water on Campus

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Jesus Renteria*, *Los Angeles City College* and Terry Boan, *Los Angeles City College*

Abstract: Chemical water analysis is crucial to studies involving water quality, contamination, and pollution. Analytical methods are used to detect and measure natural elements and inorganic compounds alike. Such methods include specific chemical tests, gas chromatography, infrared spectroscopy, and mass spectrometry. During a Biochemistry laboratory, the class encountered deionized water with a pH level of around 5, with some readings as low as 4.39. Our deionized water is kept in a separate tank above our science building and should be a neutral pH of 7. We approached this discovery using analytical chemistry in order to find an explanation. The hypothesis states that there are water impurities present from various possible sources of contamination that include air pollution affecting the DI tank, impurities coming from the building's plumbing, and or microbial & algae growth in the DI tank itself. The research project involves inorganic and organic principles, freeze drying samples with a rotary evaporator to later re-suspend them for IR spectroscopy to possibility identify bacterial strains from the infrared spectrum, and the use of a UV Spectrophotometer to detect chlorophyll-a, an indicator of possible algae growth. Water samples from different class rooms and buildings are to be analyzed, using water from both tap faucets and DI water faucets in order to see if there is difference. Preliminary results indicate the pH of our DI water around 5, which is on the acidic side of the pH scale. We hope to identify the origin of the issue in order to address it.

THU - 911 Gold Cavitand Catalyzed Alkyne-Acid Ring Closing: A Study in Regioselectivity

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Teodora Nedic*, *California State University, Long Beach* and Michael Schramm, *California State University, Long Beach*

Abstract: Gold resorcin[4]arene cavitand catalyzed transformations have piqued the interest of supramolecular chemistry. With 3-walls and one gold center a binding pocket is created around a reactive center. When internal alkyne acids are cyclized, the size-specific environment of the cavitand results in significant regioselective differences when compared to simpler Au catalysts. Regioselectivity is related to the size of the alkyne's alkyl group. 5-membered lactones become favored as the chain lengthens (e.g. propyl and butyl). 6-membered lactones dominate with shorter groups (methyl and ethyl). Contrasting, under the influence of Me2SAuCl, propyl alkyne favored 5-membered lactonization (3:1). Au cavitand skewed this to 9:1 (5:6-membered). We elaborate on these findings with the aim of describing the substrate/cavitand features that provide access to regiochemical outcomes that otherwise lack means of control.

THU - 912 Omega -3 Fatty Acid Content of Traditional Foods from the Salish Sea

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Mary Brewer*, *Northwest Indian College* and John Rombold, *Northwest Indian College*

Abstract: **Omega -3 Fatty Acid Content of Traditional Foods from the Salish Sea**

Heart disease is the leading cause of death among Native Americans in the United States and this rate is 20% higher than all other races in the US. It is believed that diets rich in omega-3 fatty acids may help reduce the risk of developing heart disease. The traditional indigenous diet of the Pacific Northwest is rich in seafood that contain high amounts of omega-3 fatty acids. This study looked at a variety of traditional food to analyze their omega-3 fatty acid content. We used heat, sonication and solvents to extract fatty acids from .5 gram freeze dried samples of locally harvested traditional native foods of the Salish Sea. Samples are being sent to Oregon State University for fatty acid content analysis. It is predicted that our results will support our hypothesis that our traditional native foods are an excellent source of heart healthy omega 3 fatty acids. In conclusion, our results will be shared with our tribal communities to help reinforce the use of traditional foods into our daily diets.

THU - 913 Selective Degradation of E2F As Cancer Therapy

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Iliana Hayes*, *University of California, Santa Cruz* and Seth Rubin, *University of California, Santa Cruz*

Abstract: The cell cycle is regulated by a series of enzymatic activities which are controlled by protein interaction in the cell. Deregulation of these proteins results in anomalous cell proliferation and cancer. By studying the structural and biochemical mechanisms of the cell cycle, more can be understood about how structural changes affect biological function. E2F is a family of transcription factors that regulate the G1 phase of the cell cycle and when deregulated, causes cancer. E2F is widely considered undruggable due to its broad, flat geometry which prevents small-molecule drugs from binding to it. To target E2F, we are designing a proteolysis targeting chimera (PROTAC): a two-headed molecule that is able to induce selective proteolysis. After recombinant expression of E2F, we will use fragment based screening, using NMR and x-ray crystallography, to identify possible E2F binding candidates. Once the screening is completed, the top binding candidates will be incorporated into the final design of our PROTAC molecule. This PROTAC is expected to suppress tumor growth by degrading the unregulated E2F through proteolysis. The knowledge gathered from researching E2F protein structure and function will tremendously contribute to the overall understanding of the causes of aberrant cell proliferation and cancer.

THU - 914 Screening a Marine Natural Products Library for Compounds with Selective Cytotoxicity Towards Pediatric Cancer Cell Lines

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Alyssa Thompson*, *University of California Santa Cruz*; Erin McCauley, *University of California, Santa Cruz*; Elizabeth Normand, *University of California Santa Cruz* and Phillip Crews, *University of California, Santa Cruz*

Abstract: Natural products continue to be an important stimulus for biomedical research and play an important role in pharmaceuticals, as over 60% of small molecule medicines are derived from or inspired by natural products. Due to the vast chemodiversity found in nature and its pharmaceutical potential, the Crews Research Group has, over the past 30 years, built an extensive repository of marine-derived natural products. Currently, there are minimal therapeutics to treat pediatric cancers that do not present aggressive and undesired side effects. In an effort to develop new drug leads for more effective treatments, the Crews repository was utilized to generate chemically diverse screening plates which were sent to our collaborator, the Moobery Research Group at UT Health San Antonio. The natural product extracts were screened in cytotoxicity assays that measured selective activity towards three pediatric cancer cell lines: Ewing's sarcoma RDES and SKES1, medulloblastoma d283, and rhabdomyosarcoma RH30. An extract isolated from a marine sponge showed potent selective cytotoxicity towards Ewing's Sarcoma cell line (A673). Liquid Chromatography was utilized to isolate three unique compounds within the extract which were identified as poecillastrin C and two novel poecillastrin analogues using high accuracy mass spectrometry and 2D NMR analytical techniques. The compounds were individually rescreened against the A673 cell line to determine which was responsible for the previously observed

potent selective cytotoxicity. All compounds exhibited nM activity, making them valuable pharmaceutical drug leads for further research on Edwing's sarcoma therapeutics. The structures and bioactivity data will be presented in this poster.

THU - 915 Synthesis of a Sialic Acid Derivative for the Development of New Anti-Hiv Agents

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Robert Perez*, *California State University, Sacramento*; Shams Makadsi, *California State University, Sacramento* and Katherine McReynolds, *California State University, Sacramento*

Abstract: Progress in the development of HIV-1 prevention options has been stagnant since the virus's discovery. At this moment, the only preventative measures available include abstinence, condoms (98% effective), or PrEP (Pre-Exposure Prophylaxis) (90% effective). Here, we propose the development of a novel glycopolymer for the prevention of HIV-1. This glycopolymer, also known as a glycodendrimer, can be designed to inhibit the binding of the HIV-1 gp120 protein to the host cells, thereby preventing infection. Here we will discuss the synthesis of a sialic acid derivative to be used in the formation of the glycodendrimers.

Our current study aims to create a glycodendrimer with terminal sialic acid derivatives. The sialic acid derivative was achieved in a sequence of four synthetic steps. The first reaction substituted the carboxylic acid at the anomeric position with a methyl ester, and was achieved in a 93% yield. The sialic acid methyl ester was next converted into a per-acetylated sugar. This crude product was pushed forward to the next step. The third reaction substituted a succinimide group at the anomeric position. The product was filtered via flash chromatography to give a 21% yield. This product then underwent a hydrazinolysis was and purified via HPLC to give the final product. Using this sugar, we aim to complete the formation of a glycodendrimer capable of inhibiting the binding of the virus to host cells, and thereby creating a new preventative agent targeting HIV-1.

THU - 916 Investigating a Photo-Responsive Material That Bends with Light

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Leslye Enriquez*, *Saint Mary's College of California*; Zuleikha Kurji, *Saint Mary's College of California* and Nicholas Rubio, *Saint Mary's College of California*

Abstract: Liquid crystal elastomers (LCEs) are stretchable, durable, and elastic materials, that can amplify microscopic molecular movements into large macroscopic mechanical motions when triggered by an external stimulus. An LCE can become photo responsive upon adding azobenzene, which undergoes photo induced change in molecular orientation when irradiated with light. A photo responsive LCE has been developed by adding an azobenzene containing monomer to the literature platform designed by Christopher Yakacki at the University of Colorado Denver. To date, our group has only performed qualitative video observations of this photo response. Thus, there is a need for more quantitative data, in particular, we are hoping to quantify the bending angle relative to azobenzene concentration. LCEs were synthesized with azobenzene concentrations that ranged from 0.25 mol%-0.10 mol%. A photo response setup was developed with a camera and a black graph paper background to reliably record the response of the LCE. ImageJ software was used to measure each bending angle. Large bending angles (>30°) were observed when all azobenzene concentrations were irradiated with a 450 nm laser (<5 W) for 1-3 seconds distanced 100 cm away. The LCE with 0.25 mol% of azobenzene still bent when the laser was 26 feet away. A 532 nm laser pointer (>200 mW) was only able to induce a bend when the light was held for a longer period of time (13 seconds) at 2.5 cm away. Continued efforts at quantifying the LCE bend angles relative to concentration are underway.

THU - 917 Optimization of a Cyclic Nucleotide-Gated Channel Blocker for the Treatment of Retinitis Pigmentosa

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Melissa Legaria Cisneros*, *Willamette University* and Sarah Kirk, *Willamette University*

Abstract: Cyclic nucleotide-gated (CNG) ion channels have been identified as a key source of rod photoreceptor loss thus making these ion channels important targets for drug development. In retinitis pigmentosa (RP), a leading genetic disorder, the uncontrolled influx of calcium causes rapid rod cell death in CNG channels, followed by the degeneration of cone photoreceptor cells and ultimately leads to complete blindness. The organic compound tetracaine has proven clinical utility due to its central aromatic ring, paired with the characteristic chain and head groups however, cytotoxicity and moderate affinity for channel binding limit the drug's activity. This research seeks to design a new small molecule, derived from tetracaine, as a potential CNG channel blocker for the treatment of RP.

The 6-aminonicotinic tetracaine derivative has the potential to increase binding affinity to CNG channels due to the presence of a strong endocyclic electron withdrawing group while maintaining a small size for the compound to diffuse through lipid membranes. It is also hypothesized that replacing the ester head linkage with an amide carbonyl linkage will enhance the lifetime of the drug while maintaining affinity. To produce the nicotinic derivative a two-step organic synthesis is proposed followed by characterization using Nuclear Magnetic Resonance and purification through High Performance Liquid Chromatography. The molecule will then be assayed using patch-clamp electrophysiology. Findings generated from this study will advance our understanding of key structural features necessary for high affinity binding and selectivity in CNG ion channels.

THU - 918 Water Oxidation Using Cobalt Compounds

Discipline: Chemistry
Subdiscipline: Organic Chemistry

David Brook, *San Jose State University* and Mario Escudero*, *San Jose State University, San Jose, Chemistry Department*

Abstract: Electrochemical splitting of water into hydrogen and oxygen is a potential source of renewable fuels, however it is limited by the large overpotentials required to oxidize water to molecular oxygen limiting the efficiency of the process. Consequently, materials that can catalyze the oxidation of water are an important area of study. We are exploring the potential of the cobalt compound [Co(dipyvd)2]2+ (where dipyvd is a redox active radical ligand) as a water oxidation catalyst. The compound undergoes several oxidation-reduction reactions and can exist as [Co(dipyvd)+, [Co(dipyvd)2]2+, or [Co(dipyvd)2]3+. Our initial tests suggest that in solution of acetone, [Co(dipyvd)2]2+ reacts with water to form the reduced species [Co(dipyvd)2]+ presumably by oxidizing water. Since the return oxidation is electrochemically facile, this may form the basis of a catalytic cycle. Currently we are investigating the water oxidation reaction using UV-visible spectrometry to investigate the reaction kinetics and stoichiometry. We will use triphenylphosphine to trap hydrogen peroxide or other reactive oxygen species that may be products of water oxidation. We will be using 31P NMR to monitor whether the trapping reaction is taking place. Further studies will include pH and solvent and temperature dependence to further understand the nature of the reaction. Ultimately, we expect to understand whether [Co(dipyvd)2]2+ or similar compounds have potential in the catalytic oxidation of water.

THU - 919 Effective Reproducibility of Microbial Fuel Cells

Discipline: Chemistry
Subdiscipline: Other Chemistry

Khala Harvey*, *Los Angeles City College* and Terry Boan, *Los Angeles City College*

Abstract: Microbial fuel cells (MFC) are an emerging technology that uses anaerobic bacteria as biological catalysts to produce electrical charge. Low electricity output and high cost are two problems facing the development of MFCs, however, MFC technology shows promising application and cost effectiveness to wastewater treatment. To study the applications of MFCs for this purpose, a simple two-chamber design was constructed the previous summer out of 1.5-L food containers, the proton exchange membrane (PEM) from a toy hydrogen fuel cell, and cow manure from a nearby farm as the bacteria source. The cell saw some success, briefly reaching a maximum voltage of 0.35

mV before the membrane deteriorated. A more durable cell was constructed for further testing, utilizing a new two-chamber cell design consisting of a small cathode chamber within a larger anode compartment and a larger membrane. Unfortunately, the first test revealed no readable voltage; the outcome arose many questions on the reproducibility of MFCs and how MFCs differ from normal concentration battery cells. The literature reveals a lack of understanding of how MFCs function and reports opposing results on the effectiveness of different components and designs. The next stages of experimentation will be to determine the materials and procedures to produce an effective MFC for study, specifically the type of PEM, the materials used for the electrode, and relevance of ions in the anode and cathode.

THU - 920 A Density Functional Computational Investigation of Derivatives of 2,4-D: Patterns That May Imply Physiological Effects

Discipline: Chemistry
Subdiscipline: Other Chemistry

Amanda Martinez*, *Humboldt State University* and Robert Zoellner, *Humboldt State University*

Abstract: The widely-used herbicide 2,4-dichlorophenoxyacetic acid (2,4-D) is a commonly used chemical throughout the Yurok Ancestral territory by timber companies and interest groups in Northern California. Natives within the Yurok lands have been exposed to chemicals such as 2,4-D, which has been controversially linked to Parkinson's Disease and other physiological effects. Density functional calculations of 2,4-D and chloro-derivatives of 2,4-D were conducted using the *Spartan '16* program. Calculations at the B3LYP-D3/6-311++G** and the ωB97X-D/6-31G* levels of theory were used to determine the equilibrium geometry, total electronic energy, the energy of the lowest unoccupied (LUMO) and highest occupied (HOMO) molecular orbitals, the molecular polarizability, zero point energy, standard molar entropy, standard Gibbs free energy, standard enthalpy, specific heat capacity at constant volume, and the dipole moment for all molecules in both the ground and excited states. Trends in these properties will be discussed with regard to both ground and excited states in these molecules.

THU - 921 The Effect of Bacterial Sustenance Composition on Microbial Fuel Cell Optimization

Discipline: Chemistry
Subdiscipline: Other Chemistry

Linda Godinez*, *Los Angeles City College*; Nallely Dominguez, *Los Angeles City College* and Terry Boan, *Los Angeles City College*

Abstract: Microbial fuel cells (MFCs) are electrochemical cells that convert organic material into energy using microorganisms as catalysts, which encourage and facilitate the movement of electrons throughout the system. The objective of this project is to investigate and optimize the processes of MFCs in a cost-effective and efficient manner. Since the biochemical mechanisms rely heavily upon bacterial culture sustenance, an understanding of the role of feed concentration and type on the energy output of the cell is critical. Out of the three primary macronutrients it is expected that feed solely composed of carbohydrates will yield the highest amount of energy, since its decomposition generates two compounds that are crucial in anaerobic metabolism- acetate and carbon dioxide. An MFC was constructed out of cylindrical plastic food containers connected by a Nafion membrane-equipped PVC pipe, as well as outfitted with a plastic spigot and valves for pressure and waste regulation. Feed was administered via syringe insertion through a duckbill valve that keeps the internal environment of the anode chamber oxygen-free. Data acquisition was performed using a 7-function digital multimeter on a bi-weekly basis. The control manure sample, without additives, produced readings that were less than 0.100 V. Conversely, the carbohydrate-rich sample replicated the system's energy output literature value of 0.350 V. It is essential to continue research in this rapidly evolving technology since it has the potential to create a sustainable and clean energy source for our increasingly energy-demanding society.

THU - 922 Developing High-Affinity Small Molecule Inhibitors of Mutant K-Ras Using 2D and 3D QSAR Models

Discipline: Chemistry
Subdiscipline: Other Chemistry

Ashley Westerfield*, *Broad Institute of MIT and Harvard* and Alisha Caliman, *Broad Institute of MIT and Harvard*

Abstract: K-Ras is an oncogenic GTPase that has been implicated in a variety of human colonic and pancreatic cancers. Endogenously responsible for controlling cell proliferation, differentiation, and development through binding to GDP/GTP, the K-Ras protein acts as a conformational switch that regulates many downstream pathways in the cell. Mutations in K-Ras – particularly the exchange of glycine for aspartic acid at the 12th amino acid (G12D) – cause the protein to become constitutively active, inducing uncontrolled cell growth. As a result, finding a small molecule drug that binds to and inactivates K-Ras can potentially halt this cell growth, allowing the cancer to become more targetable and treatable by conventional cancer therapeutics like chemotherapy. Our goal is develop K-Ras inhibitor compounds with nanomolar level affinity. To help develop such a compound, we are building QSAR models, a machine learning technique that allows us to predict the binding affinity (and other properties) of new compounds by analyzing the 2D and 3D structures from a library of known compounds. To validate this model, we will apply the leave-one-out cross validation method, and monitor several metrics, including the R_2, Q_2, and RMSE of the known activity against the predicted activity. This model will allow us to predict the binding activity of new K-Ras inhibitors before they are synthesized, which will help us triage compounds that will bind to K-Ras with nanomolar affinity.

THU - 923 Investigating the Structural Attributes and Molecular Mechanisms of Cooa (CO oxidation Activator protein) Regulation and Activity

Discipline: Chemistry
Subdiscipline: Other Chemistry

Benazir Bhutto Oluoch*, *San Francisco State University*; Kloe Elizabeth Keeter, *San Francisco State University*; Paulina Hernandez, *San Francisco State University*; Austin Kevon Murchison, *San Francisco State University* and Raymond Esquerra, *San Francisco State University*

Abstract: The use of biological sensors is increasingly prevalent in monitoring environmental pollution and in food safety. In nature, the photosynthetic bacterium *Rhodospirillum rubrum* is a biosensor that can respond to and metabolize carbon monoxide (CO) to obtain energy as an alternative to photosynthesis and aerobic respiration. Carbon monoxide oxidation activator (CooA) is a heme-containing transcriptional activator in *R. rubrum,* responsible for sensing CO and activating the expression of the CO metabolic pathway. CooA is a member of the CRP/FNR (cAMP receptor proteins/fumarate and nitrate reductase), existing as a homodimer with two domains on each monomer: the C-terminal helix−turn−helix DNA-binding domain and N-terminal heme-binding regulatory domain for detecting gaseous ligands. The CO-heme bond in CooA is proposed to induce conformational changes within the dimers, allowing for DNA binding. This project aims to reveal the heme domain regulation mechanism of CooA activity by examining how protein architecture influences ligand binding dynamics. We will use steady-state and time-resolved absorption, as well as circular dichroism (CD) and magnetic circular dichroism (MCD) spectroscopies on wild-type and mutant CooA, to reveal how the heme pocket protein environment modulates the structural changes that govern CooA activity. Specifically, MCD and absorption spectroscopies will probe the heme's electronic environment and CD spectroscopy will show changes in secondary and tertiary structures associated with ligand binding. Our work seeks to understand how natural biosensors function by examining their structural characteristics, molecular ligand interactions and regulatory activity. These studies will inform the design of efficient biosensors using CooA as an engineering template.

THU - 924 Generation of Low-Affinity Antibody Fragments for High-Density Superresolution Imaging of Endogenous T Cell Receptors

Discipline: Chemistry
Subdiscipline: Other Chemistry

Ariana De Jesús Hernández*, *University of Puerto Rico at Cayey*; Thilini Perera, *University of Illinois at Chicago* and Ying Samuel Hu, *University of Illinois at Chicago*

Abstract: Plasma membrane proteins play central roles in signal transduction and disease biology. Despite their importance, the molecular mechanisms that underlie the assembly of membrane proteins into signaling complexes of various compositions and the functional roles that individual protein clusters play remain highly controversial since there is a lack of appropriate imaging tools for nanoscale level. Even though single-molecule localization microscopy appears as a great alternative for imaging, the high molecular density present in signaling clusters hinders the appropriate labeling of molecules due to the steric hindrance from the antibodies. In this project, we generated low-affinity antibody fragments (Fabs) from OKT3 monoclonal antibody to achieve high-density labeling and imaging of endogenous T cell receptors (TCRs) on the plasma membrane. We hypothesize that through the development of this new imaging approach, we will be able to determine the clustering state of TCRs on chemically fixed Jurkat T cells attached to non-activating surfaces. To generate these low-affinity fragments, we used immobilized papain to break the peptide bonds in the hinge region of the IgG molecule, and these fragments will be subject to a newly developed method using chaotropic agents to promote a transient binding to targets. Preliminary results show that a ratio of 1:2 of antibody and papain gel is needed to obtain the desired fragments, and leave less undigested IgG heavy chain. These unique fluorescent probes should minimize the steric hindrance for TCRs clusters labeling, and enable new imaging tools for studying T cells membrane proteins.

THU - 925 **NMR Micro-Imaging Study of Broiler Chicken Livers for Cryopreservation**

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Ariga Sarkissian Nejad*, *California State University, Los Angeles*; Erick A. Avila, *California State University, Los Angeles* and Yong Ba, *California State University, Los Angeles*

Abstract: Cryopreservation is a method for long-term preservation of living cells, tissues, and organs at low temperature without causing fatal freezing damage. Cryoprotective agents (CPAs), such as dimethyl sulfoxide (Me$_2$SO) and glycerol, are commonly used as the ingredients to treat cellular tissues and organs to prevent ice crystal formation which may cause cell and tissue damages. This study focuses on investigating the freezing and melting patterns of broiler chicken livers after treatments with Me$_2$SO and glycerol modified with University of Wisconsin (UW) solutions by the method of Nuclear Magnetic Resonance (NMR) micro-imaging. Me$_2$SO and glycerol were used at various concentrations from 5.0% to 40.0% v/v with UW solution to make the CPA solutions. The use of UW solution allows for maintaining the physiological osmolarity of the organs. Treatments of the livers using the CPA solutions were done using a combined method of diffusion and perfusion. Diffusion method allows for the CPAs to enter the liver through penetrating the organ's external surface, while perfusion method allows for the CPAs to enter the organ through flushing the hepatic arteries and portal vein. Various conditions including duration and number of repetitions in the treatment were also applied. Freezing and melting points of the livers were analyzed, and also compared with two control livers which were not treated, and treated with only UW solution, respectively. The mechanical damages to the tissues were also assessed. This study provides useful information to optimize CPA solutions and the procedure of treatment for liver cryopreservation.

THU - 926 **The Transition Edge Sensor and Examination of Nitrogen Moieties on Nanoscale Diamond**

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Jocelyn Valenzuela*, *San Jose State University*; Cynthia Melendrez, *San Jose State University*; Grace Jeanpierre, *San Jose State University*; Polo Tran, *San Jose State University*; Dennis Nordlund, *SLAC National Accelerator Laboratory*; Charles Titus, *Stanford University*; Kent Irwin, *Stanford University*; Virginia Altoe, *Molecular Foundry* and Abraham Wolcott, *San Jose State University*

Abstract: The nitrogen-vacancy center in diamond is a promising tool for oncology, magnetometry, electric field sensing, quantum cryptography, and quantum communication. High-pressure high-temperature (HPHT) nanodiamonds (NDs) host nitrogen-vacancy centers (NVCs) and can be deployed in biological applications. Amine chemistry was used to activate the inert surface of HPHT NDs to provide a flexible platform for biological applications, such as bioconjugation of small molecules and plasmonic shells. To characterize the surface of aminated NDs, samples were deposited onto gold wafers and probed with 100-1300eV radiation at the Stanford Synchrotron Radiation Lightsource (SSRL beamline 10-1) with the transmission edge sensor (TES) under ultra-high vacuum conditions. The ultra-sensitive TES can provide element-specific and background-free x-ray detection without a diffraction grating. With the TES, background signal from carbon was eliminated to reveal compelling nitrogen signals from the modified HPHT NDs. X-ray emission spectra reveal amine and imide moieties at 397-410eV, verifying the success of our amination chemistry and enabling new reaction pathways targeting amine moieties. The TES detector provides unparalleled nitrogen signal-to-noise and is a powerful tool to investigate fluorescent ND surface chemistry.

THU - 927 **Measurement of Redox Potentials of Photogenerated Hot Carriers in Gold Nanoparticle Photocatalysts**

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Anthony Garcia*, *University of California, Merced*; Ziliang Mao, *University of California, Merced*; Randy Espinoza, *University of California, Merced*; Hnubci Vang, *University of California, Merced* and Son Nguyen, *University of California, Merced*

Abstract: Photo-induced hot carriers have been demonstrated to be effective catalysts in oxidation-reduction reactions. The redox potentials of these hot carriers are largely unknown and bring about complications in developing catalytic mechanisms for these reactions. We propose that the redox potentials of the hot carriers can be determined through the equilibrium constant K for the photo-oxidative etching of gold nanoparticles by Fe^{3+}. This reaction can be monitored through UV-Vis absorption spectroscopy and the concentrations of reactants and products at equilibrium can be determined. The Nernst equation is then utilized to calculate the redox potentials of the hot carriers for the photocatalyzed reaction at equilibrium. Through this method, the redox potential of hot carriers can be characterized as a function of excitation wavelength and optical power. Preliminary results indicate that reaction equilibrium is reached and shifted as the excitation wavelength changes which demonstrates that the redox potentials of hot carriers are dependent on excitation wavelength. This knowledge about hot carrier redox potential and its dependence on wavelength and optical power will provide some guidance in the search for the optimal conditions of photocatalyzed reactions in industrial applications.

THU - 928 **Computational Prediction of the Thermodynamic Stability of Solid CO2 Phases**

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Steve Peralta*, *California State University of Los Angeles* and Olaseni Sode, *California State University of Los Angeles*

Abstract: Carbon dioxide is one of the most common and readily known molecules in the world, and its increased abundance in the atmosphere as a greenhouse gas is an active area of research. Less is known about the molecule in the condensed phase (e.g. liquid and solid). There are at least seven known phases of solid carbon dioxide that exist at specific temperatures and pressures; yet, there is evidence that some of these phases have been misidentified, due to their similar structure and the lack of sensitivity of experimental methods. Empirical and ab initio theoretical methods can help clarify the solid carbon dioxide phase diagram. We have employed three different CO2 potential energy functions (SYM, Tajima, and mbCO2) to predict the finite-temperature properties of three phases(I, II, III) of solid carbon dioxide. For each phase and potential energy function, the Gibbs energy was computed at varying pressures, ranging from 0 to 50 GPa, and at varying temperatures, from 0 to 600 kelvin. From this data, partial theoretical phase diagrams were produced and compared to the experimentally determined diagrams.

THU - 929 **Determining the Presence of Hole Escape Routes in Proteins from the Protein Data Bank**

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Hector Torres*, *Universidad de Puerto Rico, Cayey*; David Beratan, *Duke University*; Agostino Migliore, *Duke University* and Ruijie D. Teo, *Duke University*

Abstract: Processes crucial for the sustainability of life on earth, such as photosynthesis and cellular respiration, are largely based on redox reactions. These reactions are catalyzed by a wide array of enzymes that allow them to achieve biochemical transformations via highly reactive intermediates. These same intermediates, if not dissipated, can cause damage to biological systems by producing reactive oxygen species (ROS), leading to protein backbone oxidation and fragmentation, or other oxidative damage. A recently proposed mechanism to neutralize potentially damaging species suggests that proteins may rely on electron-hole hopping escape routes formed by redox-active residues. These routes can direct damaging holes away from protein active sites and onto the protein surface, where they may be neutralized by reducing equivalents. This work encompasses a search of the Protein Data Bank (PDB) for the presence of redox-active residues in amino acid sequences that could constitute these escape pathways. Furthermore, an in-depth hole-hopping analysis of selected protein candidates will be conducted based on known protein crystal structures. Through this analysis, we hope to correlate the presence of redox-active residues with the proposed electron hole hopping escape routes. The results obtained will aid in the understanding of how Nature may have evolved hole hopping protective mechanisms for protein protection in an oxidizing environment.

THU - 930 Length and Charge of Water-Soluble Peptoids Impact Binding to Phospholipid Membranes

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Fabiola Gutierrez*, *Santa Clara University* and Grace Stokes, *Santa Clara University*

Abstract: Understanding how *N*-substituted glycine oligomers (peptoids) interact with human cell membranes is important because peptoids may be used intherapeutics and in coatings in biosensing applications.However, a natural human cell membrane is complex, making it difficult to study interactions on a molecular level, so our lab synthesized artificial lipid membranes to learn about adsorption at the bilayer in a much more controlled and simplified manner.Artificial lipid bilayers of different compositions, cholesterol content, and head group charge at a range of pH conditions represented lipids found in different tissue types. We used second harmonic generation (SHG), a laser-based nonlinear optical technique, to quantitatively describe adsorption of water-soluble peptoids to artificial lipid membranes.We discovered that increases in sequence length, hydrophobicity and in the overall cationic charge of the lipid resulted in higher adsorption to zwitterionic lipid bilayers. These studies elucidated the molecular-level forces that drive adsorption in order to predict how changes to sequence and 3D structure alter membrane association.

THU - 931 Mapping the Electric Potential of Weakly Electric Fish

Discipline: Physics & Astronomy
Subdiscipline: Physics

Carmen Stepek*, *California State University Channels Islands* and Brian Rasnow, *California State University Channels Islands*

Abstract: Electric organs serve several vital functions in the animal kingdom. In Physics/Biology 497, I have been conducting research with a diverse group of student researchers, alongside Dr. Brian Rasnow, to further his exploration of electric organ discharge (EOD) in weakly electric fish. Voltage and wave pattern of the dipole-like electric fields depend on size and species of fish, as well as the conductivity in the water. Our research is interested in how Mormyridae and Gymnotiformes utilize these mechanisms for communication and electrolocation. By incorporating biology, evolution, physics and computer science, our interdisciplinary research group is developing a modern apparatus to map the EOD of weakly electric fish. When the prototype, made of a robotic x-y plotter attached to four small electrodes, is combined with powerful software and algorithms, obtaining precise measurements is simple. We relay the coded instructions to an Arduino microcontroller, which directs the apparatus and provides accurate x-y-z coordinates. Then, our program in Matlab is implemented to record high-resolution data of each vector representing the electric field(s) of the EOD. Current developments are focused on reducing the uncertainty of our simulations to more accurately analyze these small, rapid waveforms. This research will better the scientific community's understanding of electrolocation and provide a systematic technique for mapping EOD of weakly electric fish.

THU - 932 Microwave Synthesis and Comparison between $NaYF_4$, LaF_3 Nanoparticles with Tm, Yb Dopant for Photobiomodulation Application

Discipline: Physics & Astronomy
Subdiscipline: Physics

Emmitt Zamora*, *University of Texas at San Antonio*; Jacob Flowers, *University of Texas at San Antonio*; Sumeyra Tek, *University of Texas at San Antonio* and Kelly Nash, *University of Texas at San Antonio*

Abstract: Lanthanide-doped nanoparticles are widely used in a variety of fields due to their tunable size and unique optical properties. Despite their use, there is continued research in the optimization of their optical emission, especially towards their use in biological applications. In this comparison study, synthesized $NaYF_4$ and LaF_3 core nanoparticles are doped with select lanthanide ions in order to observe their upconversion photoluminescence upon excitation by either 808 nm or 980 nm wavelengths. We demonstrate through a microwave-assisted synthesis technique, the core shell around the crystal host enhances energy transfer particularly in UV-blue emission wavelengths. Photoluminescence spectra were acquired through exciting the nanoparticles by 808 nm or 980 nm. Zeta potential and dynamic light scattering (DLS) reveal a surface charge and size of 35 mV and 140 nm, respectively. Transmission Electron Microscope (TEM) show the particles to have a lenticular morphology and X-ray diffraction (XRD) confirm that the structure of both LaF_3 and $NaYF_3$ is cubic. We further test the biological response of these nanoparticles using retinal pigment epithelial (RPE) cells upon uptake after 24-hours and then optical stimulation through measurement of viability and reactive oxidative species (ROS) 24-hours. The results of this study provide the basis of future applications of these materials for photobiomodulation applications.

THU - 933 Hunting the Fourth Neutrino By Simulating the Daya Bay Nuclear Reactor Experiment

Discipline: Physics & Astronomy
Subdiscipline: Physics

Charles Marrder*, *University of Notre Dame* and David Ernst, *Vanderbilt University*

Abstract: Neutrinos are light, Weakly-interacting particles that come in three types, or “flavors” – electron, muon and tau. Neutrinos of one flavor have been found to change into neutrinos of another flavor, a phenomenon called neutrino oscillation; this oscillation is governed by two parameters specific to the neutrinos – mass-squared difference and mixing angle. Numerous nuclear reactor experiments researching neutrino oscillation have detected significantly less electron antineutrinos than expected. The mass-squared difference consistent with this disappearance is four hundred times greater than the largest mass-squared difference found in experiments that reproduce oscillations consistent with the three known neutrinos. A possible explanation is the existence of a fourth neutrino, called a “sterile” neutrino, which does not interact via the Weak force. The most accurate of these reactor experiments, the Daya Bay experiment, is especially interesting due to its grand scale; it uses six nuclear reactors as antineutrino sources and collects data from eight antineutrino detectors. We investigate the antineutrino disappearance by simulating the Daya Bay experiment and examining the feasibility of the sterile neutrino via chi-square statistical analysis. We require our model be consistent with the three-neutrino analysis of the Daya Bay experimentalists. They extrapolated their analysis up to a mass-squared difference of 0.3 eV^2/c^4 and found no evidence of a fourth neutrino. Using our model, we extend this extrapolation up to 10 eV^2/c^4, thus including mass-squared differences where other experimentalists suggest a fourth neutrino. Our preliminary results indicate Daya

Bay significantly prefers the existence of a fourth neutrino in this region.

THU - 934 Developing a Supercapacitor As an Energy Source for Low-Power Flexible Electronics

Discipline: Physics & Astronomy
Subdiscipline: Physics

Danny Attiyah*, *University of California, Irvine* and Tse Nga Ng, *University of California, San Diego*

Abstract: Flexible Electronics are one of the most promising technological advancements across many different fields. From commercial products to ECG instruments, these devices have a wide variety of applications. One of the issues that arises in the production of these electronics is how to power them. The focus of this project will be to develop a supercapacitor suitable for powering a low-power device. Supercapacitors are preferred over other energy sources, such as rechargeable batteries, because of their ability to operate after a high number of charge-discharge cycles. In addition, they do not require complex charging circuits, and they can be utilized at almost any temperature. A supercapacitor will be built and its performance will be tested through state-of-charge assessments. Carbon-based material will be used for the capacitor plates and electrolytic solution will be used to separate the plates. The capacitance and lifetime will be measured after 1000 charge-discharge cycles to test the long-term performance of the device. We will model the supercapacitor using multiple branches of RC circuits, and the measurements taken will be compared with the expected results from the model.

THU - 935 Interpreting Particle Motion in Low-Gravity, Asteroidal Conditions with Image Processing and Analysis

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Gillian Gomer*, *University of Central Florida* and Adrienne Dove, *University of Central Florida*

Abstract: Asteroids and moons are small, atmosphereless bodies with dynamic surface activity that complicates remote imaging and selection of future exploration sites. To better understand the distributions of surface material (regolith), the Strata-1 experiment utilized the microgravity, vibrational environment of the International Space Station (ISS) to replicate asteroidal conditions. Image data was collected, in which we observe both times of disruptive “events” and more passive “non-events” that cause small changes. The experiment contained several types of material to simulate asteroid surfaces. Here we analyze a single tube that contained aspherical glass shards. We have written a Python routine to split the red, green, and blue (RGB) image components to isolate each set of colored particles and analyze how the surface area coverage of each color varies over time within different sections of the experiment. We are able to track changes in areas dominated by particular shard color sets, and compare those results to density of shard center coordinates manually extracted for two events and two non-events. We will use this data alongside data from qualitative descriptions of the entire dataset, as well as acceleration data from the ISS, to help understand the effect of changing acceleration vectors on regolith movement patterns. This analysis will help us interpret how similar motion might occur to mix the particles on the surfaces of asteroids and small moons.

THU - 936 Galaxy Bridges on FIRE

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Luis Martinez Patino*, *Harvey Mudd College* and Jorge Moreno, *Pomona College*

Abstract: Galaxy tails and bridges are the hallmark of the most spectacular galaxy-galaxy interactions in the night sky. In this work, we investigate the physics behind the formation and evolution of galactic bridges. We employ a suite of 24 high-resolution galaxy merger simulations, which rely on the novel “Feedback In Realistic Environments” (FIRE) model. This model is capable of resolving individual Giant Molecular Clouds, and of capturing the small-scale physics of the interstellar medium. With this framework, we can investigate how bridges are formed, their extent and duration, the amount of in-situ star formation within them, and the importance of stellar and gaseous migration as these features form. Our key science goal is to determine which orbital parameters controlling our mergers drive in-situ star formation, stellar migration and, mass transfer. Future work includes a thorough comparison with low redshift systems, to determine the relative importance of bridges in galaxy evolution.

THU - 937 Optimal Mass, Spin, and Orientation Parameters for Detecting Higher Order Gravitational-Wave Modes from Binary Black Hole Mergers

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Mahlet Shiferaw*, *Harvard University*; Alan Weinstein, *California Institute of Technology* and Liting Xiao, *California Institute of Technology*

Abstract: Thus far, the Advanced Laser Interferometer Gravitational-Wave Observatory (aLIGO) and Advanced Virgo have detected gravitational waves (GWs), or ripples in the curvature of spacetime, from dozens of binary black hole (BBH) and binary neutron star (BNS) mergers. In order to detect the GWs from these mergers, aLIGO data are optimally searched using matched filtering against a bank of model waveform templates which are well-described by General Relativity (GR). Currently, such searches only utilize waveforms for the dominant Y22 mode, neglecting higher order modes (HOMs). However, these HOMs carry information about the source and the radiation it emits, and are therefore of great interest to study. Our goal is to identify the presence of HOMs in signals found in the data in order to test GR. Using a newly-released catalog of BBH simulations with HOMs developed by the Simulating eXtreme Spacetimes (SXS) Collaboration, we will assess the capabilities of aLIGO for detecting HOMs. Such detections are currently very unlikely, as HOMs are two or more orders magnitude lower in amplitude than the dominant mode, and tend to lie outside of LIGO's sensitive frequency band for low-mass systems. Constrained by this strain sensitivity, we aim to determine the range of BBH mass, spin, and orbital orientations which optimizes the likelihood of detecting HOMs. We will do so by injecting SXS waveforms with HOMs into aLIGO recolored noise and analyzing the results, thus paving the way for a powerful test of GR in the strong-field highly dynamical regime.

THU - 938 Experimental Constraints on Ocean Wave Erosion of Icebergs and Glaciers

Discipline: Physics & Astronomy
Subdiscipline: Other Physics and Astronomy

Adriana Formby-Fernandez*, *Embry-Riddle Aeronautical University*; Alexander Robel, *Georgia Institute of Technology* and Samantha Buzzard, *Georgia Institute of Technology*

Abstract: Loss of ice from glaciers and ice sheets has been steadily increasing over recent decades due to rising oceanic and atmospheric temperatures. White (1980) developed a theoretical estimate for the erosion rate of icy surface by wave activity, which has since been used as the sole basis for calculating wave melting effects in ocean and ice sheet models. In this study, we conduct the first new experiments since White (1980) to test the established parameterization and extend it to a wider range of wave and water properties. A custom-built 1.2 meter long wave tank is used to simulate the behavior of ocean waves on ice shelves in a laboratory-scaled manner. White’s theory is tested for a wide range of conditions to within a reasonable margin of error (given the limitations of the tank and required assumptions). We further discuss how the results from this experiment can help to improve models of the high-latitude oceans for the benefit of predicting future climate, and assessing iceberg hazards to shipping.

8:45 AM – 10:45 AM

Friday Graduate Posters

FRI - G1 A Tale of Two Thiocarbonyl-Based H_2s Donors

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Matthew Cerda*, *University of Oregon* and Michael Pluth, *University of Oregon*

Abstract: In addition to nitric oxide and carbon monoxide, hydrogen sulfide (H_2S) is an important biological signaling molecule. Over the last three decades, H_2S-mediated signaling has been observed in a number of vital physiological processes including vasodilation, neurotransmission, and angiogenesis. Overall, the biological impact of H_2S has inspired researchers to harness H_2S in a therapeutic fashion to treat conditions and diseases associated with aforementioned processes. Towards this goal, our lab has developed a palette of chemical tools to deliver and study H_2S under physiological conditions. Drawing parallels to the endogenous production of H_2S via cysteine catabolism, we have developed the use of thionoesters and dithioesters as H_2S donors. Inspired by the well-established reactivity of native chemical ligation, we hypothesized thionoesters, a structural isomer of thioesters, would undergo similar reactivity in the presence of cysteine to generate H_2S. We demonstrate *via* a comprehensive mechanistic and kinetic study, a representative *bis*(phenyl) thionoester reacts rapidly ($k_2 = 9.1 \pm 0.3\ M^{-1}\ s^{-1}$) in the presence of cysteine at physiological pH to yield an equivalent of H_2S and a cysteine-derived dihydrothiazole. Improving upon this work, we identified a dithioester intermediate as a scaffold for tuning H_2S release from these donors. We observe similar H_2S-releasing efficiencies from dithioesters and find these donors provide higher selectivity for cysteine over other biological thiols including reduced glutathione. Furthermore, we demonstrate the ability to tune the rate of cysteine-triggered H_2S release via simple alkyl functionalization.

FRI - G2 Evaluation of Force Field Performance in *in Vacuo* Molecular Dynamics Simulations of Native-like Gas-Phase Protein and Protein Complex Ions

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Amber Rolland*, *University of Oregon* and James Prell, *University of Oregon*

Abstract: Ion mobility spectrometry (IMS) measures collision cross-sections (CCS), analogous to an average “shadow”, providing ion shape/size information and helping differentiate between conformations of protein complexes of equal mass. Comparing experimental CCSs to those calculated for various condensed-phase conformations is useful for determining conformation. However, experimental CCSs are often smaller than calculated values. One approach to reconcile these differences is to perform *in vacuo* molecular dynamics (MD) simulations of condensed-phase structures prior to CCS calculation. These simulations are often limited by the accuracy of the force field (FF) being used, and there has been little direct comparison of the many different FFs available.

To address this knowledge gap, we performed *in vacuo* MD simulations using five different FFs on a set of widely-used calibrant protein ions for which validated experimental CCSs are available. We calculated CCSs of the MD-simulated structures, enabling direct comparison with experiment and between FFs. All five FFs compacted structures overall but differed in detail. GROMOS96 43a2 performed best, with calculated CCSs within ~4% of experiment. We further validated these results by repeating our methods for three membrane proteins with published experimental CCSs and by using GROMOS96 43a2 to perform simulations of different conformations of pore-forming toxins, providing insight into their assembly mechanisms. These results demonstrate that simple *in vacuo* MD simulations are sufficient to accurately capture gas-phase collapse of large protein ions in IM-MS, and we expect implementation of the best FF identified here in more sophisticated computations will further improve structure determination using native IM-MS.

FRI - G4 Nature of the Magnetic Anisotropy in the Two-Dimensional Honeycomb Ferromagnet CrI_3

Discipline: Physics & Astronomy
Subdiscipline: Physics

Franz Utermohlen*, *The Ohio State University*; Inhee Lee, *The Ohio State University*; Kyusung Hwang, *The Ohio State University*; Daniel Weber, *The Ohio State University*; Nandini Trivedi, *The Ohio State University*; Chi Zhang, *The Ohio State University*; Johan van Tol, *National High Magnetic Field Laboratory*; Stephen Hill, *Florida State University*; Joshua Goldberger, *The Ohio State University* and P. Chris Hammel, *The Ohio State University*

Abstract: The recent discovery of intrinsic ferromagnetism in two-dimensional (2D) van der Waals crystals, such as CrI_3, has drawn much interest due to its potential for future 2D spintronic applications; however, the nature of the anisotropic magnetic interactions that allow 2D ferromagnetism and determine T_C in these materials remains poorly understood. In this work, we provide a detailed description of the anisotropic spin interactions in monolayer CrI_3 using a microscopic spin Hamiltonian constructed from the symmetries of the system. We present the results of our mean field theory and linear spin-wave theory calculations for this model and explain which interaction is responsible for stabilizing 2D ferromagnetic order in this system. Finally, we provide estimates for the strength of each interaction by comparing these results to our experimental data from angle-dependent ferromagnetic resonance on bulk CrI_3 single crystals.

FRI - G5 Interfacing with Nanophotonic Chips Using Two-Photon Laser Lithography

Discipline: Physics & Astronomy
Subdiscipline: Physics

Edgar Perez*, *University of Maryland* and Kartik Srinivasan, *National Institute of Standards and Technology*

Abstract: Nanophotonic devices control the behavior of light at the nanometer scale, which makes them instrumental tools for communication and quantum information, but they suffer from drastic losses at their input and output facets. Two-photon laser lithography provides the means of creating free-from optical elements at microscopic scales, which makes it possible to create novel interfaces with nanophotonic chips. Special geometric shapes such as Cartesian Ovals, hyperbolas, or other aspherical surfaces could increase the coupling efficiency into these devices based on optimized results from traditional ray optics. On the other hand, complex structures such as chiral photonic crystals, would make it possible to circularly polarize light, potentially providing another way to encode information onto a quantum source. In this work, use a Nanoscribe GmbH two-photon lithography system to create several of these surfaces for the purpose of coupling into and out of nanophotonic devices. We present the machine vision techniques that enable the correct placement of these objects, the successful construction of these shapes, and their integration into optical systems. We found that free form optical elements were effective beam shapers at the interface between devices.

FRI - G6 A Compact Core-Shell-Shell Nanoparticle Architecture for Bright Upconversion for Bioimaging

Discipline: Materials Research
Subdiscipline: Materials Research

Chris Siefe*, *Stanford University*; Randy Mehlenbacher, *Stanford University*; Chunte Sam Peng, *Stanford University*; Yunxiang Zhang, *Stanford University*; Stefan Fischer, *Stanford University*; Alice Lay, *Stanford University*; Claire McLellan, *Stanford University*; A. Paul Alivisatos, *University of California, Berkeley*; Steven Chu, *Stanford University* and Jennifer A. Dionne, *Stanford University*

Abstract: Imaging and understanding subcellular processes require small optical probes. Mapping cellular responses with fluorescent nanoparticles has led to breakthroughs in fields ranging from labeling diseases to intra-cellular interactions. While

fluorescent probes are powerful tools, they are limited by poor photostability and large autofluorescence background. Upconverting nanoparticles (UCNPs), which absorb near-infrared light and emit visible light through a multiphoton process, provide several advantages over other bioimaging probes including minimal autofluorescence background and enhanced photostability. An outstanding challenge to using UCNPs as biomarkers is synthesizing bright UCNPs in small (sub-20 nm) size regimes due to prominent surface quenching and limited light absorption. We address these challenges with a new design of UCNP that separates sensitizer and emitter ions through a core-shell-shell (CSS) structure consisting of $NaYbF_4@NaY_{0.8-x}Er_xGd_{0.2}F_4@NaY_{0.8}Gd_{0.2}F_4$, maximizing Yb^{3+} content while varying Er^{3+} concentration (from 0.01 to 0.8) to optimize for bright UCNPs. Quantum yield, single particle brightness, and lifetime measurements are used to compare the structures. Despite such distinct nanoparticle architectures, the photodynamics of the CSS structure have some similarities to those of the typical core-shell (CS) structure, particularly at low Er^{3+} concentrations in the emitter shell. While the CSS structure exhibits a decreased upconversion quantum yield of 0.16% compared to 0.8% for the CS structure, the CSS structure is up to 2x brighter than the CS structure in terms of single particle brightness. Through this work, we demonstrate that complex multi-shell architectures can be manipulated to maintain brightness and potentially leveraged for sensing of individual molecules or external fields.

FRI - G7 Deep Neural Networks for Low-Resolution Photon-Limited Imaging

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Omar DeGuchy*, *University of California, Merced*; Fabian Santiago, *University of California, Merced*; Mario Banuelos, *California State University, Fresno* and Roummel Marcia, *University of California, Merced*

Abstract: Applications in image reconstruction and compressed sensing require recovering a true signal from noisy and undersampled linear measurements. These signals – often sparse in some basis – allows for the use of penalty based algorithms to promote sparsity in its reconstruction. This modality is typically found in applications such as medical imaging and night vision where measurements at the photon detector are corrupted by Poisson noise and thus modeled using the Poisson distribution. In this work, we implement deep learning methods to recover downsampled noisy signals often present in compressed sensing applications. As an alternative to relying on previously established optimization based algorithms, we implement stacked denoising autoencoders and convolutional neural networks to perform signal reconstructions. Moreover, we propose a Poisson autoencoder inverting network (PAIN) architecture to reconstruct compressed signals imposed with Poisson noise. We observe less computational costs associated with this method while improving on reconstructions from a traditional stacked denoising autoencoder and remaining competitive with a more complex architecture in terms of Mean Squared Error (MSE). We train all proposed architectures on the MNIST dataset and establish deep neural networks as a reconstruction method.

FRI - G8 Named Entity Recognition Guided By Dependency Trees Using Recursive Neural Networks with Relative and Global Attention

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Gustavo Aguilar*, *University of Houston* and Thamar Solorio, *University of Houston*

Abstract: Recognizing named entities in a sentence is a fundamental task for many applications in natural language processing (NLP). Although significant improvements have been made due to the advances in deep learning, many linguistic properties are yet to be explored in conjunction with these methods. Particularly, state-of-the-art neural models treat sentences as plain sequences of tokens, even though the language structure is naturally recursive. We hypothesize that linguistic properties focused on syntax allow these models to understand 1) the role of the words in the sentence, 2) the relationships among words regardless of how far apart they are, and 3) the information about entities exposed by specific words.

In our method, we syntactically represent sentences with dependency trees. Our neural network extracts syntactic features from the trees using the recursive Tree-LSTM architecture. These features are weighted by two attention mechanisms: relative and global attention. The former detects the most informative words in the sentence for each word being evaluated, whereas the latter spots the most relevant words in the text as a whole. We linearly project the weighted features onto the label space and use a Conditional Random Fields algorithm for the final predictions. Our findings show that the model detects words that reveal the entity types based on their syntactic roles in a sentence (e.g., verbs such as *speak* and *write* are associated to PERSON, whereas *meet* and *travel* strongly relate to LOCATION). The results support our hypotheses and establish a new state of the art on two popular datasets.

FRI - G9 An Ophthalmic Biomaterial for the Release of Cysteamine for Corneal Crystals in Cystinosis

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Jorge Jimenez*, *Department of Bioengineering, University of Pittsburgh*; Michael A. Washington, *Department of Chemistry, University of Pittsburgh*; Ken K. Nischal, *Children's Hospital of Pittsburgh* and Morgan V. Fedorchak, *Department of Ophthalmology, University of Pittsburgh School of Medicine*

Abstract: Cystinosis is a genetic, rare disease where the intracellular accumulation of the cystine causes tissue damage in multiple organs of the body. In the eye, cystine crystals grow predominately in the cornea, and appear as reflective spindle-like structures. These crystal deposits cause severe light sensitivity, blurred vision, foreign body sensation, and if left untreated, can cause corneal erosion. Eye drops containing the active drug, cysteamine, are used to treat cystine crystals. These eye drops are administered 6-12 times per day and require a new bottle every week due to the instability of cysteamine. While the eye drops are effective in treating the crystals, the frequency of administration and high instability make this therapy inconvenient for patients. As such, the development of an alternative treatment that delivers cysteamine for a longer period in a stable form may address these issues. The purpose of this study was to develop and test a thermoresponsive gel-based eye drop that contains cysteamine-encapsulated microspheres. A poly(N-isopropylacrylamide) (pNIPAAm) gel and Cysteamine-encapsulated poly(d,L-lactide-coglycolide) acid (PLGA) microspheres were developed and fully characterized in-vitro for cysteamine drug release, stability, and cytotoxicity. Cysteamine release was observed for up to 24 hours, with 80% of cysteamine released within the first 8 hours. Cysteamine was stable in its active form for up to 7 weeks. These studies result in a more stable formulation of cysteamine that delivers cysteamine for an extended time from a single drop. These research efforts may provide cystinosis patients with an alternative eye drop therapy

FRI - G10 Development of a Tissue Engineered Skeletal Muscle Model Containing Adipocytes to Emulate Diseased Muscle

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Francisca Acosta*, *The University of Texas at San Antonio (UTSA)*; Katerina Stojkova, *The University of Texas at San Antonio (UTSA)*; U-Ter Aondo Jia, *The University of Texas at San Antonio (UTSA)*; Kennedy Howland, *The University of Texas at San Antonio (UTSA)*; Eric Brey, *The University of Texas at San Antonio (UTSA)* and Christopher Rathbone, *The University of Texas at San Antonio (UTSA)*

Abstract: Intramuscular adipose tissue (IMAT) is fat deposited skeletal muscle fibers and has been implicated in playing a role in metabolic alterations that accompany age, inactivity, and disease conditions such as Type 2 diabetes (T2D). Tissue engineered skeletal muscle (TE-SkM) is a physiologically relevant way of studying the interaction of cells. The goal of these experiments was to create a TE-SkM model using satellite cells (SCs), resident adult stem cells in skeletal muscle, as the source of both myogenic and adipogenic cells in order to better understand the interaction between myogenic and adipogenic cells and create a clinically relevant model to study metabolic disease (e.g., T2D).

SCs were cultured inside fibrin gels in either control (CON) media or adipogenic (ADIPO) media for 14 days. Myogenesis and adipogenic differentiation were analyzed using RT-qPCR and histology, and tensile strength was evaluated using the Cellscale UStretch system. Statistical analyses were performed using ANOVA with Tukey's post-hoc test for multiple comparisons (n=4).

Treatment of constructs with ADIPO increased both the myogenic and adipogenic potential of the satellite cells as seen through the significant increase in expression of both adipogenic (Adiponectin/PPARGy) and myogenic (MyoD/Myogenin/MHC) genes concomitant with an increased deposition of lipids and formation of myotubes, respectively. Furthermore, preliminary data indicates the tensile strength was unaffected by ADIPO treatment. Due to our success in creating a TE-SkM modeling IMAT, future work will use these findings to test different populations of SCs, looking at their ability to form IMAT in a clinically relevant way.

FRI - G11 Effects of Temperature and Flow Rate on Varnish Removal By Chemical Flushes

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Daniel Eduardo Sanchez Garrido*, *University of California, Merced*; Ashlie Martini, *University of California, Merced*; Mickeal Ades, *University of California, Merced*; Zhen Zhou, *Chevron Lubricants* and Elizabeth Montalvo, *Chevron Lubricants*

Abstract: Varnish is an oxidative byproduct of lubrication that forms on the surfaces of mechanical components. Varnish buildup reduces clearances on precision parts increasing wear and reducing efficiency during operation. Varnish is often removed using chemical flushes. However, there is no standard method for evaluating the efficacy of various chemicals under different operating conditions. We have developed a custom test rig that enables quantitative characterization of varnish removal rates under controlled conditions. Here, the test rig is used to characterize the effects of fluid temperature and flow rate on varnish removal for an example chemical cleaner. The results show that varnish removal increases with increasing temperature and flow rate, and demonstrate the utility of the newly developed test rig and method for chemical cleaner characterization.

FRI - G12 Spare Parts Provision Using a Reliability Framework

Discipline: Engineering
Subdiscipline: Other Engineering

Alejandro Najera-Acosta*, *New Mexico State University*; Delia J. Valles-Rosales, *New Mexico State University*; Blanca R. Venegas-Mata, *Universidad Autonoma de Ciudad Juarez* and Luis Moreno Martin, *New Mexico State University*

Abstract: In industrial practice, the availability of production equipment is influenced by the time of its repair. The latter is also influenced by the time needed to obtain a spare component or replacement. Spare parts inventories are established in order to allow rapid replacement of failed parts and ensure continuity of the operations. However, provisioning of spare parts is a significant challenge because these components have characteristics that differentiate them from other products, they are designed for a specific use, its useful life is random, and its propagation is difficult to determine. For the current work, it is proposed a reliability-based approach, to estimate the failure risk of an equipment when it is subjected to its working conditions. The study is carried out in a local manufacturing company, utilizing engineering data to quantify the impact of influencing factors (covariates) on the reliability performance of non-repairable spares and to estimate its required number to maintain in stock.

The results of the reliability analysis of the component examined using the proposed approach show that the hazard rate considering the influencing factors of working conditions is 5.3 times higher than not considering them. The suggested framework establishes scientific basis for the parts provisioning in manufacturing systems and improves spare parts management activities by providing the engineers with a theoretical foundation based on logical and rational thought processes and tools. Future research suggests analyzing different components with other covariates, its formulation and integration when provisioning spare parts.

FRI - G13 An Investigation of Fertilizer Derived Uranium in Ohio Agricultural Soils

Discipline: Geoscience
Subdiscipline: Earth Science

Adolfo E. Calero*, *The Ohio State University* and W Berry Lyons, *The Ohio State University*

Abstract: Modern agricultural practices have evolved to accommodate the food needs of the growing global population. This outcome has led to an increase in the flux of agricultural chemicals and compounds to both natural waters and soils, such as nitrogen and phosphorus. Uranium is known to be present in phosphate fertilizers due to the association of uranium-series radionuclides in phosphate rock, from which the fertilizers are sourced. A number of previous studies propose phosphorus fertilizer as a source of uranium in natural waters through agricultural runoff. Potential uranium additions to soils through agricultural management practices need to be characterized. This study will be conducted at Waterman Agricultural and Natural Resources Laboratory in Columbus, Ohio and the Western Agricultural Research Station (WARDC) in South Charleston, Ohio. Both facilities are affiliated with The Ohio State University and are managed by the College of Food, Agricultural and Environmental Sciences (FAES). Uranium concentrations will be quantified for 200 to 250 samples of agricultural and non-agricultural/residential soils, as well as different phosphorus fertilizers used in Ohio, through inductively coupled plasma mass-spectrometry (ICP-MS) and X-ray fluorescence (XRF) techniques. Comparison of the chemistry of non-agricultural, residential, and agricultural soils under different management practices with phosphorus fertilizer-treated agricultural soils will provide insight on the ability of phosphorus-rich fertilizer to add uranium to the environment. Uranium concentrations in the sampled agricultural soils are expected to have above background levels.

FRI - G14 Unconventional Reservoir Characterization of the Cretaceous Agrio Formation, Argentina: A Mixed-Carbonate-Siliciclastic Mudstone Hydrocarbon Reservoir

Discipline: Geoscience
Subdiscipline: Geology

Raul Ochoa*, *University of Utah* and Lauren Birgenheier, *University of Utah*

Abstract: The mixed-carbonate-siliciclastic, Cretaceous Agrio Formation has recently drawn new attention in the hydrocarbon-rich Neuquén Basin of Argentina as an emerging unconventional mudstone play. The proposed sequence stratigraphic study plans to characterize the most basinal marine setting of the Agrio Formation and source rock intervals through use of a subsurface geophysical logs and proposed outcrop investigations. Prior field studies have identified greater potential source rock intervals in the lower Agrio Formation from outcrop from programmed pyrolysis and facies analysis. These outcrop studies with new northern studies will be correlated into the subsurface to characterize the reservoir quality, sequence stratigraphic variability, and the reservoir's hydrocarbon potential on the eastern fringe of the basin. We predict an increase in carbonate content in more distal settings with a reduction in siliciclastic content and an increase in source rock quality. Through a subsurface reservoir characterization approach, we expect to correlate outcrop source rock intervals into the subsurface and north across the basin. This will be further validated through a detailed sedimentology and geochemical assessment of northern outcrop studies using X-ray diffraction (XRD) and programmed pyrolysis to assess source rock quality. The diagenetic impact on reservoir quality and storage capacity will be investigated using thin sections and scanning electron microscopy (SEM). This project will aid in addressing the Agrio Formation's geographic spatial extent and its potential as an international hydrocarbon source rock unconventional reservoir.

FRI - G15 Using Real World Datasets to Analyze Sensitivity to Population Size in Carbonate Clumped Isotope Measurements

Discipline: Geoscience
Subdiscipline: Other Geoscience

Robert Ulrich*, *University of California, Los Angeles*; Jesse Bateman, *University of California, Los Angeles*; Harmony Lu, *University of California, Los Angeles* and Aradhna Tripati, *University of California, Los Angeles*

Abstract: Thus far, uncertainties in carbonate clumped isotope measurements (Δ47) were based on analyses of synthetic datasets created with errors reported in the literature. Literature datasets have gone through data cleaning protocols. Since the synthetic datasets only rely on these reported errors, they likely simulate a more ideal dataset rather than a same sized real-world dataset. Our first study looked at different levels of replication and cleaning protocols on the sensitivity of the accuracy and error of measurements. Here, also using real-world data, we analyze the sensitivity of the measurement accuracy and error to the size of the sample population.

We compare a smaller population of measurements (n = 65) to a heavily replicated control population (n= 600), both comprised of measurements of standard materials. We then perform bootstrapped sampling from these populations using varied replication to see how accurately said sampling predicts the true mean of a given population and the size of the error prediction across bootstrapped replicates. Effect of sample population size is determined by comparing between the test and the control populations bootstrap analyses.

Preliminary results indicate that these analyses are sensitive to population size, with the accuracy of predicting the population mean worse in the smaller test population than the larger the control population. The uncertainty in both populations converge in bootstrapping replicate sizes greater than 30. While these results show variability when using real-world datasets of different sizes, they also indicate a minimum level of replication above which this may not be relevant.

FRI - G17 Development and Testing of Motivational Interviewing Workshops for Tribal Communities

Discipline: Health
Subdiscipline: Public Health

Marissa Tutt*, *Northern Arizona University* and Nicolette Teufel-Shone, *Northern Arizona University*

Abstract: Motivational interviewing (MI) is a client-centered approach to improve behavior change using open-ended questions, reflective listening, affirmations and summaries. The practitioner focuses on the client's stages of change and motivates the client to adjust behavior. There has been an increase in the use of MI technique within Native communities to improve health disparities. Developing culturally-tailored MI training materials will improve MI knowledge and skills among tribal healthcare workers, thereby improving health education delivery and rapport with patients served. *Development of tailored MI curriculum*: An MI training team was created, which consisted of MI mentors from Northern Arizona University, a tribal liaison, tribal members and graduate assistants. The MI mentors provided existing materials and expertise. The tribal liaison provided enhanced communication between the university and tribe. Tribal members provided cultural insight and the graduate assistants conducted training and evaluation. *Creation of MI training material*: The team met to adjust existing MI materials to include tailored information and objectives. Focus groups were conducted with tribal health workers to assess the feasibility of adjusted materials. *Training of tribal healthcare workers*: 9 hours of training was conducted and the Motivation Interviewing Self-Efficacy Questionnaire (MISE) was used to measure skills and abilities of tribal healthcare workers. Tribal healthcare workers were trained and evaluated, MI knowledge was improved and use of tribal specific techniques was observed. Culturally tailored MI training materials were created, approved, and successfully utilized by tribal healthcare workers. The use of these materials are expected to improve health outcomes among tribal communities.

FRI - G18 Advancing the Science and Practice of Conserving Hihiwai (*Neritina granosa*)*:* Using Biology and Traditional Ecological Knowledge to Identify and Overcome Threats to an Endemic Hawaiian Gastropod

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Kiloaulani Ka'awa-Gonzales*, *Colorado State University*; Liba Pejchar, *Colorado State University* and William Clements, *Colorado State University*

Abstract: Aquatic gastropods make important contributions to global biodiversity and provide vital ecological services, yet are grossly underrepresented in biodiversity assessments and aquatic conservation efforts. Hihiwai, an amphidromous gastropod endemic to Hawaii, is dependent on healthy freshwater streams and has cultural and subsistence value to local communities. The objectives of this study are 1) estimate hihiwai population densities within and among four streams in Maui County, Hawaii along a longitudinal gradient and across age classes, 2) identify the ecological and anthropogenic factors associated with hihiwai density, and 3) identify how traditional ecological knowledge of local communities can be integrated into understanding the ecology and conservation of this species and ensuring long-term community engagement in conservation efforts. Given the ecological requirements of hihiwai, we hypothesized differences in density between natural flow and diverted streams as well as among age classes within a stream. To achieve our objectives, we plan to sample hihiwai using a standardized visual survey technique, and to record density in various size classes within quadrats. We will also measure a suite of geomorphological, hydrologic, chemical, climatic, and biological characteristics perceived to impact species density. In addition to reporting our ecological findings, we will discuss preliminary plans to conduct mixed methods qualitative inquiry in the local Molokai community through surveys, interviews, and participatory mapping. We expect the results of this study to provide new insights into the value of aquatic “bioindicators”, such as hihiwai, in developing effective local stream management strategies that benefit both ecological and human communities.

FRI - G19 Using a Biomechanical Model to Explore Feeding Performance at the Lower Size Limit of Suction Feeding- in the Aquatic Carnivorous Plant *Utricularia*

Discipline: Life Sciences
Subdiscipline: Biology (general)

Krizma Singh*, *California State University, Fresno*; Fatima Hidalgo, *University of California, Berkeley*; Otto Berg, *California State University, Fresno* and Ulrike Muller, *California State University, Fresno*

Abstract: The use of mechanical models is well established in engineering and biology and has led to new insights in fluid dynamics of organism-generated flows, especially for small animals. *Utricularia,* commonly known as bladderwort, uses specialized miniscule traps (with a mouth opening of about 0.2mm in diameter) to capture zooplankton prey by generating suction flows and sucking in the prey in less than a millisecond after being triggered. These suction flows are difficult to study due to the traps' small size and fast prey capture feeding strike. Therefore, we used hydrodynamic scaling laws to build a mechanical model which lets us enlarge the size and slow down the process, while preserving similar flow conditions (flow speed, pressure) as observed in actual organism. Our model comprises an armature driving a piston, which creates a suction flow through an aperture into a transparent chamber (test section); the piston and chamber are submerged in fluid. The set-up is optimized for particle image velocimetry to quantify flow and pressure fields. We observed flow field and calculated time transects to track how flow speed changes over time at a point in space half a gape from the mouth. We can use this model not only to simulate strike kinematics of bladderwort but also explore counterfactual cases which allow us to tease apart the role of individual parameters, i.e., pressure and time to peak pressure in generating fast, high-pressure-gradient flows. This will ultimately help our goal of understanding how these parameters affect suction feeding performance.

FRI - G20 Adaptations to Deadly Diets: How Poison Frogs Metabolize Pumiliotoxin

Discipline: Life Sciences
Subdiscipline: Biology (general)

Aurora Alvarez-Buylla*, *Stanford University*; Luis Coloma, *Centro Jambatu* and Lauren O'Connell, *Stanford University*

Abstract: All animals have mechanisms to deal with ingested toxic small molecules. For humans, these molecules include commercially available oral pharmaceuticals, which once ingested are often metabolized or cleared, reducing their efficacy. South American poison frogs have evolved to sequester the small molecule alkaloids present in their normal insect diet and accumulate them in skin glands to serve as a chemical defense against predation. The toxin repertoire carried by different species or populations of frogs is variable, and some poison frog species are further able to metabolize toxins into more potent forms. One example of toxin metabolism is that of the alkaloid Pumiliotoxin (PTX), which certain poison frog species enantioselectively convert into the more toxic Allopumiliotoxin (aPTX). This project used thermal proteome profiling to screen poison frog proteins that may interact with PTX and identified several Cytochrome P450s that may be responsible for this metabolism. In parallel, the ability to metabolize PTX was assessed in the lab using tissue lysate from different species and populations of poison frogs. We then performed a P450 sequence comparison of these different species who can and cannot convert PTX into aPTX to map enzyme function to protein sequence variation. Together, these findings shed light on the enzymatic mechanism responsible for the metabolism of PTX in some poison frogs.

FRI - G21 Arsenic and Estradiol: Do They Interact to Influence Breast Cancer?

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Chloe Greenhalgh-Adam*, *Northern Arizona University* and Catherine Propper, *Northern Arizona University*

Abstract: Arsenic (As) is an environmental toxicant found in groundwater, food, and soils worldwide. Arsenic water concentrations have been measured at and well above the EPA limit in many parts of the country. This remains a problem in rural and underdeveloped areas, putting underrepresented and impoverished populations at the highest risk for arsenic exposure. Arsenic exposure has been linked to type II diabetes, liver damage, reproductive and neurological deficits, and cancers. Estrogen is a primary mediator in normal and cancerous breast development; furthermore, there is evidence that As affects cell growth through interacting with estrogenic pathways. Some studies have confirmed a correlation between the development of breast cancer and As exposure; however, the mechanism is not fully understood. To further understand Arsenic's route of breast cancer carcinogenesis, I hypothesize that 1) arsenic will dose dependently influence proliferation, metabolism, and gene expression in breast cancer cells and 2) this effect will interact with estrogen signaling. MCF-7 cells and Zebrafish as a model organism will be used to investigate *in vitro* and *in vivo* effects of As on breast cancer. Thus far, our results have shown that As effects cell proliferation and viability dependent on As dose and estradiol presence, *in vitro*. Our results suggest that As and estrogen may interact to influence breast cancer.

FRI - G22 TRIM28 As a Candidate Mutant p53 Interacting Partner in Cancer Cells

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Mariel Mendoza*, *University of Pennsylvania* and Benjamin A. Garcia, *University of Pennsylvania*

Abstract: p53 is a transcription factor that is mutated in over 50% of cancers. Missense mutations in the DNA binding domain of p53 can result in a gain-of-function (GOF) phenotype, leading to increased cell proliferation and tumor formation. Our lab previously showed that prevalent mutant p53 (mtp53) forms modify chromatin through their interaction with ETS2 and activation of non-canonical transcriptional targets (MOZ, MLL1, and MLL2). Aside from ETS2, other mtp53 partners that have been identified, including Sp1, NF-Y, and PML. However, whether specific proteins are critical for the stability and the GOF effect of mtp53 remains to be seen. We developed a quantitative mass spectrometry-based strategy, combined with molecular and genomic approaches, to identify and validate novel mtp53 binding partners from cancer cell lines with varying GOF p53 mutations. Our preliminary data identified the transcriptional corepressor TRIM28 as a candidate mtp53 interacting partner, as it was identified in all 4 GOF cell lines tested (VU1365, HUPT3, MDA468, and PANC1). Knockdown of TRIM28 in MDA468 cells (contains R273H mutation in p53) caused a decrease in cell viability. TRIM28 has been shown to interact with MDM2 to promote wild type p53 ubiquitylation and degradation; however, its role in regulating mtp53 has not been determined. Ultimately, our studies will identify and validate further novel proteins critical for the GOF activity of mtp53. Characterizing these novel interacting partners of mtp53 will shed light into the molecular mechanisms underlying cancer and thus will provide new therapeutic targets to destabilize mutant p53 interactions in cancer cells.

FRI - G23 Elucidating the Regulated Cell Surface Delivery of Delta-Opioid Receptors

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Candilianne Serrano*, *University of Michigan Ann Arbor*; Stephanie Crilly, *University of Michigan Ann Arbor* and Manoj Puthenveedu, *University of Michigan Ann Arbor*

Abstract: The delta-opioid receptor (DOR) has become a promising alternative target for pain management. However, DOR localizes intracellularly in sensory neurons resulting in the requirement of high doses of DOR agonists for pain relief. Delivery of these retained intracellular receptors to the plasma membrane increases the effectiveness of DOR agonists *in vivo*. Nevertheless, the retention mechanism of these intracellular pool of DORs remains poorly understood. We have identified two 'RXR' motifs within the C-terminus tail of DOR that are required and sufficient to mediate its subcellular localization in the trans-Golgi network (TGN). Additionally, we find that these motifs act as binding sites for Beta-COP, a well-characterized component of the COPI retrograde trafficking machinery. To further understand this distinct mechanism, in this study we design a genome-wide CRISPR/Cas9 screen targeting novel regulators of DOR regulated surface trafficking. Identification of DOR's specific mediators in this pathway could inform new strategies to specifically target intracellular pools to the plasma membrane in nociceptive neurons, thus improving pain relief properties *in vivo.*

FRI - G25 Determining the Impact of ACSL4 Isoforms on Polyunsaturated Fatty Acid Flux and Ferroptosis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

SN Sarah Morris*, *University of California, Berkeley*; Milton To, *University of California, Berkeley*; Kirill Bersuker, *University of California, Berkeley* and James Olzmann, *University of California, Berkeley*

Abstract: Ferroptosis is a form of regulated cell death that generates reactive oxygen species (ROS) in an iron-dependent fashion. The most important of these ROS are lipid peroxides, which self-propogate along the plasma membrane and result in the accumulation of oxidatively damaged lipids. This leads to a loss of membrane integrity and ultimately, cell death. Our understanding of the mechanisms underlying ferroptosis remains limited, but one method of ferroptotic regulation may be found in the enzyme acyl-CoA synthetase long-chain 4 (ACSL4). Knockout of ACSL4 prevents activation and incorporation of polyunsaturated fatty acids (PUFAs) that are susceptible to oxidative damage, thus abrogating the targets for ferroptosis. The ACSL4 gene produces two isoenzymes that differ in length and localization; the long form (ACSL4-L) co-localizes to lipid droplets (LDs) while the short (ACSL4-S) co-localizes to the plasma membrane (PM). We hypothesize that this differential localization modulates ferroptotic sensitivity as PUFA sequestration in LDs decreases the concentration of lipid peroxides on the PM and thus, mitigates ferroptotic death. We created cell lines in which endogenous ACSL4 is eliminated and replaced with a different expression construct for the two major splice forms of ACSL4. Fluroescence microscopy of these constructs depict canonical localization of the ACSL4 isoenzymes. Furthermore, induction of ferroptosis showed a 3-fold increase in ferroptotic resistance in the ACSL4-L construct when compared to WT. Conversely, ACSL4-S showed a 2-fold increase in ferroptotic sensitivity when compared to control. These results indicate that sub-cellular localization of ACSL4 is a strong determinant of a cell's ferroptotic fate.

FRI - G26 The Role of ERK2 in B Cell Activation and Differentiation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Austin Negron*, *University of Texas at San Antonio*; Sean Jeffreys, *University of Texas at San Antonio*; Nawal Abdul-Baki, *University of Texas at San Antonio*; Rebecca Perez, *University of Texas at San Antonio* and Thomas Forsthuber, *University of Texas at San Antonio*

Abstract: The regulation of B cell activation and survival is a crucial control point for the maintenance of B cell tolerance in the germinal center (GC) and involves the coordination of several intracellular signaling pathways. Dysregulation of these pathways can lead to the production and survival of autoreactive memory B cells and plasma cells (PCs), resulting in autoimmune disease. The mitogen-activated protein kinase (MAPK) pathway is involved in the transduction of stimulating and apoptotic signals such as those received through the B cell receptor (BCR) and the Fas receptor (CD95), respectively. Extracellular signal regulated kinases 1 and 2 (ERK1/2), important effectors of this pathway, play a major role in B cell activation and survival. Though ERK2 specifically regulates the pro-apoptotic protein, Bmf, its role in regulating GC B cell selection is unknown. Our lab has developed a novel mouse model in which the deletion of *Erk2* is accompanied by the expression of the fluorescent reporter protein, eYFP, allowing us to identify and isolate viable *Erk2*Δ B cells using flow cytometry. Preliminary data using this model has shown that peripheral *Erk2*Δ B cells express several surface markers associated with follicular T helper cell interactions and immunoglobulin class switching, such as DEC205 and CD80, respectively. Thus we hypothesize that ERK2 is a critical regulator of GC B cell selection. Our results will contribute to a better understanding of the molecular programs involved in B cell differentiation, potentially offering new approaches to treating B cell-driven autoimmune diseases.

FRI - G27 Elucidating the Role of TM6SF2 on Nonalcoholic Fatty Liver Disease

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Milton To*, *University of California, Berkeley* and James Olzmann, *University of California, Berkeley*

Abstract: Nonalcoholic fatty liver disease (NAFLD) is the most common form of liver disease, affecting an estimated 80-100 million Americans. NAFLD is characterized by accumulation of excess triacylglycerols (TAGs) stored in the liver, which can lead to nonalcoholic steatohepatitis, followed by cirrhosis. Previous exome-wide association studies found mutations of TM6SF2 are associated with susceptibility to NAFLD. Emerging data show that TM6SF2 promotes secretion of lipidated lipoproteins, preventing the accumulation of TAGs in hepatocytes. Surprisingly, we and others find that TM6SF2 migrates at a lower molecular weight than predicted. We therefore hypothesize that TM6SF2 undergoes proteolytic cleavage during its maturation. To test this possibility, we affinity purified a C-terminally S-tagged TM6SF2 from hepatoma cells and used Edman degradation to sequence the N-terminus of the putative truncation. Our results indicate that TM6SF2 is indeed truncated; however, the functional half of the protein is yet to be determined. We will express both halves of the protein separately to determine each half's effects on intracellular TAGs stored in lipid droplets. We can further couple this with interaction proteomics to elucidate the mechanism by which TM6SF2 affects NAFLD. Together, our results reveal a previously uncharacterized cleavage of TM6SF2 that may play a role in controlling NAFLD. A more mechanistic understanding of these truncations may provide novel targets to treat genetic causes of NAFLD.

FRI - G28 Characterizing the Role of Hopx and Nuclear Architecture in Cardiac Development

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Ricardo Linares*, *University of Pennsylvania* and Rajan Jain, *Perelman School of Medicine, university of Pennsylvania*

Abstract: Progressive lineage restriction occurs as undifferentiated cells develop into mature cell types. During cardiogenesis, multipotent cardiac progenitors (CPCs) give rise to most of the cells in the heart, including endothelial, smooth muscle, and cardiomyocyte lineages. It has been shown that Homeodomain-Only Protein X (Hopx) expression defines a pool of CPCs that exclusively gives rise to cardiomyocytes. However, it is not well understood if and how Hopx functions to restrict cell fate choice during cardiogenesis. Loss of Hopx in mice results in cardiac developmental defects and embryonic lethality. Hopx deletion during cardiac differentiation of mouse embryonic stem cells results in aberrant expression canonical endothelial genes. Importantly, preliminary experiments suggest that Hopx interacts with nuclear lamina proteins, leading me to hypothesize that Hopx regulates cardiac myocyte commitment and coordinates spatial positioning of the genome to restrict alternative lineage choices. Using a lineage tracing approach, I aim to define the role of Hopx during cardiomyocyte commitment. In addition, I aim to define regions of the genome that associate with the nuclear lamina (LADs) in murine cardiac myocytes and define changes upon loss of Hopx during cardiogenesis using Cleavage Under Targets and Release Using Nuclease (CUT&RUN). Taken together, my results will advance our understanding of how Hopx role in myocyte commitment and nuclear lamina-chromatin interactions, thereby providing a window into how spatial organization of the genome impacts coordinated gene regulation and cell fate choices.

FRI - G29 Developing an Assay to Query the Role of Nuclear RNAs in Higher Order Chromatin Architecture.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jimmy Elias*, *University of Chicago* and Alexander Ruthenburg, *University of Chicago*

Abstract: In 2009 Lieberman-Aiden et al. developed Hi-C, a technology that mapped all vs. all genomic interactions and established our first observations into higher order genomic architecture. These compartments have been shown to facilitate enhancer-promoter looping, which is deterministic for cell-type specific fates via transcriptional programming. There are multiple factors that establish these chromosomal contacts, with hints of evidence that RNAs can facilitate genomic organization. Multiple technologies have reported pervasive RNA-DNA interactions but no work has been done to see the consequences that depletion of the nuclear pool of RNA could have on genomic architecture. We hypothesize that a network of nuclear RNAs aids in the maintenance of genomic architecture. To answer this question, we plan on developing RNase Hi-C probing Nuclear Organization (RHINO). We plan on modifying the Hi-C protocol by introducing an *in situ* RNase digestion and will utilize the latest development in Illumina Sequencing technology to reach the sequencing depth needed to identify intra-TAD differences between control and RNase-treated conditions. We have performed experiments that have shown that the functionality of our RNase cocktail is preserved within the Hi-C workflow without any off-target DNase activity. Further control experiments need to be performed to assess whether our RNase digestion affects any of the downstream steps of Hi-C. The development of this technology can uncover a major factor that contributes to overall genomic architecture and provide the foundation for mechanistic studies of these RNA species or, query the differences in RNA-dependency between cell types for their genomic structural integrity.

FRI - G30 Community-Level Exposure to Lead and Human Placental Toxicity

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Chinomnso Okorie*, *San Francisco State University*; Hao Chen, *University of California, San Francisco*; Mirhan Kapidzic, *University of California, San Francisco*; Sirirak Buarpung, *University of California, San Francisco*; Elaine Kwan, *University of California, San Francisco*; Julia Varshavsky, *Program on Reproductive Health and the Environment, University of California, San Francisco*; Rebecca Mendez, *San Francisco State University*; Stephanie Gaw, *University of California, San Francisco*; Joshua Robinson, *University of California, San Francisco*; Pete Plamer, *San Francisco State University* and Leticia Márquez-Magaña, *San Francisco State University*

Abstract: Lead (Pb) is a major environmental contaminant, especially in underserved communities.

Exposures to Pb in utero may be associated with human pregnancy complications of placental origin such as preterm birth

(PTB), but the populations-at-risk and cellular targets remain undefined. Our studies aim to address this by evaluating whether Pb exposures affect 1) PTB outcome and 2) placental cell viability.

First, we evaluated the correlation between human Pb exposures and the prevalence of PTB outcomes in neighborhoods of San Francisco (SF). As a proxy of Pb exposure by neighborhood, we collected ~30 samples of pooled hair from independent salons within ~10 distinct ZIP codes and measured Pb levels via mass plasma-atomic emission spectrometry with Pb identified in 100% of samples. In general, Pb levels correlated with PTB prevalence. On average, the highest Pb levels were found in samples from zip codes 94124 and 94112, which also corresponded with currently the highest PTB rates in SF (>10%).

Secondly, we interrogated the cytotoxic effects of Pb exposures in three primary human placental cell populations: 1) cytotrophoblasts (CTBs); 2) amnion epithelial cells; and 3) amnion mesenchymal cells. We employed assays to measure function/viability after exposing cells to Pb for 24h. In general, Pb impaired viability in a concentration-dependent manner; however, effects were only significantly observed in CTBs ($p<0.05$).

Taken together, these data provide a better understanding of the relationship between community- level exposures to Pb and pregnancy complications, suggesting vulnerable placental cell populations that may be targeted by heavy metal exposures.

FRI - G31 Investigating Rab5 Distribution during Mitosis in Drosophila Neuroblast

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Bethany Kristi Morin*, *San Francisco State University*; Michelle Gbenedio, *San Francisco State University* and Blake Riggs, *San Francisco State University*

Abstract: Organelles are essential for biochemical processes, vesicular trafficking, degradation of small molecules, and transcription of proteins. The functions of organelles have been highly characterized, however, one outstanding issue that remains unknown is how they are distributed and inherited, during and after mitosis. Previous data has shown how organelles such as the Endoplasmic Reticulum (ER) can be asymmetrically distributed after mitosis, which suggests a programmed mechanism of inheritance. Although characteristics of ER distribution have been brought to light, other organelles like the endosomal network and their distribution remain less understood. Early endosomes (EE) are key in endocytosis and are controlled by Rab5 GTPases. Rab5 proteins localize on EE's and allow for docking and fusion between membranes in order for EE's to transport their cargo. Our hypothesis is that EE's are asymmetrically distributed during and after division. Here we observed a YFP-Rab5 in Drosophila neuroblasts using confocal microscopy to follow EE dynamics during mitosis. Our preliminary data has shown Rab5 motility halted at anaphase when dynein is inhibited, suggesting that microtubules are in charge of Rab5 distribution during mitosis. Additionally, we show that Rab5 appears to be asymmetrically distributed after division. This work will add to our understanding of organelle inheritance in regards to cell fate determination, and characterize endosomes as having another role in mitosis independent of endocytosis.

FRI - G32 Plastic DNA Methylation Patterns Facilitate Retina Regeneration

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Jared Tangeman*, *Miami University*; Agustin Luz-Madrigal, *Miami University*; Erika Grajales-Esquivel, *Miami University*; Sarah Kosse, *Miami University*; Lin Liu, *Miami University*; Kai Wang, *Miami University*; Andrew Fausey, *Miami University*; Chun Liang, *Miami University*; Panagiotis Tsonis, *University of Dayton* and Katia Del Rio-Tsonis, *Miami University*

Abstract: Deterioration of the photoreceptive layer of the eye, the retina, is a leading cause of blindness that impacts millions worldwide. However, a tissue known as the retinal pigment epithelium (RPE) is capable of regenerating lost retina cells in the embryonic chicken. The chick is able to regenerate a full neural retina if a source of fibroblast growth factor (FGF) is added at the time of retina injury; however, this ability is lost after day 5 (E5) of development. We hypothesize that retina regeneration in the chick is driven by the responsive epigenetic state of RPE chromatin. 3D-reconstruction of RPE nuclei during development, as well as following retina removal and FGF treatment, demonstrated robust re-patterning of DNA methylation marks throughout the regeneration process. Interestingly, over-expression of the DNA demethylation protein TET3 following injury was sufficient to induce retina regeneration, even in the absence of FGF. Bisulfite sequencing revealed 1276 genes that undergo changes in RPE methylation as response to injury or FGF, and subsequent gene ontology analysis revealed these genes are enriched for functions including chromatin remodeling and FGF production. Changes in DNA methylation were found to occur primarily within genomic regions of intermediate methylation, indicating stability in methylation patterns at hypo- and hyper-methylated loci. Furthermore, low basal methylation, indicating transcriptionally accessible chromatin, was identified in the promoters of regeneration-associated genes. Altogether, we demonstrate that RPE chromatin is in a state of epigenetic plasticity with respect to DNA methylation, and undergoes robust changes following injury that facilitate retina regeneration.

FRI - G33 Linking Hydraulic Responses to Gas Exchange and Water Stress in California Oaks

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Marissa Ochoa*, *University of California, Los Angeles*; Camila Medeiros, *University of California, Los Angeles*; Alec Baird, *University of California, Los Angeles*; Alayna Mead, *University of California, Los Angeles*; Victoria Sork, *University of California, Los Angeles* and Lawren Sack, *University of California, Los Angeles*

Abstract: Plant hydraulic traits are used to study sets of diverse species in similar climatic conditions to better understand adaptations to drought, but few studies have been applied within given genera. Studies across oak *(Quercus)* species have established some theory for the contribution of leaf traits to plant drought tolerance, but the evolution of drought tolerance and water use traits are less understood. This study focused on a range of physiological traits from *Quercus* species native to California. We tested relationships of leaf hydraulic conductance (K_{leaf}) and stomatal conductance (g_s) with climatic aridity for 15 *Quercus* species grown in a common garden, representing 75% of oak species present within California. Preliminary data show that *Quercus* leaves exhibit an array of responses to dehydration, correlating with the aridity of their native range. We will compare anatomical traits to hydraulic traits to determine correlations between structure and function. Overall, these results suggest high variability within this genus, and a broad scale of leaf responses to water stress. Oaks are critical for ecosystem function, the economy and human health; they provide resources for many types of wildlife, lumber and food for human consumption, and regulate air quality and hydrology. This knowledge could be used to inform land-managers and conservation decisions for oak habitat as we continue to face intensified drought due to climate change.

FRI - G34 Diversity and Distribution of Spiders in Cusco, Peru: A Survey and Comparison of the Yale-Peruvian Expedition of 1911

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Yvan Delgado de la flor*, *The Ohio State University* and Mary Gardiner, *The Ohio State University*

Abstract: Estimating the diversity of species is critical for setting conservation goals as they provide evidence regarding the impact of human activity and climate change. The Andes mountains in South America is one of the most biologically diverse regions on Earth; however, most species living in this area have not yet been described and are unknown to science. In 1911, Yale University surveyed spiders in the Andes of Cusco-Peru and discovered several new species.

In collaboration with Universidad Nacional San Antonio Abad del Cusco, we replicated the Yale-Peruvian expedition, following a century of land use change. Our goal was to estimate the diversity and distribution of spiders and compare our findings to the Yale expedition. We hypothesized that (1) spider endemism and diversity will be higher at intermediate altitudinal levels, and that (2) species composition will differ from the spider community sampled in 1911. In 2016-2018, we sampled spiders in the 12 locations visited by Yale using plastic cups and collection by hand. We collected 1091 specimens and identified 40 spider families using morphological features. Spiders are currently being prepared for DNA analysis and final results are expected in July 2019.

Our work serves as a foundation study to future biodiversity assessments and will be used to better understand how spider communities have responded to environmental changes in the Peruvian Andes. Our study is part of a large-scale project attempting to replicate the Yale-Peruvian expedition of 1911 for the first time in one hundred years.

FRI - G35 Nuclear Pore Protein Megator Attenuates Dosage Compensation of the Male X Chromosome

Discipline: Life Sciences
Subdiscipline: Genetics

Jennifer Aleman*, *University of Pennsylvania* and Maya Capelson, *University of Pennsylvania*

Abstract: The nuclear pore complex (NPC) is well known for its role in nuclear-cytoplasmic transport. A role for the NPC in gene expression has been an emergent topic in recent years as certain nucleoporins have been found in the nuclear interior, binding to chromatin. Megator, (Mtor) makes up the nuclear basket of the NPC and appears to form an intranuclear matrix-like structure that binds along chromatin in *Drosophila* polytenized salivary gland nuclei. Since Mtor has been implicated in both RNA biogenesis and dosage compensation, I examined the effect of Mtor on localization of a non-coding RNA that is part of the dosage compensation complex, *roX1*. Using RNA FISH in *Drosophila* salivary gland nuclei, I detected an increase in nuclear soluble *roX1* in Mtor-depleted conditions. The increased presence of *roX1* was due to increased levels of transcription of *roX1* in male nuclei. In addition to *roX1*, a number of other X-linked genes exhibited a male-specific increase in expression via qPCR assays upon depletion of Mtor. To confirm the male-specific upregulation of X-linked genes, we performed RNA-Seq in male and female salivary glands in both control and Mtor knockdown conditions. Our results confirmed our initial finding – the most notable change in gene expression observed upon Mtor depletion was an upregulation of X-linked genes in males. These results suggest that Mtor normally functions to restrict dosage compensated gene expression. Overall this work uncovers a novel gene regulatory role for a nuclear-scaffold forming nucleoporin in the context of the epigenetic phenomenon of dosage compensation.

FRI - G36 Determining the Risk of Unwarranted Investigation Due to Distant Relative Misidentification in Genealogical Searching

Discipline: Life Sciences
Subdiscipline: Genetics

Cynthia Perez*, *San Francisco State University*; Selena Hernandez, *San Francisco State University*; Emily Samperio, *San Francisco State University* and Rori Rohlfs, *San Francisco State University*

Abstract: Long range familial searching is a forensic technique used to identify a suspect through their long distant relatives, such as a third cousin, using a database containing genome wide variation data. Individuals are identified due to shared inheritance autosomal DNA segments which are Identical-by-Descent (IBD). The length of IBD segment depends on the number of meiosis events that have occurred since the last common ancestor. Therefore, more distant relationships have shorter and fewer shared IBD segments.Although, over 60% of individuals of European descent can be identified using long range familial searching, the risk of unwarranted investigation in our diverse population is unknown and may be impacted by IBD variability. Long distance relatives may share a large amount of IBD segments due to chance and investigators may inaccurately infer a closer relationship. If IBD variability is disregarded, then investigators may search family trees that don't contain the offender. In this study, we will investigate rates of misidentification by estimating IBD variability on a large empirical pedigree (familinix) containing 86 million individuals. Based on IBD inheritance models, we will determine the likelihood of long distant relatives sharing sufficient IBD to resemble closer relatives and quantify the number of people who will be erroneously investigated. Thus far, we have developed a function to identify genealogical relationships using the R package kinship2 and developed an R script to represent familinx. Results from this study will help elucidate the level of police scrutiny and privacy invasion.

FRI - G37 Illuminating Chromatin Localization and Gene Regulatory Roles of the Sperm Specific HTAS-1 Histone Variant

Discipline: Life Sciences
Subdiscipline: Genetics

Jesus Hinojosa Paiz*, *San Francisco State University*; Tomoko Tabuchi, *University of California, Santa Cruz*; Swadha Singh, *University of California, Merced*; Andreas Rechtsteiner, *University of California, Santa Cruz*; Susan Strome, *University of California, Santa Cruz* and Diana Chu, *San Francisco State University*

Abstract: A main contributor to infertility is improper spermatogenesis. For proper progression of sperm development, correct gene regulatory patterns, governed by specific proteins, are vital. Histone variants are among these specialized proteins. Histone variants differ slightly in amino acid sequence from their core histone counterpart yet have alternative tissue specific effects on gene regulation. *Caenorhabditis elegans* expresses four different histone H2A variants, one being the sperm specific HTAS-1 variant. Previous studies have shown HTAS-1 incorporates into chromatin late during male spermatogenesis and mutant strains generate less progeny. Yet, it is still unknown where HTAS-1 localizes on DNA and whether HTAS-1 directly regulates genes it binds. To investigate where on DNA HTAS-1 is present, we conducted ChIP-seq on N2 mature sperm. We identified genomic sites of HTAS-1 integration, 26.5% of which are sperm genes. From this subset of genes, we then asked whether they are regulated by HTAS-1. To explore this, I will perform RNA-seq on isolated mRNAs from *htas-1*$^{-/-}$ and N2 male germlines. From RNA-seq data, I expect to find genes both up and down regulated when comparing *htas-1*$^{-/-}$ and N2 transcripts. Subsequently, to investigate gene expression patterns established by HTAS-1 chromatin incorporation, I will perform smFISH on *htas-1*$^{-/-}$ and N2 germlines. From smFISH data, I expect to find expression patterns to differ on *htas-1*$^{-/-}$ germlines proposing HTAS-1's role in establishment of gene expression patterns. Findings from this study will help reveal new spermatogenesis gene targets for further investigation and give insight to how a histone variant is necessary for fertility.

FRI - G38 Determining the Role of DNA Methylation in the Thermal Acclimation of California Mussels (*Mytilus californianus*) Along a Natural Environmental Gradient

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Jannine Chamorro*, *University of California, Santa Barbara*; Logan Kozal, *University of California, Santa Barbara* and Gretchen Hofmann, *University of California, Santa Barbara*

Abstract: As global environmental conditions continue to change at unprecedented rates, understanding mechanisms of rapid adaptation is critical in predicting species persistence. Epigenetic mechanisms, such as DNA methylation, are thought to be processes that can drive rapid adaptation in organismal tolerance. Changes in methylation signatures not only allow organisms to deal with new or varying environments *within* a generation, but they are also heritable, thus changes in methylation markers of parental generations can be passed on to progeny i.e. *transgenerational plasticity*. My research aims at determining how long-term thermal conditioning of sessile California mussels (*Mytilus californianus*) can affect adults and progeny. I am doing this by comparing how mussels from the high and low zones of the intertidal region differ in maternal provisioning and DNA methylation patterns. My preliminary results indicate differences in offspring size with regard to adult conditioning. Using methylation sensitive amplification polymorphism (MSAP) analyses, I plan to couple these preliminary findings with measurements of methylation patterns. Findings from my research will provide a better understanding of the role of DNA methylation in the thermal plasticity of California mussels, and more broadly, the role of epigenetics in natural populations.

FRI - G39 A Comparative Study of Different Routes of Zika Virus Infection for Virus Tropism and Pathology

Discipline: Life Sciences
Subdiscipline: Microbiology

Megan Miller*, *Colorado State University* and Brian Foy, *Colorado State University*

Abstract:
Zika virus (ZIKAV) is a mosquito-borne flavivirus. The recent pandemic in the Americas resulted in over 1,000,000 cases of disease and thousands of cases of birth defects. An unexplained female bias occurs with ZIKAV disease; the incidence of ZIKAV disease is significantly higher in females vs. males, despite serological evidence of relatively equal exposure. Interestingly, ZIKAV is the only known flavivirus to be able to transmit sexually, which may be related to the female bias of disease. This study was undertaken to determine if differences in virus tropism or disease pathology occur by different routes of infections (needle inoculation, mosquito bite, and sexual transmission). We are testing the hypothesis that female A129 mice (IFNα/ßR-/-) and New World tropical fruit bats (*Artibeus jamaicensis*; AJ) will be more frequently infected with ZIKAV and have increased urogenital tract infection from sexual transmission than a mosquito bite. To test this, we will compare tropism and pathology in different tissues, by q-RT-PCR, plaque assay and histopathology of animals inoculated by different routes. We have compared needle inoculation with mosquito bite in male A129 mice and have found a significant increase in viral genomes within in tissues of mice bitten by mosquitoes. We have infected A129 female mice by needle inoculation and have determined virus present by q-RT-PCR. Additional results from sexually transmission and mosquito bite studies of female A129 mice and AJ are pending. The results of this study will begin addressing many unknown questions about the ZIKV pathology and disease from differential transmission routes.

FRI - G40 Coxiella Burnetii uses Its Type IV Secretion System to Suppress Host Cytokine Upregulation and Secretion

Discipline: Life Sciences
Subdiscipline: Microbiology

Natasha Lopes Fischer*, *University of Pennsylvania* and Sunny Shin, *University of Pennsylvania*

Abstract: Host immune cells use multiple strategies to detect and protect against bacterial infections. One common defense pathway is the activation of Pattern Recognition Receptors (PRRs) by bacterial ligands. Once triggered, PRRs activate the NFκ-B and MAPK signaling pathways to upregulate cytokine expression and secretion from the host cell, alerting the body to the infection. Some pathogens have evolved strategies to evade this defense mechanism to remain undetected by the host. The bacterium *Coxiella burnetii* is thought to evade multiple host immune pathways. *Coxiella* primarily infects alveolar macrophages and causes the emerging disease Q fever. This pathogen uses a specialized type IV secretion system (T4SS) to inject bacterial effector proteins into the host cytoplasm. These effectors modulate host cellular processes and allow bacterial replication. Despite causing major changes to the host cell, *Coxiella* does not induce a strong cytokine response. I hypothesize that *Coxiella* suppresses this host response using bacterial effectors. To test this hypothesis, I infected a human monocytic cell line with wildtype bacteria or bacteria lacking a functional T4SS, and performed qPCR, ELISA and immunoblot assays to determine differences in the immune response to these bacteria. My preliminary results suggest that *Coxiella* uses its T4SS to inhibit both NFκ-B and MAPK pathways, suppressing cytokine upregulation and secretion. In the future, I will conduct a screen of *Coxiella* effectors to identify those that may be suppressing host signaling pathways. Results from this study will provide insights into pathogen evasion strategies and may provide targets for improved therapeutics for Q fever.

FRI - 133 Association between Cotinine-*N*-Oxide Levels with CYP2C19 Genotypes and Their Potential Effect on the Nicotine Metabolic Ratio (NMR)

Discipline: Life Sciences
Subdiscipline: Pharmacology

Yadira Perez-Paramo*, *Washington State University*; Christy J. W. Watson, *Washington State University*; Gang Chen, *Washington State University* and Philip Lazarus, *Washington State University*

Abstract: The major nicotine metabolic pathway is via cotinine and subsequently 3-hydroxy-cotinine by the enzyme cytochrome(CYP) P450 2A6. The nicotine metabolic ratio (NMR; cotinine/3-hydroxy-cotinine) determines CYP2A6 activity *in vivo*, and it is widely used in clinical practice to help select smoking cessation pharmacotherapy. Cotinine is further metabolized to cotinine-*N*-glucuronide and to cotinine-*N*-oxide (CotOx), accounting for ~7 and 5% of its metabolites. The goal of the present study is to investigate the enzymes that catalyze CotOx formation and determine whether genetic variation in these enzymes may affect this pathway. Specific inhibitors of the major hepatic CYP isoforms (1A2, 2A6, 2B6, 2C8, 2C9, 2C19, 2D6, 2E1, and 3A4) were used in CotOx reactions using pooled human liver microsomes (HLM). Inhibition of CotOx formation was only observed when using inhibitors of CYPs 2A6, 2C19, and 3A4. CotOx formation was monitored by UPLC-MS/MS, and enzyme kinetic analysis was performed. CYPs 2A6 and 2C19 exhibited similar oxidation activity, with rate values of 42, and 39 $\text{nL}\cdot\text{min}^{-1}\cdot\text{mg}^{-1}$, respectively; the K_M of CYP3A4 was >10 mM. Additionally, genotype-phenotype analysis was studied in a panel of 85 HLM normal specimens. Levels of CotOx formation in 85 HLM specimens were measured and genotyped variants in CYP2A6 [*2 and *9] and CYP2C19 [*2 and *17] genes using Taqman probes. CYP2C19 genotypes were significantly associated with decreased (*2/*2;22%) and increased (*17/*17;42%) levels of CotOx formation. These results indicate that CYP2C19 genotypes affect the levels of free cotinine, potentially altering the calculated NMR in smokers and clinical practices surrounding smoking cessation therapies.

FRI - 134 Exploring Phage Structure from Head to Tail with Cryoem

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Brenda Gonzalez*, *Purdue University* and Wen Jiang, *Purdue University*

Abstract: With cryo-electron microscopy (cryo-EM), we can collect images of important biological molecules and make 3D reconstructions of them with near-atomic details in near physiological conditions. Using this powerful technology, we aim to better understand the process of infection and assembly of viruses using bacteriophage as a model system.

Phage G has the largest genome and capsid of all known phage to date. Using cryo-EM, we have reconstructed its capsid and tail structure to sub-nanometer resolution. Not only have we observed unique genome states in Phage G's capsid, but we have also observed Phage G's tail does not follow the canonical, *Myoviridae* tail contraction mechanism. Additionally, our structure studies on Phage G have led us to the clarification of Phage G's host as a *Lysinibacillus ssp.*, not *B. megaterium* as commonly cited.

In addition to our studies of Phage G, we have obtained the structure of another large phage, *Pseudomonas* phage 201phi2-1. The capsid structure of 201phi2-1 has a unique outer protein coat not reported in other phage. We have also observed protein density within its capsid under the pentamer regions, not described in other phage. We have also elucidated its non-contracted tail structure to near atomic resolution.

Altogether, the information we have uncovered about Phage G and 201phi2-1 has led us to new discoveries of phage structure and function.

FRI - 135 The Long-Term Effects of Developmental Exercise on Hippocampal Plasticity Outcomes

Discipline: Life Sciences
Subdiscipline: Neurosciences

Emma Perez*, *University of Houston* and J. Leigh Leasure, *University of Houston*

Abstract: Aerobic exercise has many positive effects on brain plasticity, but whether early life exercise effects carry over into adulthood are largely unexplored. We have previously found that developmentally exercised (Dev-ex) animals showed increased brain size in adulthood, even when animals had not exercised in months. Exercise is well known to enhance hippocampal neurogenesis. Additionally, evidence suggests that exercise increases quiescent, type-1 progenitor/stem cells (cells that activate/proliferate due to stimuli) in the dentate gyrus (DG) of the hippocampus, a structure important in mood and cognition. Type-1 progenitor cells are thus a proxy for the *capacity* for cell proliferation and provide a means for measuring experience-driven plasticity. We hypothesized that Dev-ex will increase this pool of cells with long-lasting changes into adulthood. We additionally hypothesized that Dev-ex would increase total neuron count in the DG, as exercise enhances hippocampal neurogenesis. In our experiments, Long Evans rats voluntary ran for 6 weeks starting at postnatal day 35. Quantification of NeuN (mature neuron marker) was completed in the DG immediately after Dev-ex (acute effect), after a 6-week resting period (long-term effect), and in sedentary rats. No differences were found in NeuN ($p > 0.05$) across the three groups. However, in the coming months we will quantify brain lipid binding protein in the DG, a marker for type-1 quiescent cells. Type 1 cells are a potential candidate for observing a lasting effect via exercise. Therefore, we will determine the effects of Dev-ex on adult quiescent stem cells and thus the capacity for cell proliferation.

FRI - 136 Development of Molecular Assays to Determine the Presence and Abundance of *Alteromonas Macleodii* within Marine Environments

Discipline: Life Sciences
Subdiscipline: Microbiology

Brianda Beverley*, *University of Maryland, Baltimore County* and Kathleen Cusick, *University of Maryland, Baltimore County*

Abstract: Biogeochemical cycling is an important mechanism that involves the movement of nutrients between living and non-living elements within an ecosystem. A microorganism contributing to this cycle is *Alteromonas macleodii*; a heterotrophic marine bacterium with a resilient genome that allows for survival in various marine environments. *A. macleodii* can exhibit planktonic or particle-associated lifestyles and establish a variety of relationships with many organisms including marine sponges, dinoflagellates, and diatoms. Interestingly, *A. macleodii* has low representation in metagenomic datasets but can contribute largely to the flux of carbon and nitrogen in marine environments. Furthermore, many studies have analyzed *A. macleodii* in the global ocean datasets; however, its abundance in other environments associated with marine sponges, *Prochlorococcus*, and *Trichodesmium* remain relatively unknown. To gain insight into the general ecology of *A. macleodii*, two Polymerase Chain Reaction (PCR) assays are under development in our lab to determine the presence and abundance of *A. macloedii* in marine environments. Primers specific to a 1,134 region of the *A. macleodii gyrB* gene were developed and screened against various *Alteromonas* species and other genera. PCR products were visualized with gel electrophoresis followed by Sanger Sequencing to determine specificity. The PCR assay was then used to screen DNA extracted from a variety of marine environments. To date, the *A. macleodii*-specific *gyrB* PCR assay has specifically identified *A. macleodii* in a subset of the samples. Future experiments include screening against additional marine environmental samples and development of an *A. macleodii*-specific quantitative PCR (qPCR) assay.

FRI - 137 Identification and Characterization of *Escherichia coli* Genes Associated with Grazing Resistance to the Social Amoeba *Dictyostelium Discoideum*

Discipline: Life Sciences
Subdiscipline: Microbiology

Marta Perez-Vazquez*, *Towson University*; De'Sha Johnson, *Towson University* and Michelle Snyder, *Towson University*

Abstract: Pathogenic *Escherichia coli* strains remain a significant health challenge, particularly in developing countries. The social amoeba, *Dictyostelium discoideum*, which phagocytizes bacteria for nutritional purposes, serves as a host model for several pathogenic bacteria, including *E. coli*. Here we have characterized the interactions of *D. discoideum* with 35 representative *E. coli* strains, and identified that strains sensitive and resistant to *D. discoideum* grazing were found in each *E. coli* pathotype. Whole genome Phylogenomic analysis revealed that grazing resistance is distributed among the phylotypes, although resistant strains are enriched in the B2 phylogenomic group. Comparative genomic analysis identified genes more prevalent among strains resistant to *D. discoideum* grazing, including genes associated with adhesion, carbohydrate modification, iron transport, signaling and metabolism. Interestingly, the *gipA* (growth in Peyer's Patches) gene, which has been found associated with microbiota in patients with Crohn's disease, was widely present in *E. coli* strains resistant for *D. discoideum* grazing. We are currently working to characterize the role of *E. coli* genes that have been found associated with resistance to phagocytosis by *D. discoideum*, through creation and analysis of *E. coli* strains manipulated for expression of the identified genes. Such characterization is aimed at providing insight into potentially novel *E. coli* virulence factors.

FRI - 139 Bilingual Children and Adults Do Not Engage Different Strategies When Verifying the Solutions to Multiplication Facts in Each of Their Languages

Discipline: Life Sciences
Subdiscipline: Neurosciences

Vanessa Cerda*, *University of Texas San Antonio* and Nicole Wicha, *University of Texas San Antonio*

Abstract: Most bilinguals learn math facts, like multiplication tables, through verbal rehearsal in only one language and typically prefer to do math only using that language. Behavioral studies have shown that bilingual children and adults are indeed faster and more accurate at retrieving arithmetic facts in the language in which they learned them (LA+) than their other language (LA-). Consequently, models of math cognition theorize that math facts, like multiplication, are uniquely or differentially represented in verbal memory in one language, and a qualitatively different method is required to process math in any other language. However, these models are inconsistent with evidence from bilingual language research suggesting that bilingual lexicons are highly interconnected and interactive. We tested whether Spanish-English bilingual children and adults use qualitatively different processes for math fact verification across languages. We recorded event-related potentials (ERPs) as participants verified the correctness of spoken multiplication facts presented in LA+ or LA-. In children, incorrect solutions elicited a larger negative-going ERP component, or N400, than correct solutions, reflecting differential activation of semantic memory. This effect was present in both languages and implies that bilingual children do not engage different strategies when verifying solutions in LA+ and LA-. Although adults showed modulations on a different ERP component (a target P300), the effect was not qualitatively different across languages. Overall, our findings imply that a bilingual's sense of being able to process math in only one language may be due to differences across languages that are quantitative rather than qualitative in nature.

FRI - 140 Neuronal Connexin 36 in Seizure-like Activity

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alyssa Brunal-Brown*, *Graduate Program in Transnational Biology Medicine and Health, Virginia Polytechnic Institute and State University* and Yuchin Albert Pan, *Developmental and Translational Neurobiology Center, Fralin Biomedical Research Institute at VTC*

Abstract: Connexins are transmembrane proteins that form hemichannels which allow the flow of molecules into the extracellular space. Two hemichannels from adjacent cells can dock and form a gap junction pore allowing direct intercellular signaling. Connexin 36 (Cx36) specifically, is proposed to be involved in the synchronous activity of neurons and neural circuits. Additionally, previous studies suggest Cx36 may be involved in diseases of synchronous firing, such as epilepsy, however, the exact mechanism is unknown. To better understand the role Cx36 may play in seizure genesis, we sought to answer two questions: a) how does Cx36 knock-out affect seizure susceptibility, and b) how does seizure activity affect Cx36 expression patterns. We exposed 6 days post-fertilization (6dpf) Cx35.5 (zebrafish homolog of Cx36) wild type and knock-out zebrafish larvae to 5mM Pentylenetetrazol (PTZ) for 15 minutes and examined brain activity using the Mitogen Activated Protein Mapping (MAP-mapping) technique by looking at a ratio of phosphorylated ERK (present in active neurons) to total ERK (present in all neurons). Cx35.5 mutant fish showed overall increases in activity compared to wild type controls indicating a possible increase in seizure susceptibility. Next, we examined the effect of seizure activity on Cx36 expression. We exposed 6dpf Nacre zebrafish larvae to 20mM PTZ stimulation for 3 hours and quantified Cx36 expression via immunohistochemistry. After 3-hour stimulation with 20mM PTZ, global Cx36 expression was significantly decreased. These results suggest that the role of Cx36 in seizure genesis is dynamic, and further investigation is required to understand it's function.

FRI - 145 Pathogenic Troponin T Mutants with Opposing Effects on Myofilament Ca2+ Sensitivity Attenuate Cardiomyopathy Phenotypes in Mice

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Karissa Dieseldorff Jones*, *Florida State University* and Jose Pinto, *Florida State University*

Abstract: Mutations in cardiac troponin T (TnT) associated with hypertrophic cardiomyopathy generally lead to an increase in the Ca2+ sensitivity of contraction and susceptibility to arrhythmias. In contrast, TnT mutations linked to dilated cardiomyopathy decrease the Ca2+ sensitivity of contraction. Here we tested the hypothesis that two TnT disease mutations with opposite effects on myofilament Ca2+ sensitivity can attenuate each other's phenotype. We crossed transgenic mice expressing the HCM TnT-I79N mutation (I79N) with a DCM knock-in mouse model carrying the heterozygous TnT-R141W mutation (HET). The results of the Ca2+ sensitivity in skinned cardiac muscle preparations ranked from highest to lowest were as follows: I79N > I79N/HET > NTg > HET. Echocardiographic measurements revealed an improvement in hemodynamic parameters in I79N/HET compared to I79N and normalization of left ventricular dimensions and volumes compared to both I79N and HET. Ex vivo testing showed that the I79N/HET mouse hearts had reduced arrhythmia susceptibility compared to I79N mice. These results suggest that two disease mutations in TnT that have opposite effects on the myofilament Ca2+ sensitivity can paradoxically ameliorate each other's disease phenotype. Normalizing myofilament Ca2+ sensitivity may be a promising new treatment approach for a variety of diseases. NIH-HL128683 and NIH-HL137408.

FRI - 147 Age- and Sex-Dependent Effects of Nicotine Pretreatment on Fentanyl Self-Administration in Rats

Discipline: Life Sciences
Subdiscipline: Pharmacology

Anjelica Cardenas*, *University of California, Irvine* and Shahrdad Lotfipour, *University of California, Irvine*

Abstract: Initiation of nicotine products typically occurs in adolescence. Adolescence is a critical period in development (12-18 years in humans, postnatal days (PN) 28-42 in rodents) where the maturation of brain neurocircuitry is vulnerable to nicotine. Rodent studies have shown that nicotine exposure in early adolescence increases subsequent drug intake and reward. However, this has not been studied for opioids such as fentanyl. We hypothesize that early adolescent, but not adult, nicotine exposure will increase fentanyl intake. To test our hypothesis, we pretreated male and female rats with either nicotine (2x, 0.03 mg/kg/0.1 mL, i.v.) or saline for 4 consecutive days during early adolescence (PN 28-31) or adulthood (PN 86-89). Following pretreatment, rats were allowed to nose-poke for fentanyl (2.5 ug/kg/infusion) across five days. Our preliminary data suggest that nicotine pretreated male adolescents, but not male adults or females, have enhanced reinforced responses at the end of five days. Taken together, our study highlights age- and sex-dependent effects of nicotine on fentanyl intake. Our findings have important clinical implications, given the high rate of e-cigarette use during adolescence and opioid overdose deaths in the United States.

FRI - 430 Acculturation and Help-Seeking Attitudes: Examining the Influence of Mental Health Literacy and Perceived Access to Services

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Isabel Lopez*, *California State University, Northridge*; Crystal Venegas, *California State University, Northridge*; Daniel Saravia, *California State University, Northridge*; Patricia Orozco, *California State University, Northridge*; Jose Arreola, *California State University, Northridge* and Jonathan Martinez, *California State University. Northridge*

Abstract: Extant literature suggests that acculturation influences help-seeking attitudes toward formal mental health (MH) care (Lorenzo-Blanco & Delva, 2012). Further, knowledge on MH also influences help-seeking attitudes (Thompson & Hoffman-Goetz, 2009). This study examines the associations among acculturation, MH literacy, perceived barriers to MH care, and help-seeking attitudes, and whether this translates to MH service use, utilizing the Collaborative Psychiatric Epidemiological Surveys national dataset. A subsample of 874 adults (732 US-born citizens, 107 immigrants) was achieved. MH literacy and barriers were hypothesized to mediate the relation between acculturation and help-seeking attitudes. Moreover, positive attitudes were hypothesized to predict formal MH service use, and negative attitudes to predict informal MH service use. Bivariate correlations revealed no significant association between acculturation and attitudes, changing the hypothesized path model. Model analyses revealed significant paths from literacy ($\beta = 0.42$, $p < .01$) and barriers ($\beta = 0.08$, $p < .01$) to attitudes. Limited MH literacy and more barriers related to an increase in negative attitudes. Moreover, negative attitudes related to a lower likelihood of formal MH service use ($\beta = -0.03$, $p < .05$). The model was examined separately among immigrant and US-born samples. Paths from MH literacy and barriers to help-seeking attitudes held significance in both samples, but the path from help-seeking attitudes to formal MH service use was marginally significant among immigrants ($\beta = -0.175$ $p = .07$). Findings highlight the importance of increasing MH literacy and addressing barriers to care among diverse community members to promote access to formal MH services.

FRI - 431 Income Inequality and Overdose Immunity Legislation Impact Overdose Death Rates

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Jordan Norton*, *Illinois State University* and Carl Palmer, *Illinois State University*

Abstract: From 2014-2015, the CDC saw a 72.2% and 20.6% increase in death rates related to synthetic opioid and heroin overdose, respectively. States have looked to one another for policy examples to reduce these numbers. One of the earliest of these policies was implemented by New Mexico in 2007, Drug Overdose Immunity/Good Samaritan Laws. These laws sought to remove barriers to people contacting emergency responders by granting “immunity” such that people suffering from or reporting an overdose would not be prosecuted for possession of controlled substances. We hypothesized that states implementing these overdose immunity laws would see a decrease in drug overdose death rates. To measure the effectiveness of these laws, we gathered 8,773 observations from 800 counties between 2006-2016 and used a Pooled OLS multivariate regression model to determine the effects of the breadth of protections provided by the laws, average income, income inequality, educational attainment, and categories of race/ethnicity. Inequality had the largest effect on overdose death rates, where a one unit increase in our inequality measure resulted in a 72.94 increase in death rate. Breadth of protections had the second largest effect, where each increase in protection resulted in a 1.38 increase in death rate, perhaps explained by late adoption of protections. Future work will use pooled regressions among individual years, as well as fixed and random effects models to control for county and state effects. This approach will provide a more well-rounded means of evaluating how overdose immunity legislation impacts overdose death rates in the United States.

FRI - 432 Engaging STEM Students from Non-Dominant Backgrounds in Discussions about Stereotype Threat during a First-Year Experience Course

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Tatiane Russo-Tait*, *University of Texas* and Leticia Márquez-Magaña, *San Francisco State University*

Abstract: Stereotype threat (ST) has been shown to lower performance by increasing anxiety and lowering cognitive capacity in domains a person cares about, and where this person's group is negatively stereotyped. Women and some racial/ethnic minorities are particularly susceptible to ST in science, technology, engineering, and mathematics (STEM) classrooms. This impacts the ability to recruit people from these underrepresented populations into STEM careers. Certain interventions have been successful in ameliorating ST, including explicitly teaching students about the phenomenon. This case study explores the effects of engaging students in sustained discussions, readings, and reflections about ST and its underlying sociopolitical causes. We predicted that this comprehensive pedagogical approach not only ameliorates ST, but also helps students to develop the critical consciousness and agency needed to disrupt the status quo in STEM. To test this prediction, student data was collected for a 7-week period during a semester of a first-year experience course for underrepresented students in STEM (N= 30, 70% female, 100% students of color). This included pre-post surveys of psychosocial measures (e.g., perceptions of ST, sense of belonging, identity, etc.), written responses from in-class discussion prompts, reflections on assigned readings, and a group project. Preliminary data analyses show positive associations between the curriculum and pedagogical approaches used and persistence to degree. In addition, providing students with the opportunity to critically examine the sociopolitical context in which ST operates appears to enable them to challenge the status quo and promote equity efforts in STEM, which have the potential to further diversify the field.

FRI - 433 Asynchronous Discussions to Engage Students in Scientific Argumentation

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Iresha Jayasinghe*, *Illinois State University*; Ranija Turner, *Illinois State University*; Rebekka Darner, *Illinois State University*; James Wolf, *Illinois State University* and Kristine Callis-Duehl, *East Carolina University*

Abstract: Scientific argumentation facilitates knowledge-building, bridging claims and evidence. This study examines scientific argumentation occurring in an asynchronous online discussion board to answer the questions: 1. Does gender composition of discussion groups affect students' engagement in productive scientific argumentation? 2. To what extent does gender composition of groups engaging in scientific argumentation influence the development of scientific literacy? 3.To what extent does gender composition of discussion groups and the quality of scientific argumentation affect students' satisfaction with the discussion experience? Participants were recruited from an online introductory biology course taught at a large, Midwestern, R2 university. Assigned discussion groups remained throughout the 6-week course. Groups were either all-male (2), all-female (6), or mixed-gender (4). Students' pre-course scientific literacy was measured using 10 items from the Test of Science Literacy Skills. Discussions occurring in week 5 of the course were downloaded, de-identified, and coded using the Assessment of Scientific Argumentation in the Classroom protocol to measure the quality of scientific argumentation. Post-course science literacy was measured using 10 different but matched items from the TOSLS, administered with a survey of students' satisfaction with their discussion experiences. A one-factor analysis of variance, using group composition to predict ASAC score, was performed to address the first research question. A repeated-measures ANOVA was used to assess the influence of group composition on pre/post-course growth in scientific literacy to answer the second research question. A two-factor ANOVA, using group composition and ASAC scores to predict satisfaction scores, was performed to answer the last research question.

FRI - 849 RIG-I-like Receptor Mediated Cell Death Regulation By TRIM16

Discipline: Other
Subdiscipline: Other Professional Fields

Brittany Ulloa*, *University of Washington* and Michael Gale Jr., *University of Washington*

Abstract: Most malignant cells are poorly immunogenic and fail to elicit an effective anti-tumor response. Viral infections of cancer cells can trigger intracellular innate immune defenses that impart oncolytic signaling. Innate immune molecules that trigger oncolytic signaling hold great promise for cancer therapy. Our lab has identified a viral pathogen associated molecular pattern (PAMP) RNA motif from hepatitis C virus (HCV) that when delivered to cells in a liposomal formulation it engages RIG-I to induce innate immune signaling. Unexpectedly, we found that PAMP RNA can direct RIG-I dependent signaling to drive tumor cell death. Preliminary studies reveal that RIG-I binds to a novel protein TRIM16, and that TRIM16 is required for this oncolytic phenotype. Therefore, we hypothesize that TRIM16 mediates a non-canonical RIG-I dependent cell death pathway. Preliminary in-vitro studies using CRISPR knockout cell lines confirms that this cell death pathway requires RIG-I and the down stream adaptor protein MAVS. Additionally, we found that TRIM16 does not affect interferon expression nor does interferon affect TRIM16 expression. Our observations indicate that TRIM16 is not involved in innate immune signaling but instead mediates a novel and non-canonical RIG-I oncolytic signaling pathway. We are currently working to identify the structural components of RIG-I and TRIM16 required for cell death signaling and are developing an in-vivo model of TRIM16 mediated PAMP RNA tumor therapy through RIG-I activation. The results of this research will reveal a novel RIG-I mediated oncolytic signaling pathway that can be leveraged for the design of anti-tumor therapeutics.

FRI - 850 How Does Adjacent Land Use Affect the Deposition and Transport of Pollutants in Urban Forest?

Discipline: Other
Subdiscipline: Other Professional Fields

Luis D Rivera Cubero*, *Michigan State University*; Asia Dowtin, *Michigan State University* and David Rothstein, *Michigan State University*

Abstract: Trees provide numerous environmental benefits, including helping to improve air quality by intercepting airborne gases and particles, causing them to be captured on plant surfaces. After being deposited on the urban canopy, these gases and particles can be mobilized in the urban ecosystem by different transport mechanisms, including throughfall and stemflow. The transport of these solutes via throughfall and stemflow to urban soils may impact the health and function of trees in cities. For methodology I will utilize in situ sampling to quantify hydrologic and solute fluxes via throughfall and stemflow in three woodlots, each surrounded by a different land use: agricultural, residential and interstate highway. Stemflow and throughfall will be sampled along gradients from forest edge to interior on an event basis, with data collection being limited to storm events during the spring and summer of 2019. Stemflow and throughfall samples will be analyzed in the laboratory to determine the amount of acids, nutrients, and pollutants that are transported beneath the urban canopy as a function of the surrounding landscape matrix. This will ultimately strengthen our current understanding of the transport and fate of deposited aerosols through the canopy and the vadose zone, and the related impact on the function of urban trees and woodlots.

8:45 AM – 10:45 AM

Friday Undergraduate Posters

FRI - 100 Role of Pregnancy-Associated Plasma Protein-a (PAPP-A) in the Pathogenesis of Polycystic Kidney Disease

Discipline: Health
Subdiscipline: Medicine

Paola Vidal*, *The University of Texas Rio Grande Valley*; Sonu Kashyap, *Department of Anesthesiology and Robert and Arlene Kogod Center on Aging, Mayo Clinic*; Kyaw Zaw Hein, *Department of Anesthesiology and Robert and Arlene Kogod Center on Aging, Mayo Clinic*; Claudia C.S. Chini, *Department of Anesthesiology and Robert and Arlene Kogod Center on Aging, Mayo Clinic*; Jorgo Lika, *Department of Anesthesiology and Robert and Arlene Kogod Center on Aging, Mayo Clinic*; Gina M. Warner, *Department of Anesthesiology and Robert and Arlene Kogod Center on Aging, Mayo Clinic*; Vicente E. Torres, *Division of Nephrology and Hypertension and supported in part by the Mayo Clinic Robert M. and Billie Kelley Pirnie translational PKD center*; Laurie K. Bale, *Division of Endocrinology and Metabolism, Endocrine Research Unit, Mayo Clinic*; Peter C. Harris, *Division of Nephrology and Hypertension and supported in part by the Mayo Clinic Robert M. and Billie Kelley Pirnie translational PKD center*; Claus Oxvig, *Department of Molecular Biology and Genetics, Aarhus University*; Cheryl A. Conover, *Division of Endocrinology and Metabolism, Endocrine Research Unit, Mayo Clinic* and Eduardo Chini, *Department of Anesthesiology and Robert and Arlene Kogod Center on Aging, Mayo Clinic*

Abstract: Pregnancy-associated plasma protein-A (PAPP-A) is a key component of the IGF-1 pathway that plays a crucial role in IGF-signaling through degradation ofIGF-binding proteins (IGFBPs), thereby increasing the tissue bioavailability of free IGF-1 and 2 to activate the IGF-1 receptor (IGF1R). It has been speculated that the IGF-1 pathway may also play a role in autosomal dominant polycystic kidney disease (ADPKD), characterized by fluid-filled cysts in renal tubules, whose progression and expansion often leads to end-stage renal disease. Treatment options for ADPKD are limited.In the present study, we tested the hypothesis that the IGF-1 pathway and its components play an important role in ADPKD pathogenesis. Expression of IGF-1 and its components was analyzed in ADPKD patient cystic fluid and kidney tissues, in *Pkd1*$^{RC/RC}$ mice and 9-12 human ADPKD cells. We observed that among IGF-1 components, PAPP-A expression was higher in ADPKD patients as well as experimental ADPKD models compared to controls. Histopathological studies showed that PAPP-A accumulation was localized in the cyst-lining epithelium and cystic fluid in ADPKD patients. To study the role of PAPP-A in the pathogenesis of ADPKD, PAPP-A deficient ADPKD mice were generated. Homozygous as well as heterozygous deletion of the *Pappa*gene in *Pkd1*$^{RC/RC}$miceremarkably reduced the development of cysts and kidney inflammation markers, fibrosis and injury. Treatment of *Pkd1*$^{RC/RC}$mice with a monoclonal antibody to PAPP-A ameliorated the cystic disease *in vivo*in ADPKD mice. These data demonstrate that PAPP-A/IGF-1 pathway plays a role in the growth and expansion of cysts in ADPKD.

FRI - 101 Pituitary Tumor Database Development: Preliminary Results

Discipline: Health
Subdiscipline: Medicine

Emmanuel Makanjuola*, *Indiana University - Purdue University Indianapolis*; Diane Donegan, *Indiana University Health Hospital* and Heather Cero, RN, *Goodman Campbell Brain & Spine*

Abstract:
The pituitary is often referred to as the “master gland” and is found at the base of the brain. It is responsible for regulating the actions of a variety of endocrine glands. Pituitary adenomas are tumors that start from the pituitary gland. The estimated prevalence based on autopsy studies or MRI imaging is 16.7%; however, not all of these are clinically apparent. Most of these are benign and non-cancerous, but growth can be problematic due to their location and proximity to neurological structures, and excess hormone production can lead to increased morbidity and mortality. Additionally, growth may also compromise normal pituitary function.

Treatment of pituitary tumors is dependent on neurological and hormonal complications; however, assessment of outcome is challenging given the slow growth of the tumors. Moreover restrictive medical coding (ICD-9/ICD-10) of the tumors further complicates identification and assessment of these tumors. National registries or databases have been suggested for conditions which are less prevalent. Therefore, to better observe the long term significance and effects of pituitary tumor treatments, a database of IU Health patients was generated to keep track of their progress and response to treatment received.

FRI - 102 The Effect of Electronic Cigarette Liquids on *Staphylococcus Aureus* Antibiotic Susceptibility and Resistance

Discipline: Health
Subdiscipline: Medicine

Joshua García-Colón*, *Universidad Ana G Méndez, Recinto de Cupey*; Saira Ahmad, *University of North Carolina* and Robert Tarran, *University of North Carolina*

Abstract: Electronic Cigarettes have grown in popularity since 2007 and are estimated to become an $86.43 billion global market by 2025. Following inhalation, vapers expose their airways to an aerosol produced by heating an E-Liquid that contains propylene glycol-vegetable glycerin, nicotine, and flavorings. The alarming factor of this situation is that human airways have a dynamic microbiota with the potential of threatening human health and disease. Previous studies have shown that environmental factors present in vivo may influence bacterial susceptibility to antibiotic killing. We have seen that *Staphylococcus aureus* strain COL tolerates low concentrations of E-liquids. In this study, we tested the hypothesis that E-liquid stressed bacteria could develop multiple responses that may antagonize or potentiate antibiotic efficacy. We therefore chose E-liquids by their chemical compositions, which were previously identified by a GC-MS analysis. COL was incubated at 10^5 CFU/mL and stressed with E-liquids for 2 hours to evaluate the effect on the antibiotic’s minimum inhibitory concentration through an optical density analysis. Our results demonstrated that E-liquid stressed bacteria are more susceptible to Ciprofloxacin but not to Vancomycin or Tobramycin. We observed how the effectiveness of antibiotic treatment is determined by a holistic manner that not only involves the antibiotic but also the target pathogen and other environmental factors. Our data suggest that E-liquids may alter the pathogenicity of bacteria and its chemical composition should be considered prior antibiotic treatment. Thus, future studies should be performed to better understand the effects of E-cigarette use on antibiotic efficacy.

FRI - 104 A Role for Ceramides in Vascular Function

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Tahno Warren*, *University of Utah* and Scott Summers, *University of Utah*

Abstract: Cardiovascular complications are the leading causes of morbidity and mortality in individuals with obesity, type 2 diabetes mellitus (T2DM), and insulin resistance. Complications include pathologies specific to large (atherosclerosis, cardiomyopathy) and small (retinopathy, nephropathy, neuropathy) blood vessels. Common among all of these diseases is an altered vascular endothelial cell dysfunction that is characterized by reduced nitric oxide (NO) bioavailability. Understanding the mechanisms linking obesity and dyslipidemia to the impairment in endothelial function is essential for developing new therapeutic strategies to combat these debilitating disorders.

The persistent exposure of blood vessels to elevated fatty acids and lipoproteins leads to the aberrant production of ceramides, a class of sphingolipids that inhibit NO production. Previous work has shown that pharmacological approaches that inhibit enzymes required for ceramide synthesis systemically prevent endothelial dysfunction, ameliorate hypertension, and lessen the development of atherosclerosis in rodents. These data strongly suggest that ceramides are important drivers of the endothelial dysfunction that underlies cardiovascular disease.

To test the relevance of ceramides in endothelial function in vivo, we studied mice lacking *Sptlc2*, the rate-limiting enzyme in *de novo* ceramide synthesis, selectively within the endothelial cell using a tamoxifen-inducible knockout mouse model. Animals were maintained on a high-fat diet for 12 weeks. Animals were then administered tamoxifen and underwent a vascular function testing protocol. In line with the aforementioned studies, animals lacking *Sptlc2* displayed improved endothelial dependent vascular flow mediated dilation (FMD). These data suggest ceramides affect vessel function in a cell-autonomous manner and reveal new therapeutic strategies for combating hypertension.

FRI - 105 Exercise Decreases Estrogen Receptors & Inflammation in the Mesenteric Fat in an Endometriosis Rat Model

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

María Del Mar Méndez*, *University of Puerto Rico in Ponce*; Myrella Cruz, *Ponce Health Sciences University*; Johnathan Velazquez, *Pontifical Catholic University of Puerto Rico*; Gladys Chompre, *Pontifical Catholic University of Puerto Rico; Ponce Health Sciences University, Ponce Research Institute* and Caroline B. Appleyard, *Ponce Health Sciences University*

Abstract: Endometriosis, a gynecological disorder, is characterized by increased levels of the estrogen receptor β (ERβ) in endometrial tissue. Estrogen receptors (ER) are also present in visceral fat and dysregulation of their function is known to correlate with increased white adipose tissue. Preliminary data in our lab found increased mesenteric fat and serum leptin levels in endometriosis animals, which are decreased by exercise. **Hypothesis:** Voluntary exercise can decrease endometriosis through modulation of ER in the mesenteric fat and a decrease in inflammatory cytokines. **Methods:** Endometriosis (ENDO) was induced in female Sprague Dawley rats by the implantation of uterine tissue next to the intestinal mesentery while control group (SHAM) received only sutures. The exercised endometriosis group (ENDO-Ex) had access to a running wheel before and after surgery. After sixty days, rats were sacrificed and mesenteric fat was collected for measurement of ERβ, ERα, interleukin-1β (IL-1β), and interleukin-6 (IL-6) by RT-PCR. **Results:** Across all groups a significant correlation was found between percentage of fat/body weight and ER-β ($p=0.011$; $n=12$). Increased mesenteric fat also correlated with increased levels of IL-1β ($p=0.024$) and IL-6 ($p=0.030$) in the endometriosis animals ($n=4$/group). ENDO-Ex animals developed less endometriotic lesions and these were smaller in size. Exercise significantly decreased ERβ levels ($p=0.045$) and IL-1β ($p=0.008$, $n=4$/group) compared with ENDO. No significant differences were found in ERα levels between groups. **Conclusion:** Our results demonstrate that exercise can reverse the increased levels of mesenteric fat, ERβ and inflammatory cytokines found in an animal model of endometriosis. *Supported by P20GM103475-16 & R15AT009915.*

FRI - 106 Optical Measurement of Basal Forebrain Neuromodulation of the Olfactory Bulb

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jaime Richards*, *University of Utah*; Thomas Eiting, *University of Utah* and Matt Wachowiak, *University of Utah*

Abstract: The basal forebrain (BF) is thought to be involved in attention and active sampling of sensory information. Neurons within the BF regulate functions associated with learning, reward, decision-making, emotive responses, and sensory processing. However, little is known about how BF neurons are activated during olfactory related behavior. In this project, our goal was to understand how neurons in the basal forebrain are activated in the behaving animal in the context of active sniffing, attention, sensory input and reward. The olfactory bulb is advantageous for investigating BF function, as it is the only primary sensory structure modulated by BF neurons. Neural activity will be tracked with GCaMP6f reporters in cre-ChAT and GAD-2-cre transgenic mouse lines to monitor activity in cholinergic and GABAergic neurons, respectively. We are using in-vivo fiber photometry to monitor activity within the basal forebrain to record real-time neural population activity. Mice are trained in a Go/No-Go paradigm to discriminate between two odors using a water reward. While mice are performing the task, BF neuron activity is monitored using implanted fiber optics, and sniffing is measured using an implanted thermistor. The implanted thermistor provides precise measurements of inspiration onset in response to odor presentation. This data, along with neuronal activity data, will indicate if behavior is driving neural responses. We hypothesize basal forebrain neurons will respond to active sniffing during odor presentation in awake mice. Ultimately, this experiment will highlight the role of neural BF projections to the OB, and shed light on their role in olfactory processing.

FRI - 108 Investigating the Relationship between Income and Housing Quality on Women's Risk of Preterm Birth

Discipline: Health
Subdiscipline: Medicine

Phiwinhlanhla Ndebele-Ngwenya*, *Philander Smith College*; Mary Regina Boland, *University of Pennsylvania*; Jessica A Patterson, *University of Pennsylvania*; Silvia Canelon, *University of Pennsylvania* and Samantha Butts, *University of Pennsylanis*

Abstract: The purpose of this study was to understand the relationship between the condition of the housing occupied by the mother and pregnancy-related conditions and complications, especially among low-income populations.

We investigated the correlation between preterm birth rates and income, and also imminently dangerous housing violations and unsafe housing violations. We incorporated data on housing quality from the Licenses and Inspections Code Violations dataset obtained from OpenDataPhilly (*https://www.opendataphilly.org/showcase/li-imminently-dangerous-violations-visualization*). We used the software language R to visualize communities and regions within the Philadelphia Area at risk for preterm birth and assess statistical significance.

Our dataset contained 42,390 pregnancies where the mother lived in a Philadelphia zip code having a population greater than 20,000 individuals. We linked these pregnancies with information of whether the mother was billed with a preterm birth code at any point in her medical records. We found that 3,861 pregnancies corresponded to mothers having had a preterm birth. Our dataset contained 10,909 pregnancies (25.73%) where the mothers lived in a zip code having a median income less than $25,000. Our preliminary results revealed that income was not correlated with preterm birth rate in Philadelphia ($p=0.787$, $r=0.053$). However, preterm birth rate was correlated with unsafe housing ($p=0.039$, $r=0.415$) and marginally associated with imminently dangerous housing ($p=0.055$, $r=0.388$).

Our preliminary results demonstrate that housing quality is more important than income in determining preterm birth. This suggests that the role of socioeconomic disparities on preterm birth is multifactorial and warrants further investigation.

FRI - 109 The Effect of C1q and gC1qR in Breast Cancer: Racial Health Disparities

Discipline: Health
Subdiscipline: Medicine

Tiana Reyes*, *Stony Brook University*; Jennie Williams, *Stony Brook University*; Berhane Ghebrehiwet, *Stony Brook University* and Matthew Digiovanni, *Stony Brook University*

Abstract: Breast cancer is one of the most highly diagnosed cancers in the US with African American (AA) women developing a more aggressive form of the cancer at a younger age. The complement system, part of the immune system, is tightly regulated and able to eliminate foreign invaders. Complement proteins can induce cancer cell apoptosis or increased proliferation. Cell surface expression of C1q, classical pathway of the complement system, and its receptor, gC1qR, is enhanced in malignant cells. Upon treatment with antibody to C1q, antiproliferative effect in breast cancer cells was observed *in vitro*. Antibody recognizing gC1qR enhances breast cancer cell survival by promoting angiogenesis and metastasis. It was noted in a panel of breast cancer cell lines that MDA-MB-468, an AA derived cell line, did not express gC1qR compared to three Caucasian American (CA) derived cell lines. In a second study, a lower expression level of gC1qR in the membranes of three AA breast cancer cell lines (MDA-MB-468, HCC70, and HCC1500) compared to a CA cell line (MDA-MB-231) was observed. We hypothesize that treatment with anti-C1q will have an antiproliferative effect on breast cancer cell lines, while treatment with anti-gC1qR will have a pro-proliferative effect. One CA (MDA-MB-231) and three AA (MDA-MB-468, HCC1500, and HCC7) breast cancer cell lines were treated with anti-C1q in solution at increasing concentrations and an antiproliferative effect was observed. Coating the culture plate with C1q will determine differential expression. Therefore, role of C1q and gC1qR on cytokinetics and in racial health disparities are being accessed.

FRI - 110 Sexual Function in Ulcerative Colitis Patients with an Ileal Pouch Anal Anastomosis

Discipline: Health
Subdiscipline: Medicine

Jocelyn Durán-Martinez*, *Pomona College* and Sushila Dalal, *University of Chicago Medicine*

Abstract: Ulcerative colitis (UC) is a type of Inflammatory Bowel Disease (IBD) that involves inflammation beginning in the rectum and progressing proximally into the colon. UC affects about 3 million Americans, and is often diagnosed between the ages of 15 and 35, a time in which body image and exploration of sexual activity are important. High rates of sexual dysfunction have been reported in UC patients. About 25% of UC patients fail medical therapy and require surgery to remove the colon. After colectomy, patients can elect to have an ileal pouch anal anastomosis (IPAA) created. Colectomy with IPAA formation requires a deep pelvic dissection that has been associated with decreased fertility, but its affects on sexual function are unknown. We hypothesize that patients in the first year post IPAA may also report high rates of sexual dysfunction. We are performing a retrospective observational study of adult UC patients who underwent colectomy and IPAA at the University of Chicago IBD Center between 2013-2018. Patients filled out a standardized questionnaire regarding their sexual function and quality of life every three months for the first year after surgery. The study is ongoing. We will be reporting percentage of both female and male patients reporting a change in interest in sexual intercourse since surgery, change in ability to reach orgasm, and change in quality of life as compared to before the operation. This is the first study to report upon the effect of colectomy and IPAA on sexual function in UC patients.

FRI - 111 Characterization and Comparison of Collagen Structure between Chronic Rhinosinusitis with Nasal Polyps Tissue and Healthy Tissue Using Two Photon Microscopy.

Discipline: Health
Subdiscipline: Medicine

Andre Benally*, *Fort Lewis College*; Jeremiah Alt, *University of Utah*; Abigail Pulsipher, *University of Utah*; Nithya Subrahmanyam, *University of Utah*; Jorgen Sumsion, *University of Utah*; Chelsea Pollard, *University of Utah* and Elijah Alt, *University of Utah*

Abstract: Chronic rhinosinusitis with nasal polyps (CRSwNP) is characterized by sustained mucosal inflammation, epithelial barrier breakdown, and tissue remodeling. Increased collagen deposition and collagen fiber misalignment have been correlated with disease progression in various cancers and inflammatory conditions. The role of collagen dysregulation with respect to structure, orientation, and content in CRSwNP-associated tissue remodeling and disease progression, however, remains poorly understood. Herein, we assess the overall differences in collagen structure, content, and fiber alignment between normal controls and patients with CRSwNP, as well as differences between subsites within anterior ethmoid and nasal polyp tissues. Tissue biopsies (n = 7 controls; n = CRSwNP) were stained with hematoxylin and eosin and imaged using two-photon microscopy. The non-centrosymmetric properties of collagen yield second harmonic generation, which can be used to quantify collagen deposition and fiber alignment. Regions of interest (ROIs) that included epithelial, basal lamina, submucosa, and nasal polyp subsites using CurveAlign software were then subjected to collagen alignment quantification. Collagen alignment and content was found to decrease from submucosa to the apical side of the sinonasal tissues, with a marked reduction in nasal polyps in tissues obtained from CRSwNP compared controls, suggesting that dysregulation of collagen and tissue remodeling may contribute to the pathology of CRSwNP. Further elucidating the role of collagen in CRSwNP-associated tissue remodeling may ultimately help us develop more effective and targeted therapeutics for CRSwNP.

FRI - 112 Prediction of Plasma and Salivary Pharmacokinetics of Atropine in Pediatric Sialorrhea Patients Using a PBPK Modeling Approach.

Discipline: Health
Subdiscipline: Medicine

Drisanna Watson*, *University of Utah, NARI internship.* and Venkata Yellepeddi, *University of Utah, Pediatric School of medicine.*

Abstract: Sialorrhea is excessive salivation and is a significant quality of life issue in children with neurodevelopmental disorders. Sialorrhea is currently treated off-label using adult formulations of anticholinergic agents such as atropine. Sublingual administration of atropine eye drops is the present approach for the treatment of sialorrhea because of the low-cost and easy availability. However, due to its off-label use, there are no approved pediatric dosing guidelines for atropine in sialorrhea. We hypothesize that a validated physiologically based pharmacokinetic model (PBPK) of atropine can be used to predict the blood plasma and salivary pharmacokinetics of atropine in children across various age groups. A validated PBPK model can, therefore, be used to develop dosing recommendations for atropine in pediatric sialorrhea patients. The PBPK model was developed using PK-Sim®Version 8, software. The input parameters for atropine were obtained from the published literature. The simulations of atropine pharmacokinetics after oral administration were performed in virtual pediatric populations with age groups: 0-5, 6-10, 11-15, and 16-21 years. The pharmacokinetic parameters maximum plasma concentration (C_{max}), half-life ($T_{1/2}$), and Area Under the Curve ($AUC_{0-\infty}$) of atropine in plasma and saliva were calculated using PK Sim®. Our results indicated that the plasma and salivary pharmacokinetics varied significantly across all age groups studied. Specifically, $AUC_{0-\infty}$, a pharmacokinetic parameter representing bioavailability was approximately 3.5-fold lower in 16-21 years when compared to 0-5 years. The atropine PBPK model developed after validation with observed data can be used to develop an age-based dosing regimen of atropine in pediatric sialorrhea patients.

FRI - 113 Blacmy-2 Gene Mobilization into Environmental *Escherichia coli* incf Plasmid By IS*1294* Transposase

Discipline: Health
Subdiscipline: Public Health

Sarah Singh*, *University of California, Irvine* and Luis Mota-Bravo, *University of California Irvine*

Abstract: The AmpC beta-lactamase CMY-2, encoded by *blaCMY-2*, confers resistance to cephalosporin and penicillin classes of antibiotics. It is commonly carried on plasmid incompatibility (Inc) types IncA/C and IncI1. Finding antibiotic resistance genes mobilized between plasmids of different Inc-types shows how those genes are disseminating. The objective of our study was to describe the genetic environment of *blaCMY-2* found on an IncF plasmid from the environmental *Escherichia coli* isolate, SW4104. We hypothesized that cephalosporin resistance by *blaCMY-2* was transferred between different Inc-types by mobile genetic elements. The isolate was collected in San Juan Creek, California and identified as an *E. coli* using MALDI-TOF. The resistance phenotype was determined through disk diffusion tests (DDT). The plasmids were sequenced, assembled and annotated. Plasmid 1 was an IncFII-type and 67,876 bp long. The DDT revealed that the bacterium was resistant to ten antibiotics from the beta-lactam class. Plasmid 1 encoded *blaCMY-2,* which conferred resistance to all these antibiotics and was preceded by the mobile element IS*1294*. Its 60 kb backbone was 99% similar to IncF plasmids in GenBank, and its 7.9 kb region, surrounding the IS*1294* and *blaCMY-2*, corresponded to two IncI1-types. Earlier studies showed that *blaCMY-2* was mobilized and transferred on the IncI1 plasmids from an IncA/C plasmid by the IS*1294* transposase. We show that the IS*1294* further transferred this region onto the IncF plasmid in SW4104. It can be difficult to infer the evolutionary path of gene mobilization, but our finding shows a clear example of *blaCMY-2* mobilization.

FRI - 114 Maximizing Retention of Nutritional Knowledge and Healthy Behaviors through the Teen Teaching Model

Discipline: Health
Subdiscipline: Public Health

Anaderi Iniguez*, *WASHINGTON STATE UNIVERSITY* and Elizabeth Weybright, *WASHINGTON STATE UNIVERSITY*

Abstract: Despite widespread implementation of nutrition programs targeting adolescents, obesity remains a prevalent issue (Center for Disease & Control Prevention, 2017).

Nonetheless, nutrition interventions are still essential for adolescents, as they remain one of the only ways to reach and educate youth about nutrition. One promising approach has been using teens as instructors that teach a nutrition education curriculum, as research demonstrates teens adopt the skills and knowledge they impart (Weybright et al., 2018). Similarly, we expect to see improvement in teens making healthier choices after they have completed the nutrition intervention program.

The current study evaluates the effectiveness of a nutrition education program by looking at teen teacher nutrition knowledge and healthy behavioral change. The sample includes pre and post surveys of 46 adolescents (M_{age} = 15.5 years old; 67% female; 52% Hispanic; 41% White Non-Hispanic) enrolled as teen teachers in a 4-H youth development program. A paired sample t-test was conducted to identify significant changes in nutrition knowledge and behaviors.

Significant improvements from pre to post were found in knowledge of making healthy food choices (t= 3.38, p<.001), what makes up a balanced diet (t=4.56, p<.001), and what foods to eat daily (t=4.33, p<.001). Other significant improvements were found in behaviors of eating fruits and vegetables (t=2.66, p<.01), and drinking water (t=2.14, p<.05).

These results demonstrate the teen-teaching approach should be disseminated throughout nutrition interventions to produce optimal results. Future studies should examine the potential benefits and outcomes of incorporating a teen-teaching component in other positive youth development interventions.

FRI - 115 Poor Sleep Health and Psychological Distress: A Nationally-Representative Study

Discipline: Health
Subdiscipline: Public Health

Samuel J. Goldstein*, *University of North Carolina at Chapel Hill*; Symielle A. Gaston, *Epidemiology Branch, National Institute of Environmental Health Sciences, National Institutes of Health, Department of Health and Human Services*; John McGrath, *Social & Scientific Systems, Inc.* and Chandra L. Jackson, *Epidemiology Branch, National Institute of Environmental Health Sciences, National Institutes of Health, Department of Health and Human Services*

Abstract: Prior studies investigating the association between poor sleep and mental health have been mainly conducted among special populations (e.g., medical students; battered women) prone to stress. Few studies, however, have used nationally-representative data. To address this important gap in the literature, we investigated associations between sleep health and psychological distress using nationally-representative data collected from the National Health Interview Survey (2004-2017). Participants self-reported sleep duration and measures of sleep quality (trouble falling asleep, trouble staying asleep, and restorative sleep). Psychological distress was assessed using the Kessler-6 scale. We used Poisson regression with robust variance to estimate prevalence ratios (PRs) and 95% confidence intervals (CIs) of psychological distress for each sleep characteristic. Models were adjusted for sociodemographic, other health behavior, and clinical characteristics. Among 303,590 adults, psychological distress was more prevalent among adults with poor sleep characteristics. Whites with long (>9 hours) vs. recommended (7-9 hours) sleep had an over 3-fold increased prevalence of psychological distress (PR=3.31 [95% CI: 2.93-3.75]), and Blacks with short (<7 hours) vs. recommended (7-9 hours) sleep had an over 5-fold increased prevalence of psychological distress (PR=5.24 [95% CI: 4.42-6.21]). Hispanics/Latinos reporting trouble vs. no trouble falling asleep had an almost 9-fold increased prevalence of psychological distress (PR=8.90 (95% CI: 6.30-12.6). Compared to Whites reporting the recommended amount of sleep, Blacks and Hispanics/Latinos reporting either short or long sleep were more likely to be psychologically distressed. The poor sleep-psychological distress relationship appears to vary by race, and additional studies investigating the determinants and health consequences are warranted.

FRI - 116 Persistence of Anti-Zika Virus Antibodies over Time in Nicaraguan Cohort Studies

Discipline: Health
Subdiscipline: Public Health

Samantha Hernandez*, *Department of Molecular and Cell Biology, University of California*; Robin Hauscher, *Division of Infectious Diseases and Vaccinology, School of Public Health, University of California*; Damaris Collado, *Laboratorio Nacional de Virología, Centro Nacional de Diagnóstico y Referencia, Ministerio de Salud*; Tatiana Miranda, *Laboratorio Nacional de Virología, Centro Nacional de Diagnóstico y Referencia, Ministerio de Salud*; Raul Zapata, *Laboratorio Nacional de Virología, Centro Nacional de Diagnóstico y Referencia, Ministerio de Salud*; Leah Katzelnick, *Division of Infectious Diseases and Vaccinology, School of Public Health, University of California*; Angel Balmaseda, *Laboratorio Nacional de Virología, Centro Nacional de Diagnóstico y Referencia, Ministerio de Salud* and Eva Harris, *Division of Infectious Diseases and Vaccinology, School of Public Health, University of California*

Abstract: Zika virus (ZIKV) is a flavivirus that is transmitted primarily by infected *Aedes* mosquitoes and, to a lesser extent, sexual transmission. In 2016, the World Health Organization declared a Public Health Emergency due to the massive epidemics of Zika in the Americas. Recent epidemics of Zika have demonstrated association of ZIKV with birth defects in newborns and Guillain–Barré syndrome in adults. ZIKV was first detected in Nicaragua in January 2016, and the epidemic peaked between late June and September of 2016. This study analyzes serum samples from adult and pediatric cohorts in Managua, Nicaragua, from 2017-2019 processed by the ZIKV Inhibition Enzyme-Linked Immunosorbent Assay (iELISA) and ZIKV NS1 Blockade-of-Binding (BOB) ELISA. Serological cross-reactivity between ZIKV and the related dengue virus (DENV) is common. Given that cross-reactive antibodies are known to decay more rapidly than virus-specific antibodies, we hypothesize that we will observe an age-related decline in anti-ZIKV antibodies since older individuals are more likely to have had prior DENV infection(s). Because the ZIKV iELISA has a lower specificity than ZIKV NS1 BOB ELISA, we hypothesize that a greater rate of decay of anti-ZIKV antibodies will be seen in ZIKV iELISA. Findings from this study will help 1) assess the persistence of anti-ZIKV antibodies, 2) determine the differential profiles of anti-ZIKV antibodies in adults vs. children, and 3) provide more insight into the sensitivity and specificity of the ZIKV iELISA and ZIKV NS1 BOB ELISA.This investigation is important for Zika surveillance, calculation of seroprevalence, epidemiological preparedness, and vaccine development.

FRI - 117 Developmental Manganese Exposure Causes Lasting Alterations of Catecholaminergic System Protein Levels Due to Epigenetic Mechanisms

Discipline: Life Sciences
Subdiscipline: Neurosciences

Thi Lan Chi Nguyen*, *Mission College*; Nicholas Santiago, *University of California, Santa Cruz*; Shanna Howard, *University of California, Santa Cruz* and Donald Smith, *University of California, Santa Cruz*

Abstract: Developmental manganese (Mn) exposure is associated with cognitive impairment and fine-motor dysfunction in children. While the mechanism(s) of how Mn causes these impairments in humans are not well-known, studies in rats have shown that developmental Mn exposure causes lasting impairments in attention and fine-motor function associated with changes in levels of several catecholaminergic system proteins in the prefrontal cortex (PFC). The PFC catecholaminergic systems are important mediators of executive functions, including attention and impulse control. Catecholamine neurotransmitters, such as dopamine and norepinephrine, are biomolecules that contain catechol and amine functional groups. The catecholaminergic systems also involve several enzymes, transporter, and receptor proteins responsible for the synthesis, transport, and signal transduction of these neurotransmitters. My research will use a human immortalized neuronal cell culture line and an *in vivo* rat model of developmental Mn exposure to analyze changes in expression levels of the catecholaminergic system proteins tyrosine hydroxylase, dopamine transporter, and the dopamine 2 receptor using immunohistochemistry and fluorescence microscopy. In addition, the research will use RT-qPCR to quantify gene expression in the cell model for these catecholaminergic system proteins, as well as gene expression levels of DNA methyltransferase (DNMT) and histone deacetylase (HDAC), which are enzymes responsible for epigenetic modifications of DNA. Through looking at changes in gene transcript and protein levels,

together with further experiments, I expect to find out whether the changes in catecholaminergic system protein levels caused by developmental Mn exposure are due to epigenetic modifications of their genes.

FRI - 118 Optimization of the VAST Imaging System for High-Throughput Morphological Characterization of Neurodevelopmental Phenotypes in Zebrafish

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alejandra Quezada*, *California State University, Sacramento State* and Megan Dennis, *University of California, Davis*

Abstract: In recent years, zebrafish have become commonly used as a model for studying neurodevelopmental disorders. Their high fecundity and rapid development allows us to conduct more robust, higher-throughput experiments. In addition, zebrafish share ~80% gene homologs with humans, making it a suitable genetic model of humans. The goal of this study is to optimize a high-throughput protocol for consistent zebrafish morphological and behavioral characterization. For this we are using the VAST automated system, which allows us to image 96 fish larvae in an automated fashion. Utilizing wildtype zebrafish larvae, we tested the following approaches: (1)VAST imaging of fish at two time points (2 days post fertilization (dpf) and 5 dpf); (2)VAST imaging of fish at 2 dpf, followed by motion-tracking and VAST imaging at 5 dpf; (3)VAST imaging fish only at 5 dpf; and 4)VAST imaging fish at 5 dpf first tested with motion tracking. First, we assayed the impact on fish survival with each experimental approach. Our preliminary results show that experimental approach 1, in which larvae undergo VAST imaging at two separate time points, do not present any developmental or physical damage. We did observe a 20% loss of fish within the microfluidic system of the system in each run. This suggests that to maximize our number of larvae we should limit our VAST imaging to one developmental time point. Once optimized, we will use it to to characterize mutant larvae produced via CRISPR gene editing of disease-candidate genes.

FRI - 119 Identifying Palliative Care Interventions Used By Community Health Workers in Southern Thailand.

Discipline: Health
Subdiscipline: Public Health

Yanique Duffus*, *The City College of New York* and Cathy Campbell, *The University of Virginia*

Abstract: Palliative care promotes comfort care for patients who are suffering from life-limiting illnesses. Recently in Thailand there have been several initiatives to enhance the quality of palliative care across the country.The goal for this project was to identify palliative care interventions used by community health workers (CHWs) in Southern Thailand. We conducted focus groups at two community hospitals. We used a 6-step thematic analysis method to analyze the transcripts of the interviews. Across the two hospitals forty-one CHWs participated in the focus groups, 90 % women and 10 % men. Approximately 54% of the sample provided data on mean age, mean years worked in the facility, and years in current position. Mean age was 45.45 years, and the mean number of years spent at the facility and in current position where both 10.36 years. Three major themes were identified: 1) Interventions to support mental and emotional health such as presence, encouraging the patient, and focusing on the needs of the caregiver were important. 2) Coordinating with the interprofessional team and community organizations is an intervention that is a component of quality palliative care. 3) Culture and religion influences the interventions used by the CHWs to care for their patients. Understanding the role of CHWs is important because they play a vital role in caring for patients within their community.

FRI - 120 Exploring Relationships between Vigorous Physical Activity, and Caffeine, Alcohol and Smoking in a Nationally Representative Sample.

Discipline: Health
Subdiscipline: Public Health

Gwendolyn Lind*, *California State University Fullerton*; Koren Fisher, *California State University Fullerton* and Archana McEligot, *California State University Fullerton*

Abstract: Physical activity (PA) plays a predominant role in health and therefore, understanding the behaviors that influence our choice to be physically active is important. Caffeine, being the key ingredient in pre-workout supplements, has been linked to performance enhancing effects on exercise. Alcohol use and smoking, both potentially risky behaviors may also impact PA, however, the role of alcohol use and smoking with vigorous PA has yet to be fully explored. Therefore, we examined the association between alcohol use, caffeine intake, and smoking cigarettes with vigorous PA. Data were obtained from the 2005-06 National Health and Nutrition Examination Survey (NHANES), with a nationally representative sample size of 5,563. Separate univariate regression analyses were performed to assess the association between caffeine intake (mg/day), alcohol use (g/day), and smoking (number of cigarettes/day) with vigorous PA (defined as any physical activity above 6 METS). Alcohol use was significantly inversely associated with vigorous PA (β = - 0.016; p = <0.001). Caffeine intake likewise was significantly associated with vigorous PA (β = - 0.004 ; p = < 0.001), as was smoking (β = - 0.004 ; p = < 0.001). Our findings suggest that higher caffeine, alcohol, and smoking is associated with lower levels of vigorous PA. Therefore, potentially we showed that higher levels of vigorous PA may promote reduced caffeine intake and alcohol use, and smoking less, however temporal sequence has yet to be established. Further studies are needed to assess the combined influence of other factors on vigorous PA.

FRI - 121 Relationship between Diabetes Control and Cognitive Decline Among Cameron County Hispanic Cohort

Discipline: Health
Subdiscipline: Public Health

Paola Bojorquez-Ramirez*, *University of Texas Health Science Center at Houston*; Isela De La Cerda, *University of Texas Health Science Center at Houston*; Miryoung Lee, *University of Texas Health Science Center at Houston* and Susan P. Fisher-Hoch, *University of Texas Health Science Center at Houston*

Abstract: Findings on the association of diabetes and diabetes-related conditions with cognitive decline have been inconsistent. Furthermore, no studies have evaluated the association between diabetes risk factors and cognitive decline among Mexican American adults, a population with a higher burden of diabetes. We aim to determine if control of diabetes is associated with cognitive decline among Mexican American adults aged ≥18 years with cognitive deterioration in the Rio Grande Valley. The cross-sectional analysis included 2991 participants 18-94 years of age from the Cameron County Hispanic Cohort. Mini-Mental State Examination (MMSE) scores were dichotomized as an indication of ‘mild to severe’ cognitive impairment (MMSE ≤24, n=333, 11.13%) or normal cognition (MMSE>24, n=2658, 88.87%). Logistic regression models controlled for age and education were used to assess the odds of cognitive impairment using a multi-factorial variable based on the American Diabetes Association 2010 criteria. At baseline visit, 16.14% of diabetic participants and 8.64% of participants without diabetes were identified as having ‘mild to severe’ cognitive impairment. Participants with diabetes have 2.04 (95%CI: 1.53-2.69) times the odds of having ‘mild to severe’ impairment compared to participants without diabetes. However, diabetes no longer had a significant association with ‘mild to severe’ cognitive impairment (adjusted OR: 1.15[95%CI: 0.84-1.57]) in models adjusting for age and education. Diabetes was independently associated with cognitive impairment among Mexican Americans across a wide age range, but this association attenuated when adjusted for age and education. These findings indicate the need to objectively identify risk factors for cognitive decline in Mexican Americans.

FRI - 122 The Impact of Host Factors on Antibody Response to Influenza Vaccine

Discipline: Health
Subdiscipline: Public Health

Amali Stephens*, *Iowa State University of Science and Technology*; Danielle Wagner, *Iowa State University*; Joshua Borwick, *Iowa State University*; Jessica Alley, *Iowa State University*; Megan Slattery, *Iowa State University*; Daniel Taylor, *University Of North Texas*; Kimberly Kelly, *University of North Texas* and Marian Kohut, *Iowa State University*

Abstract: Immunizations are a cornerstone of public health in reducing or eliminating the threat of infectious disease. Antibody response to vaccination determines the degree of protection from infection. However, host factors such as advanced age or comorbidity may influence antibody response. The goal of this project is to determine how body mass index (BMI) (normal, overweight, or obese) and underlying inflammatory status impact antibody response to influenza immunization. Many comorbid conditions including cardiovascular disease, diabetes, neurodegenerative disease, etc., are characterized by low-level chronic inflammation. Obesity and comorbidities may increase the risk of complications from influenza infection. In this study, serum has been collected from > 300 nurses before influenza vaccination (pre-immunization), and at 1, 6, and 11 months post-immunization. The hemagglutination inhibition (HI) assay is being used to measure the quantity of anti-influenza antibody against the 4 strains of influenza contained in the vaccine. The inflammatory status (as a surrogate marker of comorbidity) is determined using ELISA technique to measure inflammatory proteins, IL-6, TNFα, IL-1β, and CRP. A microneutralization assay will be used to determine antibody quality. Preliminary results show that higher BMI (overweight/obese) or greater IL-1β are associated with reduced antibody (HI) response to the vaccine, particularly for Influenza A H1N1. Given that the Influenza A H1N1 strain of virus was the only new strain of virus contained in the vaccine, these early findings may suggest that obesity impairs antibody response to newer antigens. Pending final analysis, a review of current influenza immunization practices for obese individuals may be warranted.

FRI - 123 Pain Sensitivity and Central Pain Mechanisms Among Immigrant Hispanics and Non-Immigrant Hispanics: The Role of Sociocultural Factors

Discipline: Health
Subdiscipline: Public Health

Erika De Santiago*, *Northern New Mexico College*; Aaron Smiley, *The University of Texas at El Paso*; Megan Giron, *The University of Texas at El Paso* and Carolina Valencia, *The University of Texas at El Paso*

Abstract: Chronic pain is a common problem in the general population that is associated with alterations in the central nervous system. However, the social context in which persons live, could explain why certain populations experience pain differently. The aims of this study are to examine central pain mechanisms among Hispanic Americans who consider themselves immigrants (Hi) and those who consider themselves non-immigrant (Hn-i), and to identify the potential effect of ethnic identity, optimism, and resilience in pain perception and central mechanism. This preliminary analysis included 14 Hispanic subjects (7 Hi and 7 Hn-i). Validated questionnaires were gathered at the beginning of the session. Participants underwent quantitative sensory testing which included heat pain threshold, heat pain tolerance, suprathreshold heat pain response (SHPR), and conditioned pain modulation (CPM). Analysis showed non-significant difference on the level of ethnic identity, and resilience; however, optimism showed significant difference [$t(12)=-2.410$; $p=0.03$] between Hi and Hn-i where Hi reported lower level of optimism (mean= 1.904, SD=0.46) than Hn-i (mean=2.42, SD=0.34) In addition, SHPR and CPM showed non-significant difference between groups; however, the heat pain tolerance significantly differed [$t(12)=2.259$; $p=0.04$] between groups, where Hi reported higher tolerance than Hn-i. The results of this study suggest that Hi and Hn-i have a non-significant difference in the level of ethnic identity, and resilience; however, testing optimism may provide a better understanding on why certain populations experience pain differently. Further analysis in a larger sample will provide stronger evidence about the interrelationship between sociocultural factors and central pain mechanisms.

FRI - 124 Association between Metal Exposures and Maternal Autoantibodies: Potential Role in Neurodevelopment

Discipline: Health
Subdiscipline: Public Health

Adrianna Rojas*, *California State University, Northridge*; Joseph Hoover, *Community Environmental Health Program, College of Pharmacy, University of New Mexico Health Sciences Center*; Esther Erdei, *College of Pharmacy, University of New Mexico Health Sciences Center*; Johnnye Lewis, *College of Pharmacy, University of New Mexico Health Sciences Center* and Debra MacKenzie, *College of Pharmacy, University of New Mexico Health Sciences Center*

Abstract: Studies investigating the etiology of developmental disorders in children are challenging due to the vast amount of factors that could influence these outcomes which include environmental factors, genetics as well immune interactions between mother and child. On Navajo Nation, the prevalence of developmental disorders is of concern due to chronic exposure to mixed metals such as uranium and arsenic from the more than 500 abandoned uranium mines that are located on Navajo Nation, many of which remain unmarked, unfenced and in close proximity to communities. The Navajo Birth Cohort Study (NBCS) is investigating the relationship between exposure to environmental metals and child development. These studies have found higher than expected levels of anti-nuclear antibody (ANA) and literature has shown that maternal autoantibodies with specificity for fetal brain tissue increases risk for neurodevelopmental disorders (ND), suggesting that metals exposure could increase risk for ND through induction of these antibodies. Serum from NBCS mothers were tested for presence of anti-mouse fetal brain reactive antibodies (AFB) using immunohistochemistry. We will determine if the detection of AFB is associated with increased overall detection of ANA, metals levels, as well as developmental assessments in these mothers. We will use a linear regression model to look for associations between metals determined through biomonitoring assays and AFB. We will also use a 2 X 2 contingency table to look for associations between AFB and anti-nuclear antibodies (ANA). Addressing the origins of developmental disorders can help in diagnosing developmental disorders early in communities impacted by mixed metal exposure.

FRI - 125 The Association between Physical Activity and Metabolic Syndrome in Older Women

Discipline: Health
Subdiscipline: Public Health

Mimi Ngo*, *California State University, Fullerton*; Koren Fisher, *California State University Fullerton* and Archana McEligot, *California State University, Fullerton*

Abstract: Metabolic syndrome (MetS), a cluster of health conditions, has been associated with developing subsequent diabetes and/or heart disease. Both moderate/vigorous physical activity (MVPA) and sedentary behavior (SB) have been shown to be associated with MetS risk in adults, but little is known about PA/SB and MetS in older women. Therefore, we investigated the link between MVPA and SB with MetS indicators in older (≥50 yrs., n=1,035) and younger women (≤49 yrs., n=1,620), utilizing 2005-06 National Health and Nutritional Examination Survey (NHANES) data. Separate univariate analyses were conducted using weighted questionnaire and laboratory data to assess associations between MVPA and SB with MetS indicators. In older women, MVPA was significantly associated with waist circumference ($\beta= -.276$, $p < 0.001$), fasting glucose ($\beta= -0.370$, $p < 0.001$), triglycerides ($\beta= -0.575$, $p < 0.001$), and systolic ($\beta= -0.246$, $p < 0.001$) and diastolic blood pressure ($\beta= 0.119$, $p < 0.001$). Similarly, for younger women, significant associations were observed between MVPA and waist circumference ($\beta= -.278$, $p<0.001$), triglycerides ($\beta= -.808$, $p<0.001$), and systolic ($\beta= -.084$, $p<0.001$) and diastolic blood pressure ($\beta= -.094$, $p<0.001$). In older women, stronger associations in magnitude were evident between MVPA and MetS indicators compared to those found between SB and MetS (waist circumference: $\beta= -0.276$ vs. 0.02; glucose: $\beta= -0.376$ vs. 0.003) suggesting that MVPA may have stronger influence on MetS in this population. Our findings suggest that MVPA may play an important role in improving MetS indicators in older women, potentially curbing later onset diabetes and heart disease.

FRI - 126 The Ethical Inclusion of Indigenous Individuals in Clinical Research Studies That Are Not Specific to Tribal Nations: The Intramural Research Program at the National Institutes of Health, a Model

Discipline: Health
Subdiscipline: Public Health

Deionna Vigil*, *National Institute of Neurological Disorders and Stroke* and Barbara Karp, *National Institute of Neurological Disorders and Stroke*

Abstract: The National Institutes of Health, as a federal entity and the world's largest biomedical research agency, often sets research practice precedents and has a responsibility to the nation and the individuals it serves, including Indigenous peoples (IP). In 2017, the National Institutes of Health Intramural Research Program (NIH-IRP) enrolled over 19,000 IPs in clinical studies that were not based in or on tribal nations. 41% of those studies enrolled one IP while other studies enrolled over 1,000 IPs, even though not targeted to an Indigenous community. Whether a study enrolls one person or 1,000 persons, the possibility of unintended negative consequences (UNCs) exists at individual, tribal, and national levels.

We conducted this mixed methods study using the NIH-IRP as a model to identify circumstances under which UNCs for Indigenous individuals, their tribal nations, and IPs as a whole could arise. Literature reviews, NIH-IRP investigator interviews, and interviews with departments related to bioethics and the protection of human subjects in research were conducted. We found several studies where an individual's participation carried implications for their tribal nation and/or IPs in general. We similarly identified cases where the Indigenous community could have an adverse impact on the individual's ability to receive potential benefits of participation in clinical studies. Examples of each of these situations will be presented. These cases demonstrate a need for the establishment of a mechanism to monitor, ensure the protections of, and serve as a liaison for IPs, tribal nations, and the NIH-IRP while minimizing barriers to IP participation.

FRI - 127 Examining Mindfulness and Body Image in the Context of Yoga

Discipline: Health
Subdiscipline: Other Health

Veronica Garcia*, *Washington State University* and Anne Cox, *Washington State University*

Abstract: Many young girls are dissatisfied with their bodies, and this has been shown to continue and worsen over time. The purpose of this study was to examine the relationships of mindfulness and self-compassion to body appreciation and body surveillance in women during a 16-week yoga course. It was hypothesized that higher state mindfulness and self-compassion would predict decreases in body surveillance and increases in body appreciation over the 16 weeks. It was also hypothesized that there would be an increase in trait mindfulness, self-compassion, and body appreciation, and a decrease in body surveillance throughout the course. The study included 147 female participants (M age = 20.28). Self-report surveys were administered to participants 3 times throughout the course to assess trait mindfulness, self-compassion, body appreciation, and body surveillance. Surveys assessing state mindfulness were administered every two weeks for a total of seven surveys. Average scores of state mindfulness were used in the main analyses. All correlations between variables were significant and in anticipated directions. State and trait mindfulness, self-compassion, and body appreciation all related positively to each other, and they all negatively related to body surveillance. In looking at whether mindfulness and self-compassion predicted body surveillance and body appreciation, we found that higher state mindfulness and self-compassion related to decreases in body surveillance and increases in body appreciation. Interestingly, trait mindfulness was not a significant predictor in either case. Understanding these relationships is essential so that women can begin to work on implementing strategies that will support more positive body image.

FRI - 128 Antibiotic Resistance Gene Mobilization into Escherichia coli By a Single IS26 Transposon

Discipline: Health
Subdiscipline: Other Health

Micah Lawrence*, *University of California, Irvine* and Luis Mota-Bravo, *University of California Irvine*

Abstract: Antibiotic resistant Gram-negative bacteria are currently a concerning occurrence in environmental and clinical settings as they can harbor antibiotic resistant genes (ARGs) on plasmids, which are capable of mobilizing through horizontal gene transfer (HGT). The objective of this study was to describe and analyze antibiotic resistant genes from bacteria found in the environment in order to better understand the evolution and propagation of these ARGs. Disk diffusion tests and plasmid DNA sequencing were performed on an *Escherichia coli* isolated from Sulphur Creek, CA and revealed that the isolate is resistant to 4 different classes of drugs, conferred by genes on two plasmids. When analyzing the multi-drug resistant region (MDR) of one of these plasmids (p1) with comparative genomic mining public databases, five plasmids displayed a 99% nucleotide identity. Upon further analysis of the MDR a section containing the *aac(3)*-IIa gene, conferring aminoglycoside resistance, and an IS26 transposon present in p1 was missing in four of the similar plasmids. Directly upstream of *aac(3)*-IIa in p1 there is another IS26 transposon found in the five similar plasmids mentioned above. This IS26 potentially acted as a recognition site, mediating the integration of *aac(3)*-IIa and an IS26 transposon. After this integration, the two IS26s are in the same orientation forming a composite transposon, capable of further HGT. The mobilization of the *aac(3)*-IIa gene into a MDR region by a single IS26 allows for a more effortless dissemination of the ARG between environmental and clinical settings.

FRI - 129 Perception of Odor Blends By *Caenorhabditis Elegans*

Discipline: Life Sciences
Subdiscipline: Neurosciences

Micah Ayah Maglasang*, *Pomona College* and Elizabeth Glater, *Pomona College*

Abstract: The nematode *Caenorhabditis elegans* provides a simple model to study how sensory stimuli are received, encoded, and perceived by the nervous system. *C. elegans* uses chemosensation to locate food, avoid potentially harmful substances, and reproduce (Bargmann 2006). However, how *C. elegans* recognizes combinations of odorants to detect bacteria, its major food source, is not yet fully understood. In this study, we elucidate how *C. elegans* recognizes an odor bouquet consisting of multiple odorants. We will conduct an associative conditioning assay in which *C. elegans* are starved in the presence of a specific odorant or odor blend, called the conditioning odor. After the starvation period, we will conduct chemotaxis assays to observe the chemotactic response of conditioned and well-fed worms to the conditioning odor. We expect that conditioned worms will have a reduced attraction to the conditioning odor blend, but not other odor mixtures, because the worms have learned to associate starvation with the specific odor mixture. Preliminary results suggest that worms conditioned with starvation with the specific odorant, 2-butanone, learn to avoid the odorant, even in a mixture with another attractive odorant, such as acetone. We plan to conduct further associative conditioning assays as well as calcium imaging to study the activity of sensory neurons in response to odors in conditioned and well-fed worms. Through behavioral assays and calcium imaging studies, we hope to gain a better understanding of the mechanisms underlying sensory processing and perception.

FRI - 131 Projections from the Paraventricular Nucleus of the Thalamus to the Striatum Can Evoke Dopamine Transients through Glutamatergic and Cholinergic Signaling

Discipline: Health
Subdiscipline: Other Health

Sean Hernandez*, *California State University of San Marcos* and Veronica Alvarez, *National Institute of Health*

Abstract: The paraventricular nucleus of the thalamus (PVT) is a brain region important for behavioral adaptations to stress. However, the understanding of how PVT neurons control behavioral responses to stress is incomplete. The PVT projects to the striatum, a part of the basal ganglia which is involved in motor learning, motivation, and reward processing. Dopamine (DA) signaling in the striatum is essential for these functions and is also involved in PVT mediated stress adaptations. We hypothesize that PVT inputs to the striatum can trigger DA release in this brain region to facilitate certain motor patterns that drive the behavioral responses to stress. Here we tested this hypothesis and used optogenetics to specifically stimulate PVT inputs to the striatum while measuring DA with fast-scan cyclic voltammetry in ex vivo brain slices. DA transients were observed in the dorsal medial striatum, but not in other striatal regions. The mechanism underlying PVT-triggered dopamine release depended on both glutamatergic and cholinergic signaling. We speculated that Channelrhopdopsin-2 expressing glutamatergic inputs from the PVT synapse onto striatal cholinergic interneurons to evoke release of acetylcholine, which in turn binds to presynaptic nicotinic acetylcholine receptors on DA axons to release DA. Furthermore, PVT-triggered DA transients were inhibited by acute application of cocaine, suggesting this mechanism of dopamine signaling in the striatum is sensitive to drugs of abuse. These findings contribute to our understanding of how the PVT influences striatal dopamine release at a circuitry level and may provide the framework for how the PVT elicits behavioral responses to stress.

FRI - 132 Studies on How High Levels of BPA in Mothers Adversely Affects Enamel Formation in-Utero.

Discipline: Health
Subdiscipline: Other Health

Desiree Quintana*, *Arizona State University* and Rena D'Souza, *University of Utah*

Abstract: Bisphenol A (BPA) is used worldwide in the production of polycarbonate plastics, epoxy resins, dental composite resins, food packaging and daily products. BPA affects multiple human organ systems as it acts as a disruptor of endocrine functions. Exposure to BPA during prenatal development has been shown to adversely affect deciduous dentition (baby teeth) and many permanent teeth. Since disturbances in enamel formation manifest as irreversible defects that are visible clinically, they provide a permanent record of exposures to BPA and other environmental toxins during pregnancy.

The objective of our studies was to evaluate the current literature for reports on the effects of BPA exposure on enamel formation in rodents and humans. Exogenous delivery of BPA to pregnant and newborn rats resulted in enamel defects that correlated with the developmental of tooth development. Mandibular incisors from BPA treated-rats after 30 days exhibited hypomineralization similar to human MIH (Molar-Incisor Hypomineralization). Human teeth with MIH were compared with BPA-treated rat incisors, and both presented asymmetrical white enamel lesions. In comparison to control rats that showed completely normal dentition, over 75% of rats exposed to BPA showed enamel lesions. Comparing the results of human MIH teeth to the features of BPA-affected rat enamel, there are similarities between BPA-induced enamel defects in the rat model and human MIH lesions. In conclusion, rodents offer a valuable experimental model system to test the controlled exposure to BPA during prenatal development as enamel formation in rats closely mimics that seen in humans.

FRI - 141 Characterization of VIP Interneuron Ablation in the Visual Cortex

Discipline: Life Sciences
Subdiscipline: Neurosciences

Hannah Selwyn*, *Yale University*; Katie Ferguson, *Yale School of Medicine*; Rima Pant, *Yale School of Medicine* and Jessica Cardin, *Yale School of Medicine*

Abstract: Inhibitory interneurons function to maintain stable activity within local neural circuits and have been hypothesized to play a key role in shaping the processing of sensory information. Despite their sparseness, comprising approximately 1% of all cortical neurons, vasoactive intestinal peptide (VIP) expressing interneurons have been hypothesized to play a key role in shaping cortical activity. They are positioned at an interesting intersection between long-range inputs, including neuromodulatory inputs such as acetylcholine and serotonin afferents, and the local cortical circuit. The primary goal of this project is to examine how cortical activity is shaped by VIP interneurons through chronic manipulations of these cell populations. To determine how chronic VIP interneuron manipulations affect cortical population activity, we will compare the efficacy of a virally injected genetically-targeted toxin, Caspase3, in mice in which Ca^{2+} transients have been imaged *in vivo* using two-photon laser scanning microscopy (2PLSM). We will quantify how many cells have been successfully ablated and compare this result with *in vivo* Ca^{2+} imaging data. Disruptions of inhibitory interneurons have been shown to lead to perturbations of primary cortical functions, such as the encoding of sensory information and higher-order cognition. This disruption has been suggested as a strong candidate mechanism underlying several neuropsychiatric and developmental diseases, such as schizophrenia and autism. This project, therefore, can provide insight not only into the distinct roles of inhibitory interneuron populations in shaping visual cortical activity and their distribution in the healthy brain but also on the effects their disruption on primary cortical functions in disease.

FRI - 142 Mapping Central and Peripheral Nervous System Myelin in a Mouse Model

Discipline: Life Sciences
Subdiscipline: Neurosciences

Aleezah Balolia*, *University of Colorado Denver, Department of Integrated Biology*; Marios Georgiadis, *Stanford University, Department of Radiology* and Michael Zeineh, *Stanford University, Department of Radiology/Neuroimaging and Neurointervention*

Abstract: The myelin sheath is a multi-layered membrane that surrounds neuronal axons in both the central and peripheral nervous systems (CNS/PNS), effectively “insulating” them and enabling fast signal transduction. CNS myelin is formed by oligodendrocytes, while PNS myelin is formed by Schwann cells, resulting in structural and chemical differences between the two tissue types. Diseases associated with demyelination of axons have devastating health effects and affect over 2.5 million people worldwide. Moreover, there are diseases specific to CNS myelin, such as Multiple Sclerosis (MS), whereas Gillian Barré Syndrome (GBS) is a PNS demyelinating disease. Interrogating differences between the different forms of myelin can shed light on demyelination and re-myelination in a variety of CNS/PNS disorders. Small-angle X-ray scattering (SAXS) is sensitive to ordered nanostructure, like the myelin sheath, and can thus be used to selectively probe CNS or PNS myelin, given their demonstrated differences in periodicity. Furthermore, the recent advent of SAXS Tensor Tomography (SAXS-TT) has enabled tomographic studies on bulk specimens without the need for invasive tissue preparation or staining. In this work, we present the first maps of myelinated axons specific to the CNS or PNS using SAXS-TT in a mouse model. We highlight the technique’s potential to provide quantitative information specific to CNS or PNS myelin, and contribute to the development of novel diagnostic, monitoring and eventually therapeutic tools for nervous system-specific demyelinating diseases such as MS and GBS.

FRI - 200 Developing Tools to Study Zika Virus Infection *In Vivo* Based on Cre-Lox Reporter Systems

Discipline: Life Sciences
Subdiscipline: Microbiology

Karina Flores*, *The University of Oklahoma*; Margarita Rangel, *New York University School of Medicine*; Maria Noval, *New York University School of Medicine* and Kenneth Stapleford, *New York University School of Medicine*

Abstract: Zika virus (ZIKV) is a mosquito-borne virus transmitted by *Aedes sp.* of mosquitoes. ZIKV has become a major public health concern after the 2015-2016 explosive outbreak occurred in the Americas where it was linked to congenital microcephaly, and Guillain-Barré in adults. To date, there are no approved vaccines or effective antivirals against ZIKV, highlighting the need to develop new strategies to understand fundamental aspects of ZIKV biology. The use of the *Cre-loxP* system has been shown to be a powerful genetic tool to edit genomes in mammalian models. This system can be used to study genes of interest in a tissue/cell and/or time specific manner. In addition, previous studies have shown that ZIKV genome can be modified and tolerate insertions of reporter genes without altering viral fitness. In this study, we coupled both concepts and developed a ZIKV-Cre reporter system that will allow tracking the course of ZIKV infection *in vivo* by studying infected cells in *Cre-loxP* mouse models. We developed two ZIKV variants that codify for the Cre recombinase, with or without a green fluorescent protein tag

(GFP) to allow visualization of Cre expression in cells. In this study ZIKV-Cre viruses and a control mCherry-ZIKV were tested for stability, fitness and functionality. We addressed Cre functionality *in vitro* by infecting flox-stop reporter fibroblasts. The results of this study will provide the foundation needed to establish a *Cre-loxP* system in ZIKV infection model that will be used to address the progression of ZIKV infection in animal models.

FRI - 201 ***Listeria Monocytogenes*** **requires Electron Acceptors to Maintain Redox Balance and Virulence inside Human Macrophages.**

Discipline: Life Sciences
Subdiscipline: Microbiology

Davy Deng*, *University of California, Berkeley*; Sam Light, *University of California, Berkeley*; Andrea Sanchez, *University of California, Berkeley* and Dan Portnoy, *University of California, Berkeley*

Abstract: *Listeria Monocytogenes* is a deadly facultative anaerobic intracellular pathogen that constitutes a serious global health burden. It invades and replicates inside human immune cells such as macrophages in an attempt to evade humoral immunity. Previous studies have pointed out that aerobic respiration is essential to its virulence inside macrophages however the details behind it is still unclear. We set out to explore the mechanisms behind its oxygen-dependence and found our that mutants in terminal oxidases have a dramatic NAD+/NADH ratio imbalance. The inability to use oxidize oxygen depletes NAD+ and causes redox stress. By correcting the imbalance via a constitutive heterologous expression of NADH oxidase, we are able to restore the growth curve in broth media to wild-type level. Furthermore, we tested the virulence in bone-marrow derived macrophages *in vitro*, and saw that the intracellular replication is completely restored in NADH oxidase-expressed mutants. Similarly, fibroblast plaque assays also show a restoration of cell-to-cell transmission in NADH oxidase transformed mutant strains. Finally, we show that there is also a significant increase in liver and spleen colonization *in vivo*. Biochemically, when we knock out acetoin and acetate fermentation pathway and overexpress lactate and ethanol fermentation pathway, in an attempt to increase NAD+ level, we are also able to rescue the virulent phenotype. In summary, we show that a proper NAD+/NADH ratio is important for *listeria monocytogenes* to infect and replicate inside host cells, thus could be exploited as new strategies for therapeutic developments.

FRI - 203 **Fungal Pathogen** ***Candida Albicans*** **GAL10 Gene Is Imperative to Biofilm Formation**

Discipline: Life Sciences
Subdiscipline: Microbiology

Diana McMahon*, *University of Detroit Mercy*; Jonathon Finkel, *University of Detroit Mercy*; Marcelio Shmmami, *University of Detroit Mercy*; Nikol Shllaku, *University of Detroit Mercy*; Angelina Antonyan, *University of Detroit Mercy* and Alexander Jackman, *University of Detroit Mercy*

Abstract: Infections by the opportunistic fungal pathogen *Candida albicans* is a critical health issue with a ~30% mortality rate and few available antifungal drugs for treatment. While *C. albicans* is commensal in the human gut, it can become virulent and form biofilms in the body on implanted devices such as artificial joints, catheters, and pacemakers, especially in immunocompromised individuals. The cell wall of *C. albicans* is the outermost component of a fungal cell and is comprised of cell wall proteins along with chitin and glucans. Cell wall proteins are of great importance to the survival of the *C. albicans* as they are the first to encounter the cell's environment and report the external environmental condition including whether the location is an appropriate site for cellular adherence. Once the yeast cells have adhered, a biofilm can develop. In this study, we identified from a screen of cell wall insertion mutants that the gene *GAL10* is essential for biofilm formation. Here we report the results of study of two mutant isolates of *gal10* for their ability to form biofilms in anaerobic conditions and aerobic conditions, and their sensitivities to different cell wall perturbing agents in an attempt to identify the cause of the biofilm defect. Our results show that *GAL10* has an essential role in the ability of *C. albicans* to form a biofilm and that one possible role in biofilm formation is *GAL10* important function of galactose metabolism.

FRI - 204 **Development of a Fluorescently Activated Cell Sorting Technique to Identify Gut Microbiota Important in Host Protein Metabolism**

Discipline: Life Sciences
Subdiscipline: Microbiology

Madisen Mason*, *The University of New Mexico*; Cristina Takacs-Vesbach, *The University of New Mexico*; Marilyn Fogel, *University of California, Riverside*; Kelli Feeser, *The University of New Mexico* and Seth Newsome, *The University of New Mexico*

Abstract: Gut microbiota contribute to the health and fitness of animals. Within a single host, hundreds or even thousands of different microbial species form tight symbiotic communities influenced by many factors, including host diet. These communities often metabolize and synthesize compounds that their host species cannot and supply essential compounds needed to maintain host homeostasis and reproduce. These processes are likely important for hosts that consume low-quality diets and experience seasonal or persistent protein limitation. To date, the role gut microbiota play in host protein metabolism has not been systematically explored. We hypothesize that taxonomic and functional differences in gut microbiota correlate with diet and that microorganisms are largely responsible for supplying essential amino acids (AA_{ESS}) to hosts with protein-poor diets. This project combines amino acid carbon isotope ($d^{13}C$) analysis with fluorescently activated cell sorting (FACS) to quantify the relative contribution of key microbial taxa to the production of AA_{ESS} used to synthesize host tissues. Pilot data are currently being analyzed to identify the most abundant species of *Bacteroidetes* and *Firmicutes* in gut contents to develop nucleotide-specific probes. Mouse gut microbiota will be hybridized with phylum-specific probes, using a fixation-free protocol, and individual populations from gut contents will be sorted and their amino acid $d^{13}C$ values will be measured to quantify the proportion synthesized by gut microbiota from non-protein macromolecules (e.g., carbohydrates) in the host's diet. This approach enables us to directly link AA_{ESS} production to specific gut microbiota taxa and determine the relative importance of different populations to the host.

FRI - 205 **Determining the Trigger of Anti-Phage Island Excision in** ***Vibrio Cholerae***

Discipline: Life Sciences
Subdiscipline: Microbiology

Maria Nguyen*, *University of California, Berkeley* and Kimberley Seed, *University of California, Berkeley*

Abstract: *Vibrio cholerae,* the causative agent of the diarrheal disease cholera, is antagonized by predatory bacteriophages. One specific bacteriophage, ICP1 is locked in a dynamic co-evolutionary arms race, in which *V. cholerae* has evolved to block ICP1 infection using a conserved mobile genetic element referred to as PLE (phage-inducible chromosomal island-like element). Upon ICP1 infection, the PLE excises from the chromosome, replicates to a high copy number, and blocks phage infection through an unknown mechanism. We screened PLE 2 operon knockouts and identified the integrase to be necessary and sufficient for PLE 2 excision. Previous studies show that PLE 1 respond specifically to ICP1 infection through a direct interaction with a phage encoded protein (PexA) and the integrase to catalyze PLE 1 excision. We hypothesize that the PLE 2 integrase has evolved to recognize a unique phage encoded factor. An amino acid alignment of the integrase from the five PLEs shows that PLE 2 integrase is the most divergent, consistent with the idea that it requires a different RDF than other PLEs. In addition, we made a miniaturized PLE2 (miniPLE2) containing only the integrase, an antibiotic resistance cassette, and the recombination sites needed for excision. Upon infection with ICP1, miniPLE2 excises from the *V. cholerae* chromosome, demonstrating that the integrase directs excision and that the RDF is not PLE encoded. Studying the interactions between *V. cholerae* PLE and ICP1 helps to uncover strategies that bacteria use to protect against bacteriophages and contribute to understanding of their coevolution.

FRI - 206 **Chemical Communication of a Natural Cheese Rind Fungus with** ***P. Psychrophila*** **Vs.** ***E. coli***

Discipline: Life Sciences
Subdiscipline: Microbiology

Itzel Lizama-Chamu*, *University of Illinois at Chicago*; Jessica Cleary, *University of Illinois at Chicago College of Pharmacy* and Laura Sanchez, *University of Illinois at Chicago College of Pharmacy*

Abstract: Previous studies have shown that cheese rinds represent a simplified model of a microbiome that can be experimentally manipulated and reproduced to elucidate pair-wise and community interactions of microbial species. Since the specialized metabolites that drive microbial interactions within these communities are poorly understood, we examined how a cheese fungus (*Penicillium* sp. #12) altered its specialized metabolites in the presence of either a natural cheese rind bacterium (*Pseudomonas psychrophila* sp. JB418) or a food pathogen (*Escherichia coli).* Specifically, we used mass spectrometry techniques to investigate the molecules produced by the fungus and bacteria in response to their interaction. *Penicillium* sp. #12 and bacterium *P. psychrophila* grow commensally while *E. coli* was inhibited by *Penicillium* sp. #12. Therefore, we hypothesize that *Penicillium* sp. #12 excretes metabolites that interact with bacterial partners that produce different phenotypes in *P. psychrophila* and *E. coli*. Matrix-assisted laser desorption/ionization time-of-flight imaging mass spectrometry (MALDI-TOF IMS) was used to visualize the spatial distribution of the molecules produced in both pure bacterial and fungal cultures to quickly detect molecules involved in microbial interactions. Molecules produced in each interaction were extracted from a large-scale culture and analyzed via liquid-chromatography tandem mass spectrometry to obtain molecular fragmentation data. IMS data was used to prioritize signals for future isolation and purification using high-performance liquid chromatography to identify the molecule(s) responsible for different phenotypic expression. A long-term future direction of this research will help us to understand the impact the cheese microbiome may have on human health via dietary intake.

FRI - 207 ***Barp*** **Regulates Peptidoglycan Biosynthesis of** ***Borrelia Burgdorferi***

Discipline: Life Sciences
Subdiscipline: Microbiology

Jessica O'Berry*, *University of Texas at San Antonio* and Janakiram Seshu, *Department of Biology The University of Texas at San Antonio*

Abstract: Lyme disease is the most prevalent tick-borne disease in the US with more than 300,000 cases estimated to occur each year by the Center for Disease Control and Prevention (CDC). Lyme disease is caused by the spirochete, *Borrelia burgdorferi (B. burgdorferi)*, which is transmitted to humans following the bite of an infected *Ixodes scapularis* tick. Since there are no vaccines available to prevent this illness, it is critical to prevent the survival of the Lyme disease spirochetes in infected reservoir hosts or in the transmission vector. *B. burgdorferi* has a peptidoglycan layer that is unique among bacterial pathogens and the integrity of this layer is critical for survival of the pathogen in its different hosts. Hence, our *central hypothesis* is that disrupting or degrading the peptidoglycan layer of *B. burgdorferi* will reduce pathogen burden during its infectious cycle in nature which will lead to a reduction in the incidence of Lyme disease. One of the genes of *B. burgdorferi* that contributes to the integrity of the borrelial peptidoglycan is *BarP*. In order to determine the role of *BarP* in the survival of *B. burgdorferi,* we will generate recombinant *BarP* and determine its biochemical functions and substrate specificity. Deletion of *BarP* in *B. burgdorferi* strain B31-A3 will enable us to determine the role of *BarP* in the pathogenic mechanisms of *B. burgdorferi* in mouse-tick-mouse model of Lyme disease.

FRI - 208 **Investigating the Role of Chvi in Regulating Srnas in** ***Sinorhizobium Meliloti***

Discipline: Life Sciences
Subdiscipline: Microbiology

Jesus Ortega*, *California State University, Fullerton* and Esther Chen, *California State University, Fullerton*

Abstract: *Sinorhizobium meliloti* forms an endosymbiotic relationship with legume plant hosts, including *Medicago sativa.* This symbiosis provides plants with biologically available nitrogen, an important determinant of agricultural productivity. The conserved ExoS/ChvI two-component system (TCS) regulates genes associated with symbiotic and free-living phenotypes of *S. meliloti.* The ExoS/ChvI TCS controls the expression of many genes, including genes involved in exopolysaccharide production, motility, and nutrient utilization. ExoS, a membrane-bound histidine kinase, phosphorylates its cognate response regulator ChvI, which binds to promoter regions and regulates gene expression. Previous work in our laboratory identify small RNA (sRNA) genes that may be regulated by ChvI. Many sRNAs regulate gene expression post-transcriptionally by interacting with messenger RNA. To test whether these sRNA genes are regulated by ChvI, the upstream region of each sRNA gene was fused to the β-glucuronidase (GUS) reporter gene. These fusions were integrated into *chvI* gain-of-function (GOF), *chvI* partial loss-of-function (LOF), and wild-type *S. meliloti* strains, and GUS activity was compared. A subset of the sRNA transcriptional fusions showed higher, expression of GUS in *chvI* GOF mutants compared to WT and *chvI* LOF strains. Meanwhile, some of the sRNA transcriptional fusions showed no differences in GUS expression between the *chvI* mutant and WT *S. meliloti* strains. These results indicate that ChvI may regulate the expression of certain sRNAs. Our study provides a more comprehensive understanding of the regulatory roles of ChvI in *S. meliloti,* and therefore may provide insight into the regulation of sRNAs by TCS and their function for successful symbiosis.

FRI - 209 **Identifying Genetic Regulators in** ***Candida Albicans*** **that Lead to Phenotypic Switching through Mutant Screening**

Discipline: Life Sciences
Subdiscipline: Microbiology

Gabriel Romero*, *University of Puerto Rico at Cayey* and Dana Davis, *University of Minnesota*

Abstract: *Candida albicans,* a commensal fungus, causes life-threatening infections in immunocompromised individuals. Colony morphology phenotypic switching (CMPS) is employed by *C. albicans* to generate phenotypic diversity, potentially promoting pathogenicity and resistance to anti-fungal treatments. A clear role for the target of rapamycin complex 1 (TORC1) growth control pathway in CMPS has been established, but the specific TORC1-dependent processes that contribute to CMPS are unknown. The main objective of this research is to identify mutants that regulate CMPS to determine how TORC1 governs CMPS. CMPS occurs after prolonged growth in strains defective for TORC1, thus our collection of mutants were incubated for >10 days on solid medium and liquid medium. Mutants on solid medium that led to changes in CMPS are possible inhibitors of CMPS. Mutants in liquid medium that did not exhibit CMPS are possible inducers of CMPS. We previously showed that CMPS isolates showed altered sensitivity to the TORC1 inhibitor, rapamycin. To determine if new mutants may affect the TORC1 pathway we screened them for rapamycin sensitivity. Here we identified mutants for two genes that affect CMPS on solid medium, VACuolar segregation (*vac7)* and General Control Nonderepressible (*gcn1).* The *vac7* mutants also showed heightened sensitivity to rapamycin. These results identify two potential inhibitors of CMPS and suggest that *VAC7* is likely linked to the TORC1 growth control pathway. By understanding the molecular aspects of CMPS, we can develop effective ways to arrest phenotypic diversity, weakening *C. albicans* pathogenicity and resistance to anti-fungal treatments.

FRI - 210 **Comparative Growth on and Metabolism of Sugars and Artificial Sweeteners By Common Bacteria of Mammalian Gut**

Discipline: Life Sciences
Subdiscipline: Microbiology

Nicol laura*, *Cañada College*; Dalila Gonzalez, *Cañada College*; Maria Garduño, *Cañada College*; Kaitlyn Burke, *Cañada College* and Nathan Staples, *Cañada College*

Abstract: Unhealthy diets with high caloric intake from added sugars are associated with the incidence of obesity, type II diabetes, and cardiovascular disease. The effect of non-nutritive sweeteners (NNS) has a major impact on bacterial growth, but the underlying mechanisms still remain unclear. Little is known about the ability of gut microbial species to grow on NNS in vitro.The purpose of this research work is to study the effects of various NNS in several bacterial strains found in the mammalian gut, *Escherichia coli*, *Klebsiella aerogenes*, and *Bacillus subtilis.* With this work we aim to better understand the impact NNS have in the

metabolic and growth profiles of these bacterial species in vitro. We hypothesize that NNS that promote the growth of enteric microbiota may over-balance the presence of these species in the gut and will produce growth on media containing only these sugars. We tested strains of bacteria for differences in growth rates on rich media with added individual and combined NNS (sucralose, sucrose, acesulfame K, and aspartame, and glucose). Comparative growth rates were analyzed evaluating optical density as a measurement of bacterial growth. So far, all NNS tested show a bacteriostatic effect in some bacterial species. However, the effect on different bacteria varies. Our findings show that glucose and sucrose inhibit the most growth on *Escherichia coli* whereas aspartame tends to show an inhibitory effect throughout with glucose. These findings are a crucial initial result that helps us clarify the potential implications of NNS consumption on human health.

FRI - 211 Evaluation of Antimicrobial Properties of *Usnea* Lichen

Discipline: Life Sciences
Subdiscipline: Microbiology

Sokleng Kelley Leong*, *Skyline College* and Christine Case, *Skyline College*

Abstract: Microbial spoilage results in the loss of global food resources. In recent decades, the investigation of phytochemicals as antimicrobials and preservatives has been attracting scientific interest to eliminate or reduce synthetic additives. Historically, lichens were used to treat external wounds and tuberculosis. Research has shown that lichens are promising sources of antimicrobial components due to their secondary metabolites. The purpose of this study is to determine whether aqueous, ethanolic, and acetonic extracts of *Usnea* sp. have antimicrobial properties. Each extract (100 mg/mL) was tested against gram-positive *Staphylococcus aureus, Mycobacterium phlei, Bacillus cereus,* and *Streptococcus mutans* and gram-negative *Escherichia coli* bacteria, and *Aspergillus niger* and *Candida albicans* fungi. All three extracts inhibited gram-positive bacteria and *A. niger* and *C. albicans* fungi in disk-diffusion assays. The minimum lethal concentration against *S. aureus* is 150 mg/mL, against *A. niger* is 18.75 mg/mL, and against *C. albicans* is 37.5 mg/mL. The effect of *Usnea* extracts on growth of *S. aureus* and fungi in food is being determined. Preliminary results indicate that *Usnea* has the potential to be used as an antimicrobic to prevent growth of gram-positive bacteria and fungi in food.

FRI - 212 In Vitro Antimicrobial Activity of *Mimulus Aurantiacus*

Discipline: Life Sciences
Subdiscipline: Microbiology

David Dela Cruz*, *Skyline College*; Tyler Ma, *Skyline College* and Christine Case, *Skyline College*

Abstract: Since the identification of methicillin-resistant *Staphylococcus aureus* (MRSA) in 1962 there has been a need for novel antibiotics as continued development of resistance limits the lifespan of any one antibiotic. The practice of using plants medicinally dates well into prehistory and due to the rapid rate of plant species extinction, investigation into plant-derived antimicrobial compounds has increased as these potential antimicrobials may be irrecoverably lost. The objective of this study is to investigate and characterize the antimicrobial properties of *Mimulus aurantiacus*, a plant used in traditional Native American Miwok medicine. Crude whole-plant extracts of *M. aurantiacus* (500 mg/mL) were prepared from the flowers, stems, and leaves in acetone, ethanol, and water. The crude extracts were then tested for antimicrobial properties against *Candida albicans* fungus, gram-positive *Staphylococcus aureus* and gram-negative *Escherichia coli* bacteria by disk-diffusion assays. Crude whole-plant extracts inhibited *S. aureus* and *C. albicans*. Determining the individual antimicrobial activity of the stems, flowers, and leaves and testing against other gram-positive bacteria and fungi is in progress. The minimal inhibitory concentrations and method of action are being determined.

FRI - 213 Multiple Antibiotic Resistance Profiles of Enterococcus Spp. Isolated from Sea Water in Puerto Rico

Discipline: Life Sciences
Subdiscipline: Microbiology

Frances Vélez González*, *Universidad Ana G. Mendez*; Yaidelice Rodríguez Álamo, *Universidad Ana G. Mendez*; Jose Santoni, *Universidad Ana G. Mendez*; Orlando Santiago, *Universidad Ana G. Mendez* and Nydia Rodríguez-Bonano, *Universidad Ana G. Mendez*

Abstract: Enterococci are Gram-positive bacteria that are normal inhabitants of human and animal gastrointestinal (GI) tracts. These microorganisms can survive for extended periods of time and grow in 6.5% NaCl and in the presence of 40% bile salts. Also, they can tolerate pH and temperature variations. *Enterococcus* spp. are a common cause of community-acquired and foodborne diseases. Moreover, recent published reports indicate that enterococci isolated from environmental samples can exhibit multiple antimicrobial resistance traits. The primary objective of our research was to assess the presence of *E. faecalis* and *E. faecium* with multiple antibiotic resistance properties in sea water from recreational areas in the eastern region of Puerto Rico. We used the membrane filtration method and cultivated the isolated enterococci in m-E, BHI with nalidixic acid and bile esculin agars. We studied the antibiotic susceptibility and resistance patterns using prepared microtiter plates with 18 antibiotics to determine their Minimum Inhibitory Concentration (MIC). The control strains for antibiotic testing were *E. faecalis* ATCC 29212 and *E. faecium* ATCC 27270. Results showed that there is a great variability in antibiotic resistance among the isolate. The isolates were all resistant to one or more antibiotics, especially to levofloxacin, clindamycin, erythromycin, and ceftriaxone. Future studies will be focused on verifying the DNA content of each isolate to determine the presence of R-plasmids encoding for antibiotic resistance traits in the isolates.

FRI - 214 The Unexplored Bacterial Diversity Lurking in Protist Cell Cultures

Discipline: Life Sciences
Subdiscipline: Microbiology

Ameris Aponte*, *University of Puerto Rico, Rio Piedras* and Sally Warring, *American Museum of National History- Richard Gilder Graduate School*

Abstract: Microbes, especially Bacteria, are abundant in marine habitats and heavily affect the biogeochemical cycles of the Earth. Yet our knowledge of these microbial ecosystems is critically inadequate as the vast majority of species are not culturable and/or cannot be isolated from their microbial communities. This limits our ability to study microbes and microbial genomes from individual species. Consequently, metagenomic approaches have become important in the study of these microorganisms. For this work, we took assembled genomic sequencing data from mixed-species cultures of microbial organisms obtained from temperate and tropical oceans around the globe. These cultures consist of a single isolated microbial eukaryote species, co-cultured with unidentified bacterial species, many of which originate from the oceanic water source. The bacterial sequence data is often discarded, as the cultures come from a lab that focuses on microbial eukaryotes, but we hypothesized that we could use existing bioinformatics tools to pull out and identify complete bacterial genomes from these metagenomic assemblies, and thus contribute potentially new bacterial genomes to public databases. From four separate metagenomic assemblies of mixed culture, we identified 28 complete bacterial genomes. Using BLAST and TSGS, we found that only four of the 28 genomes were already present in the NCBI genome database, demonstrating the value of this often-discarded data. We annotated each genome using Prokka and are in the process of depositing each full genome sequence and their gene complement to the NCBI genome database, where they will be a resource for further studies into the marine bacterial diversity.

FRI - 215 The Rotateq Vaccine Elicits a Broader Neutralizing Antibody Response Against Contemporary Rotavirus Outer-Capsid Proteins Than the Rotarix Vaccine

Discipline: Life Sciences
Subdiscipline: Microbiology

Shania Sanchez*, *The University of New Mexico*; Maximilian Carter, *Vanderbilt University*; Julia Diller, *Vanderbilt University*; Yuta Kanai, *Osaka University*; Takeshi Kobayashi, *Osaka University* and Kristen Ogden, *Vanderbilt University*

Abstract: Rotaviruses cause severe diarrheal disease resulting in approximately 150,000 annual deaths in children under five years of age. VP7 is the major rotavirus outer-capsid protein and a primary target for neutralization. Two vaccines, Rotarix and RotaTeq, respectively present one and four different VP7 genotypes to the immune system and have each been used to prevent rotavirus disease for more than a decade. However, differences in the genotypic makeup of circulating rotaviruses have been detected following widespread vaccine uptake, suggesting they elicit differing immune responses. Based on the more diverse VP7 composition of RotaTeq compared to Rotarix and published seroconversion data, we hypothesize that sera from infants vaccinated with RotaTeq will provide broader neutralization of human rotavirus VP7 genotypes than sera from infants vaccinated with Rotarix. To test this hypothesis, we used plasmid-based reverse genetics to engineer chimeric rotaviruses that each contain 10 genes from simian lab strain SA11 and a single human VP7 outer-capsid gene, either from a vaccine strain or a sequenced circulating rotavirus. We are quantifying neutralization of chimeric rotaviruses by serum antibodies elicited in infants vaccinated with RotaTeq, Rotarix, or both vaccines using a fluorescent focus reduction neutralization assay. Our preliminary results suggest that sera from infants vaccinated with RotaTeq neutralize viruses containing a broader range of VP7 genotypes than those neutralized by sera from infants vaccinated with Rotarix, including genotypes not represented in the vaccine. Understanding the breadth and specificity of rotavirus neutralization may provide insight into vaccine efficacy and rotavirus evolution following vaccine introduction.

FRI - 216 Synergistic Properties of Essentials Oils with Antibiotics Against Multidrug Resistant *Pseudomonas Aeruginosa*

Discipline: Life Sciences
Subdiscipline: Microbiology

Alexis Hamm*, *Northeastern Illinois University* and Emily Booms, *Northeastern Illinois University*

Abstract: The World Health Organization estimates that by the year 2050 multidrug resistant (MDR) infections will affect 9 million people per year globally. This estimation highlights the importance of identifying additional treatment sources outside of antibiotic therapies alone to overcome MDR infections. Multidrug resistant bacteria of the ESKAPE group of pathogens, like *Pseudomonas aeruginosa,* are responsible for the sharp rise in untreatable bacterial infections. *P. aeruginosa* is a gram-negative bacterium and nosocomial pathogen that causes a diverse range of infections and has multidrug resistant (MDR) strains*.* Our study explores the ability of essential oils to synergize, or enhance, the efficacy of antibiotics to overcome MDR *P. aeruginosa*. We previously identified essential oils that have strong inhibitory activity against *P. aeruginosa* MDR strain, ATCC BAA 2110. We also confirmed that our MDR strain of *P. aeruginosa* was resistant to three antibiotics, intermediate to three other antibiotics, and susceptible to three additional antibiotics. Initial synergy testing was performed at 20% oil concentration using a modified disc diffusion assay method in triplicate. Synergistic activity between antibiotics and essentials oils has been observed in overcoming MDR *P. aeruginosa* with the following combination: cefoxitin/ajowan, cephazolin/ajowan, nitrofurantoin/ajowan, sulfamethoxazole trimethoprim/ajowan, cefotaxime/wintergreen, and cinnamon branch/cefotaxime. Our results suggest that some essential oils and antibiotics can synergize to enhance the efficacy of antibiotic treatment against MDR *P. aeruginosa.* We are setting up additional trials to confirm our findings and further analysis of our data is being conducted to establish a method to quantify synergy using ImageJ software.

FRI - 217 Regulatory Roles of Loquacious in Dengue Virus Life Cycle

Discipline: Life Sciences
Subdiscipline: Microbiology

Deyri Garcia Torres*, *Yale University*; Shwetha Shivaprasad, *Stanford University* and Peter Sarnow, *Stanford University*

Abstract: Dengue Virus (DENV) is a single stranded RNA virus that is transmitted to humans via the bite of an infected *Aedes aegypti* mosquito, resulting in dengue fever. DENV interacts with and co-opts several host proteins for efficient propagation in both human and mosquito cells. To better understand the interaction between DENV RNA and host proteins in mosquito cells, the Sarnow lab conducted a high throughput screen that identified Loquacious (Loqs) as one of the several protein candidates that can interact with the 3’ untranslated region of DENV RNA. When Loqs, a double stranded RNA binding protein (dsRBP), was partially depleted, it resulted in a significant decrease in DENV RNA levels, indicating a pro-viral role for Loqs in mosquito cells. Since Loqs is a core component of miRNA/siRNA processing pathways, we hypothesize that Loqs might be utilizing other core components of this pathway such as Dicer for regulating viral replication. To test this hypothesis, we will use RNA interference (RNAi) to induce depletions of Loqs and PACT, the human paralogs of Loqs. We will then use Dicer knockout cells to test the effect of Loqs depletion on DENV replication in mosquito cells. In parallel, we will also study the role of PACT on the DENV life cycle in human Dicer knockout cells. We expect that Loqs effect may be Dicer dependent and that we will see little changes in DENV RNA levels. Understanding the mechanisms by which DENV co-opts these host proteins for survival will be critical to developing antiviral interventions.

FRI - 218 Identifying Antibiotic-Resistant Mutants in a Non-Tuberculosis Mycobacterial Pathogen

Discipline: Life Sciences
Subdiscipline: Microbiology

Jesus Alain Gonzalez Camba*, *Chabot Community College*; Ronald Rodriguez, *University of California, Berkeley* and Sarah Stanley, *University of California, Berkeley*

Abstract: Non-tuberculosis mycobacteria (NTM) are environmental saprophytes that are capable of causing a wide variety of opportunistic human infections. *Mycobacterium abscessus* is one of the most pathogenic NTM species, causing various pulmonary and skin infections. These infections are incredibly difficult to treat due to its high level of intrinsic resistance to most clinically relevant antibiotics, which has portrayed *M. abscessus* as an “antibiotic nightmare”. The genetic basis of this intrinsic resistance has been largely unexplored. Identifying novel genes associated with antibiotic resistance can allow for identification of drug targets that can be utilized for therapeutic strategies. The isolation of spontaneous, antibiotic resistant mutants has identified novel genetic determinants of resistance to functionally diverse antibiotics in *M. abscessus*. Here, we utilized this approach to identify mutants resistant to Isoniazid (INH) and Ethionamide (ETH), two antibiotics that interfere with cell wall biosynthesis in mycobacteria. *M. abscessus* is highly resistant to INH and ETH, but the basis of this resistance has never been explored. We were able to isolate bacteria exposed to inhibitory concentrations of ETH, but not INH. Minimum inhibitory concentration experiments revealed that the isolated bacteria grew at higher ETH concentrations compared to wild-type (WT) bacteria, classifying these cells more resistant than WT. Our results have identified a bonafide ETH resistant mutant. We are currently in the process of sequencing candidate genes to search for mutations that may explain the high-levels of ETH resistance observed. Future work will focus on characterizing the roles of genes containing mutations in ETH resistance.

FRI - 219 Increasing Protein Retrieval from an Uncultured Bacterium Associated with Human Oral Periodontal Disease

Discipline: Life Sciences
Subdiscipline: Microbiology

Lex Dias*, *Gavilan College*; Joshua Garcia, *San Jose State University* and Cleber Ouveney, *San Jose State University*

Abstract: Uncultured microorganisms comprise most of the microbial diversity existing on our planet. TM7 is one such phylum of uncultured bacteria and it has been associated with adult human periodontal diseases. The long-term goal of this project is to better understand the role TM7 bacteria play in human health.

For this project we aimed to purify the TM7 lactase soluble protein using BL21 cells via the pET28a vector expression system. Previous results showed that overexpression of lactase gene in BL21 cells can lead to misfolded aggregated protein and, hence, a low yield of soluble proteins. In order to improve the level of the soluble native form of the protein we plan to increase the cellular concentration of osmolytes, including high salt and betaine, which have been shown to help proteins fold properly. Total and soluble proteins yields were observed in 12% SDS page gels. We predicted that by using betaine coupled with cool temperature growth our protein samples will be able to be observed in the soluble proteins SDS gel which will be same kDa size as our total proteins of 60 kDa. Preliminary results for culture samples collected every hour for five hours suggest that betaine increases the expression of soluble proteins compared to controls. Our method suggests growing cells under these conditions provides improved soluble protein expression and allows for more efficient purification of the TM7 lactase protein compared to previous methods.

FRI - 221 Characterization of the Role of Neuropeptide Receptors in a Multi-Sensory-Dependent Decision-Making Process

Discipline: Life Sciences
Subdiscipline: Neurosciences

Natalie Shink*, *California State University Channel Islands* and Gareth Harris, *California State University Channel Islands*

Abstract: An environment is represented by numerous sensory cues where our nervous system is optimized to process, interpret, and act upon such cues. For example, an area containing food can produce attractive and repulsive cues, stimulate specific modality pathways, therefore allowing an organism to integrate multiple simultaneous pieces of information to coordinate decision-making behavior. Neurological diseases, including autism spectrum disorder, Parkinson’s disease, depression, schizophrenia, and gambling behaviors, share deficits associated with sensory processing or decision-making when encountering multiple sensory stimuli that evoke certain behavioral choices under normal conditions.

By using nematode, *C. elegans* to examine a multi-sensory behavior, we expose worms to a food patch and repulsive cues, 2-nonanone, then assess the food patch leaving rate during exposure to this repellant. We examine the role of neuropeptides and their corresponding neuropeptide receptors in this 2-nonanone dependent food leaving assay through testing mutant worms that lack these different neuropeptide receptors. We hope this study will provide more insight into how neuropeptide signaling via neuropeptide receptors shape an organism’s sensory behavior as well as proving insight into how neuropeptide receptors modulate sensory-dependent decision-making.

So far, we have found potentially 1 neuropeptide receptor that mediates this food-leaving behavior when worms are exposed to repellant cues based on this mutant exhibiting a delayed food leaving ability. Through the identification of new neuropeptide receptor genes, we are able to analyze the deeper functions of these pathways to see what is happening at the mechanistic level and apply it back to what is happening in humans.

FRI - 222 A Neurobehavioral Analysis of the *Trapped in Endoderm 1* GPCR Pathway in *Drosophila Melanogaster*

Discipline: Life Sciences
Subdiscipline: Neurosciences

Emily Mu*, *San Jose State University*; Cac Tran, *San Jose State University* and Rachael French, *San Jose State University*

Abstract: Understanding how genes direct neurodevelopment is one of the main goals of neuroscience. Elucidating the role of a gene with regard to a particular behavior has the potential to be a powerful set of tools to map out the molecular pathways that direct the wiring of the central nervous system. *Drosophila melanogaster* is an excellent model for behavioral research. Male *Drosophila* perform an elaborate courtship ritual consisting of a series of stereotyped behaviors that must be performed correctly and in the right order to ensure female receptivity. These behaviors, while complex, are innate – male flies are born knowing how to perform them. Additionally, all steps of the ritual are established and regulated by the behavioral sex determination gene *fruitless (fru),* making this set of behaviors an ideal model for studying the genetic and neural programming of behaviors. We previously identified a novel function for *Trapped in endoderm 1 (Tre1)* in courtship. *Tre1* encodes an orphan G-protein coupled receptor (GPCR) that we now know is regulated by *fru* and is required for normal courtship behavior. Loss-of-function in *Tre1* results in mutants that initiate courtship twice as fast as control males, on average. Here, we characterize the signaling cascade downstream of Tre1 by testing mutations in *Drosophila* G-proteins. Our results demonstrate that Gαi is a candidate downstream effector for Tre1 while also implicating Gγ30A in courtship behavior. Future goals include completing the characterization of the G-protein mutations and performing experiments to explore the complex interaction between G-protein signaling and courtship initiation.

FRI - 223 The Basic-Helix-Loop-Helix (bHLH) Transcription Factor *Cnd-1*controls the Expression of the Homeobox Transcription Factor *Ceh-5*

Discipline: Life Sciences
Subdiscipline: Neurosciences

Trae Dunn*, *Kennesaw State University* and Martin Hudson, *Kennesaw State University*

Abstract: Accurate control of gene expression in the central nervous system (CNS) is essential for development. Irregularities in gene regulation have been linked with several neurodevelopment disorders including epilepsy and schizophrenia. In order to better understand the molecular mechanisms behind these disorders, we utilize the nematode *Caenorhabditis elegans* as a model organism to examine CNS defects. *cnd-1*is a predicted ortholog of the human NeuroD1 gene, and mutations in this gene have been associated with seizures and diabetes mellitusType II. We performed a comparative transcriptome analysis of *cnd-1*and wild-type animals to identify genes that are controlled by *cnd-1*.Our data indicates that *cnd-1*positively regulates expression of the homeobox transcription factor *ceh-5*, which ismost closely related to vertebrate ventral anterior homeobox 2 gene (Vax2), andis expressed in the ventral portion of the retina during development. We used quantitative PCR to confirm that*ceh-5*transcript levels were significantly reduced in *cnd-1*mutants. We also examined expression of a *ceh-5-GFP*reporter gene in wild-type and *cnd-1*mutants. We find that the *ceh-5-GFP*expression level is significantly lower in *cnd-1*mutants, although the expression pattern is not altered. We are now corroborating these data by examining *ceh-5*mutants to determine if they control their own expression and have any roles in CNS development.

FRI - 224 Environmental Enrichment and Amantadine Confer Individual but Non-Additive Enhancements in Motor and Spatial Learning after Controlled Cortical Impact Traumatic Brain Injury

Discipline: Life Sciences
Subdiscipline: Neurosciences

Melissa Alvarez*, *University of Pittsburgh*; Anthony Kline, *UPMC Children's Hospital of Pittsburgh Safar Center for Resuscitation Research*; Isabel Bleimeister, *Safar Center for Resuscitation Research*; Mia Wolff, *University of Pittsburgh*; Tracey Lam, *University of Pittsburgh*; Jeffrey Cheng, *University of Pittsburgh Physical Medicine & Rehabilitation Safar Center for Resuscitation Research University of Pittsburgh* and Corina Bondi, *Safar Center for Resuscitation Research*

Abstract: Environmental enrichment (EE) and amantadine (AMT) improve recovery after traumatic brain injury (TBI). However, there are no data on the effects of combining therapies. The importance of knowing how both treatments affect recovery is relevant because during rehabilitation a pharmacotherapy will also be added to the treatment regimen. The aim of the study was to combine EE and AMT to determine if their net effect further enhances performance. Isoflurane-anesthetized adult male rats received a cortical impact or sham injury and then were randomly assigned to EE or standard (STD) housing and daily administration of AMT (20 mg/kg; i.p.) or vehicle (VEH, 1 mL/kg; i.p.) beginning 24 hours after injury for 19 days. Motor and cognitive function were assessed on post-surgical days 1-5 and 14-19, respectively. Cortical lesion volume was quantified on day 21. There were no differences among the sham groups, so the data were pooled. EE, AMT, and their combination (EE+AMT) improved beam-balance, but only EE and EE+AMT enhanced the more beam-walking. All

three treatments improved learning and memory compared to the VEH-treated STD controls (p<0.05). No differences were observed between the EE groups, but both were better than AMT-treated STD on beam-walking and spatial learning (p<0.05). Both EE groups reduced cortical lesion relative to the STD-housed AMT and VEH groups (p<0.05). The results indicate that although beneficial on their own, EE+AMT do not provide additional benefits after TBI. Despite the lack of additive effects, the findings provide insight for future combination studies for TBI.

FRI - 225 Aging and Neurodegeneration: Investigating the Role of Protein Quality Control Proteins in the Aging Brain.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Keyshla Negron*, *University of Michigan*; Henry Paulson, *University of Michigan* and Lisa Sharkey, *University of Michigan*

Abstract: The purpose of this research to identify the relationship between protein homeostasis pathways and aging. Protein homeostasis is the ability of the cell to balance the synthesis of new proteins with the degradation of damaged or misfolded proteins. Failures in the quality control pathways that regulate protein homeostasis in the cell can lead to aging-related neurodegenerative diseases such as Alzheimer’s disease. This project is designed to determine whether there are changes in the levels of key quality control proteins between young and old mice. Specifically we are investigating Ubiquilin2, a protein that regulates protein degradation. Rare mutations in this protein lead to neurogenerative diseases including Amyotrophic Lateral Sclerosis (ALS). To measure levels of Ubiquilin2, brain lysates are prepared from young and old mice, protein quantification is determined using a bicinchoninic acid assay (BCA assay) and Western blots are run to quantify the amount of Ubiquilin2 in each mouse brain based on the band intensity. Our preliminary data suggests that the level of expression of Ubiquilin2 is increased in older mice. Ongoing experiments are focused on determining levels of other key quality control proteins that are critical for maintaining protein homeostasis in the aging brain.

FRI - 226 A High-Throughput Platform for Neurophysiological and Behavioral Monitoring Combined with Optogenetic Capabilities in Awake-Behaving Rodents

Discipline: Life Sciences
Subdiscipline: Neurosciences

Marlyn Torres*, *Novartis Institute for Biomedical Research*; Michelle Sidor, *Novartis Institute for Biomedical Research*; Daniel Graziano, *Novartis Institute for Biomedical Research*; Steve Legare, *Novartis Institute for Biomedical Research*; Shushi Kabu, *Novartis Institute for Biomedical Research* and Brent Kuzmiski, *Novartis Institute for Biomedical Research*

Abstract: There is a growing need for a high-throughput system to study specific neural circuit perturbations, while simultaneously recording electrophysiological and behavioral responses to these inputs in awake-behaving rodents. Multiple ways to modulate circuit activity exist, either endogenously through opotogenetic-based technologies and/or exogenously through sensory evoked potentials. However, current available tools have a relatively low-throughput in design. Here we describe an innovative system using a wireless radiofrequency telemetry device for EEG recordings (Data Sciences International) combined with both optogenetic and auditory sensory stimulation that permits real time simultaneous modulation of neural activity and EEG recordings in awake-behaving rodents. The telemetry device permits a 24 hour collection of continuous activity data, which was validated using a video tracking software to be an accurate measure of ambulatory activity. Several TTL triggered optogenetic laser set-ups can be integrated to the EEG recording system via BNC inputs. The enclosed-laser system is comprised of simultaneously controlled lasers, which allows individual modulation of light intensity output at each fiber end. Optogenetic chronic stimulation is emerging as a powerful tool to represent a more disease-relevant approach. In order to verify the functionality of the optogenetic-EEG system, an acute stimulation of VTA (ventral tegmental area) dopamine neurons in TH:cre mice will be tested. This stimulation has been proven to induce hyperactivity and a time-locked increase in VTA neural firing. This offers a unique system by which to interrogate specific cortical circuitry involved in sensory evoked responses which are perturbed across multiple neuropsychiatric diseases and which are modeled in rodents.

FRI - 227 Molecular Identification of Androgen Receptor Isoforms in *Mus Musculus* Brain

Discipline: Life Sciences
Subdiscipline: Neurosciences

Summer Jordan*, *California State University, Long Beach* and YuanYu Lee, *Center for Education in Proteomics Analysis (CEPA), California State University, Long Beach*

Abstract: Androgens are essential for the development and maintenance of male sexual characteristics by acting on target organs and tissues via the activation of androgen receptor (AR). Previous studies shown that androgen insensitivity in the testicularly feminized (Tfm) male mouse caused by a frame-shift mutation in the *Ar* gene, which results in a prematurely, C-terminally truncated AR isoform of 411 amino acids in length lacking the DNA-binding and ligand-binding domains. Despite this, a N-terminally truncated AR isoform containing the DNA- and steroid-binding domain of the AR can be produced from the internal translation initiation of the mutated Ar mRNA by *in vitro* translation. However, there is no evidence showing the existence of this internally translated AR isoform *in vivo*. To address this, we first performed sequence analysis of male and Tfm mouse *Ar* cDNA by ATG pr to search for potential translation initiation sites. We found 17 translation initiation sites and at amino acid position 1, 503, 507, and 517 as reported and others 13 potential new sites. Interestingly, amino acid 503 became most favorable site in Tfm AR mRNA for ribosome decking. To determine the expression of the potential AR isoforms *in vivo*, we performed immunoblotting of male and Tfm mouse testicular extracts with the antibodies recognized the N- or C-terminal regions of AR. So far, we observed the full-length AR protein (~100 kDa) in wild-type, but not in Tfm males. We will continue examining the expression of the potential AR isoforms in different mouse tissues.

FRI - 228 Investigating the Function of a Novel UBQLN2 Interactor in Protein Homeostasis Pathways in the Nucleus

Discipline: Life Sciences
Subdiscipline: Neurosciences

Francisco Padron*, *University of Michigan*; Amit Pithadia, *University of Michigan*; Henry Paulson, *University of Michigan* and Lisa Sharkey, *University of Michigan*

Abstract: Ubiquilin2 (UBQLN2) belongs to the ubiquilin family of proteins characterized by their ubiquitin-like (UBL) and ubiquitin–associated (UBA) domains. UBQLN2 plays an important role in maintaining protein homeostasis by binding and shuttling ubiquitinated substrates to the proteasome for degradation. UBQLN2 has been implicated in various neurodegenerative diseases including amyotrophic lateral sclerosis, frontotemporal dementia, Huntington's Disease and Alzheimer’s Disease, via its inclusion in the protein aggregates characteristic of each disease. Recent findings have shown that UBQLN2 has the ability to translocate to the nucleus where it clears protein aggregates of mutant expanded polyQ Huntingtin (Hjerpe et al. 2016). However, the mechanism by which UBQLN2 clears aggregates in the nucleus or its nuclear translocation is not yet understood. To gain insight into UBQLN2’s role in protein homeostasis we performed a mass spectrometry screen to identify novel UBQLN2 interacting proteins. We identified a small, nuclear-expressed protein with no known function that strongly interacts with UBQLN2. When co-expressed with UBQLN2, it promotes UBQLN2 translocation into the nucleus. To identify the function of this uncharacterized protein and its interaction with UBQLN2, I am using CRISPR/Cas9 to knock-out the gene in a mammalian neuronal cell line, Neuro2a (N2a). Upon creating knockout (KO) cell lines, I will perform RNA sequencing on wildtype and KO cells, enabling a Go Pathway analysis which should provide insight into the protein function. Preliminary results have shown that CRIPSR/Cas9 is effective for knocking out the target protein in N2a cells. Ongoing experiments are focused on submitting KO cell lines for RNA sequencing.

FRI - 230 Lesion Tracer: A Supervised Image Analysis Tool to Investigate the Role of Immune-Mediated Penumbral Collapse in Focal Stroke.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Naomi Carter*, *Hampton University*; Kathleen Miller-Rhodes, *University of Rochester School of Medicine*; George Albert, *University of Rochester School of Medicine*; Viollandi Prifti, *University of Rochester School of Medicine* and Marc Halterman, *University of Rochester School of Medicine*

Abstract: Acute ischemic stroke (AIS) is a common health concern and a leading cause of disability in the aging population. While current interventions for AIS focus primarily on reestablishing blood flow to the brain, complementary strategies capable of reducing ischemia-reperfusion injury are desperately needed. Historically, preclinical models of CNS injury rely on changes in ischemic core volumes to evaluate effects of putative therapeutic interventions. However, this approach fails to adequately capture the cascade of cell-autonomous and inflammatory responses active within the ischemic penumbra. Approaches that assess the volume of at-risk penumbral tissue, the burden of innate immune activation, and extent of perilesional regulated cell death (RCD) in a robust, quantitative manner will expedite our ability to identify therapeutic interventions for AIS. To address this gap, we developed the image analysis platform Lesion Tracer in the filament model of transient focal stroke in C57bl/6 adult male mice. Lesion Tracer streamlines the process of manually outlining regions of interest to estimate stroke lesion volume via simultaneous measurements of volume, area, average intensity, and spot counts. Following 30-minute middle cerebral artery occlusion (MCAO) mice were sacrificed at 24 and 72 hours post-injury and immunohistochemistry was performed using established markers for the ischemic core, penumbra, and infiltrating immune cells. Our results indicate that Lesion Tracer is a useful platform to quantify the dynamic spatial and temporal relationships between lesion growth and immune activation after AIS.

FRI - 231 Cholinergic Input to Vasoactive Intestinal Peptide Neurons of the Inferior Colliculus

Discipline: Life Sciences
Subdiscipline: Neurosciences

Kevin Cruz-Colón*, *University of Puerto Rico at Ponce*; Luis Rivera-Peréz, *University of Michigan* and Michael Roberts, *University of Michigan*

Abstract: The inferior colliculus (IC) is the hub of the central auditory system. Although it is known that the IC plays important roles in sound and speech processing, the full anatomy, physiology and computational mechanisms underlying these functions are still unclear. Vasoactive intestinal peptide (VIP) neurons are a class of neurons that we recently identified in the IC. While examining the physiology of VIP neurons, we found that VIP neurons are strongly excited when acetylcholine (ACh) is applied. ACh is a potent neuromodulator that controls attention-based processing in a number of brain regions. Because it is known that the IC receives cholinergic input from the pontomesencephalic tegmentum (PMT), we hypothesized that cholinergic axons synapse directly onto VIP neurons. To test this, we used immunostaining to determine whether synaptic terminals that stain for the Vesicular Acetylcholine Transporter (VAChT) are located adjacent to the cell bodies and dendrites of VIP neurons. Preliminary results indicate the presence of VAChT+ synaptic terminals adjacent to VIP neurons that were labeled in the VIP-IRES-Cre mouse line. These preliminary results support our hypothesis that cholinergic cells from the PMT provide cholinergic input to VIP neurons. Since previous studies from our lab showed that VIP neurons project to several brain regions, these results suggest that cholinergic modulation of VIP neurons in the IC may have wide-ranging effects on auditory processing.

FRI - 232 Evaluating the Genotypic Frequencies within the Chitinase Gene

Discipline: Life Sciences
Subdiscipline: Genetics

Joshelle Tsinnijinnie*, *Northern Arizona University* and Jason Wilder, *Northern Arizona University*

Abstract: The purpose of my research is to correlate people's genotype with the microbial residents of their mouths. Chitinase (CHIT1), an antimicrobial protein, is expressed in the components of a person's saliva and is secreted from activated macrophages. This enzyme hydrolyzes the chitin from fungal pathogens. The presence of a mutation within chitinase, specifically a 24 base pair duplication (dup-24 bp), prevents the gene from encoding a functioning protein, potentially allowing fungal pathogens to thrive. Thus, we will analyze the dup-24 bp within CHIT1 by performing a polymerase chain reaction assay on DNA sampled from healthy Native American, Indonesian, Northern Arizona University student, and Chronic Rhinosinusitis (CRS) populations. Initially, we had hypothesized that a person who is deficient in CHIT1 may be more susceptible to CRS. However, our results indicated that the CRS population had the lowest homozygosity frequency of the dup-24 bp in the CHIT1 gene compared to any of the healthy populations we surveyed. We have concluded that a deficiency in chitinase is not a predisposition for developing CRS. Moreover, we observe substantial heterogeneity in the frequency of CHIT1 dup-24 among populations. Future studies will examine whether CHIT1 deficiency genotype correlates with any aspects of microbiome composition and related disease.

FRI - 234 A Robust Platform for the Genome Engineering of Primary Human Myeloid Cells

Discipline: Life Sciences
Subdiscipline: Genetics

Devin Cavero*, *University of California, San Francisco*; Joe Hiatt, *University of California, San Francisco*; Michael McGregor, *J. David Gladstone Institutes*; David Gordon, *University of California, San Francisco*; Kelsey Haas, *University of California, San Francisco*; Kristoffer Leon, *University of California, San Francisco*; Krystal Fontaine, *J. David Gladstone Institutes*; Jeff Cox, *University of California, Berkeley*; Alexander Marson, *University of California, San Francisco* and Nevan Krogan, *University of California, San Francisco*

Abstract: Efficient genome engineering of primary human cells with CRISPR-Cas9 has transformed our ability to study complex immune functions, notably in the context of host-pathogen interactions. While significant progress has been made to develop technology that can edit different primary immune cell types, myeloid cells remain genetically intractable. This presents a challenge for host-pathogen studies, where myeloid cells comprise some of the most important bacterial and viral targets. To this end, we sought to leverage CRISPR-Cas9 technology to genetically perturb myeloid-lineage cells for the identification and analysis of host-pathogen interactions. To do this, we purified CD14+ human monocytes from healthy donors and edited them *ex vivo* by delivery of CRISPR-Cas9 Ribonucleoproteins (RNPs) via electroporation. We show that these cells can be precisely edited and efficiently differentiated into monocyte-derived macrophages or dendritic cells for subsequent challenge with diverse pathogens including HIV, Influenza, and Zika virus. Importantly, this pipeline allows us to broadly assess the impact of perturbed candidate genes on pathogenesis in a scalable fashion, utilizing flow cytometry and high-throughput microscopy to quantitatively compare the levels of infection in isogenic edited cells. Using this method, we observed that efficient genetic deletion of SAMHD1, a canonical viral restriction factor in macrophages, dramatically enhanced HIV infection, while knockout of entry factors diminished HIV susceptibility. We thus demonstrate a robust pipeline for the genetic engineering of primary human myeloid cells to enable the rapid identification and prioritization of key host factors specific to and shared between diverse human pathogens for novel therapeutic development.

FRI - 235 Using Novel Mitogenome Capture Methods on Non-Invasively Collected DNA to Compare Genetic Diversity and Population Structure in Two Sympatric Mustelids in Valdivia, Chile: The Endangered Native Southern River Otter and the Invasive North American Mink

Discipline: Life Sciences
Subdiscipline: Genetics

Natalí Chávez*, *Smithsonian Institution*; Lillian D. Parker, *Smithsonian Institution*; Margad-Erdene Ochirbat, *Smithsonian Institution*; Jessica D. Quinta, *Center for Consevation Genomics, Smithsonian Biology Conservation Biology Institute, Smithsonian Institution*; Maximiliano A. Sepúlveda, *Departamento de Conservación de la Diversidad Biológica, Gerencia de Áreas Silvestres Protegidas del Estado, Corporación Nacional Forestal* and Jesús E. Maldonado, *Smithsonian Institution*

Abstract: The Southern River Otter, *Lontra provocax*, is an endangered mustelid with a limited distribution in southern Chile and Argentina. The region we focus on in this study is the Valdivian Coastal Reserve in southern Chile, where the otters share habitat with the invasive American mink, *Neovison vison*. The mink population was established from individuals that escaped from fur farms in the 1970s. The terrestrial movement of the minks means that there is potential for them to transmit diseases from domesticated dogs to the otters, including canine distemper virus (CDV). This threat, in addition to predation from dogs and habitat destruction, makes the river otters susceptible to local extinction. This goal of this research is to use non-invasively collected samples to assess the genetic diversity and structure of the otter and mink populations. We use 7 microsatellite loci to identify unique individuals from DNA derived from 47 mink and 37 otter scat samples. We then use a novel set of in-solution hybridization probes to enrich and sequence mitochondrial genomes from fecal DNA derived from each individual. Our preliminary analysis of mitogenomes reveals greater genetic diversity in the otters than in the minks, and a genetic signature of population expansion in the minks. Future analysis will investigate population structure and gene flow. This research provides data critical for assessing and maintaining the genetic health of the endangered Southern River Otter, and applies novel methodology that enables the use of non-invasively collected samples for conservation genetics.

FRI - 236 Characterizing Genetic Suppressors of Spt5 Cs-

Discipline: Life Sciences
Subdiscipline: Genetics

Patrick Fuller*, *University of California, Santa Cruz* and Grant Hartzog, *University of California, Santa Cruz*

Abstract: Spt4/Spt5 is an essential transcription elongation factor, found in all eukaryotes, that directly associates with and regulates RNA Pol II (Pol II) during transcription elongation. We believe that one function of Spt4/Spt5 is to enable elongating Pol II to transcribe through chromatin. Nucleosomes, the basic repeating subunit of chromatin, must be temporarily removed and then replaced to permit transcription elongation. Although Spt4/Spt5 does not appear to directly touch histones, it does interact with many proteins that are required to overcome the nucleosome barrier to transcription elongation. Previously, we showed that a cold sensitive (Cs-) allele of the *Saccharomyces cerevisiae SPT5* gene can be suppressed by mutations that either decrease the rate of Pol II elongation or that perturb chromatin. Among these *spt5* suppressor mutations are a large number of dominant mutations that fall into at least two distinct linkage groups. The goal of this project is to identify the genes carrying these mutations. We sequenced the complete genomes of several mutant strains containing the suppressor mutations. Based on these data, we will present evidence for the identities of 4 new suppressor genes . Furthermore, we will describe our strategies for verifying the identities of these suppressors and our interpretations for the roles of these proteins in modulating chromatin structure and transcription elongation.

FRI - 237 Investigating the Interaction between NGLY1 and Other Cdg Genes in *Drosophila Melanogaster*

Discipline: Life Sciences
Subdiscipline: Genetics

Adetunji Adeniran-Adetoye*, *Morgan State University*; Emily Coelho, *University of Utah*; Nathan Clark, *University of Pittsburgh* and Clement Chow, *University of Utah*

Abstract: Glycosylation involves many genes that encode proteins involved in forming and modifying glycans. Mutations in many of these genes lead to a variety of multi-organ disorders. Congenital disorders of glycosylation (CDG) is an umbrella term for rare autosomal recessive disorders of metabolism affecting glycosylation. Mutations in the N-Glycanase 1 (NGLY1) gene cause NGLY1 deficiency, the only known disorder of deglycosylation. NGLY1 is thought to deglycosylate misfolded proteins that are degraded by ER-associated degradation (ERAD). Patients with NGLY1 deficiency present with various symptoms, including developmental delay, movement disorder, seizures, and liver dysfunction. It is unknown why mutations in NGLY1 results in these symptoms. To better understand what might be disrupted in NGLY1 deficiency, we employed evolutionary tools. We identified genes that co-evolved with NGLY1 using evolutionary rate covariation (ERC) analysis. ERC measures correlated evolutionary rates across the animal phylogeny. We hypothesized that genes that co-evolve with NGLY1 must function in similar pathways as NGLY1. Surprisingly, of the ~150 known CDG genes, 29 co-evolve with NGLY1, suggesting that there is an essential connection between NGLY1 and the broader glycosylation pathways. Some of these CDG genes include components of N-linked glycosylation and GPI anchor biosynthesis, among others. To test for interactions between NGLY1 and co-evolving CDG genes, we used RNAi technology to knockdown candidate genes in neurons and glia of a *Drosophila Melanogaster* NGLY1 deficiency model using a UAS/GAL4 system. We will present data on how NGLY1 interacts with these co-evolving CDG genes. Understanding NGLY1 deficiency will likely provide insight into other CDGs.

FRI - 238 CRISPRa-Based Upregulation of Mitochondrial Genes and Effects on α-Synuclein Fibril Aggregation

Discipline: Life Sciences
Subdiscipline: Neurosciences

Miguel Hernández-Rovira*, *University of Puerto Rico - Mayaguez Campus*; Stephanie See, *University of California, San Francisco*; Merissa Chen, *University of California, San Francisco* and Martin Kampmann, *University of California, San Francisco*

Abstract: Parkinson’s disease is morphologically characterized by the formation of Lewy bodies, proteinaceous aggregates in neurons. Among the most recognizable components of Lewy bodies is α-synuclein, a protein usually found in presynaptic terminals that can aggregate in a prion-like manner. The introduction of preformed α-synuclein fibrils into cells can induce conformation change of cellular α-synuclein, which contributes towards the growth of these fibrils. However, the mechanism by which this transformation and assembly occurs is yet to be completely understood. Previous studies have linked mitochondrial dysfunction to synucleinopathies, suggesting that malfunctioning mitochondrial gene expression may be related to the resulting phenotypes. To determine the factors involved in this process, a CRISPRa genetic screen with a mitochondrial sgRNA library was performed on a FRET-based cell reporter for aggregation seeded with pre-formed α-synuclein fibrils. CRISPRa technology allows for the highly-targeted augmentation of gene expression via a modified CRISPR complex where the knockdown function has been replaced with an activating domain. Fluorescence-activated cell sorting (FACS) was used to sort cells into aggregation-positive and aggregation-negative populations based on FRET signal. Both populations were deep sequenced and compared to identify sgRNAs involved in increased and decreased aggregation. These results can then be used to identify new mechanisms that control the intracellular aggregation of α-synuclein.

FRI - 239 Development of a Gene Therapy for Unfolded Protein Regulation As a Treatment for Alpha-Synucleinopathies

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jocelyn Ortiz*, *University of Michigan*; Angel Santiago-Lopez, *Emory University School of Medicine*; Claire-Anne Gutekunst, *Emory University School of Medicine* and Robert E. Gross, *Emory University School of Medicine*

Abstract: Parkinson’s disease (PD), a neurodegenerative disease (or alpha-synucleinopathy), is characterized by the intracellular aggregation of improperly folded alpha-synuclein proteins. The accumulation of misfolded alpha-synuclein causes endoplasmic reticulum (ER) stress, which subsequently activates the unfolded protein response (UPR) pathway and disrupts protein homeostasis. Direct monitoring of UPR activation in response to PD-induced ER stress would allow for a better understanding of the temporal dynamics of this response and its relationship to cellular homeostasis. This work introduces the implementation of a genetically-encoded ATF4-based expression vector, whose expression is contingent on activation on the UPR, that allows for the assessment of the UPR stress response in live cells. We have characterized the kinetics and dynamics of this expression using time-lapse fluorescence microscopy in cells experiencing abnormal protein folding due to chemically-induced ER stress. Current *in vitro* studies are being conducted to implement this expression in PD models and gain insights into the cellular mechanisms associated with mutant A53T alpha-synuclein protein expression. We expect that these results will inform the development of therapeutic strategies harnessing the UPR as a mechanism to prevent neurodegeneration.

FRI - 300 Isotopic Labeling of Tryptophan Synthase

Discipline: Life Sciences
Subdiscipline: Biochemistry

Lucia Diaz*, *Scripps College* and Mary Hatcher-Skeers, *Keck Science Department*

Abstract: In collaboration with the Mueller group at UC Riverside, the Hatcher-Skeers group is using newly developed techniques to grow and purify isotopically labelled protein samples for NMR studies. Tryptophan synthase is an enzyme that catalyzes the final two steps in the biosynthesis of tryptophan. The discovery that it is a dimer of dimers (α2β2) caused debate over its mechanism of subunit interaction. In the mechanism of tryptophan, there is beta elimination and replacement reaction with the beta hydroxl group of L-serine. It is eliminated and replaced with indole to produce tryptophan. In the mechanism, two of the intermediates were long thought to be quinonoids but recent NMR crystallography experiments determined them to be carbanions. The purpose of these studies is to gain a better insight into the structure and mechanisms of tryptophan synthase. The Hatcher-Skeers group has developed a method whereby the dimers can be dissociated and recombined with different labelling schemes. Unlabeled tryptophan synthase was grown and purified. We will be expressing deuterium labelled tryptophan synthase by using labelled glucose, ammonium chloride, and Bioexpress. Once we have deuterium labelled protein, we will separate and purify the α and β subunits of both the labeled and unlabeled protein. The labeled subunits will then be recombined with the unlabeled protein to make samples with alternatively NMR silent subunits. This process will allow us to solve complete structures of each subunit while in the native, dimerized form. This should provide a better insight into the structure and mechanism of tryptophan synthase.

FRI - 301 Determining the Role of Linker Region Phosphorylation in Polypyrimidine Tract Binding Protein 2 Neuronal Splicing Regulation

Discipline: Life Sciences
Subdiscipline: Biochemistry

Elizabeth Hitch*, *California State University, Fullerton*; Dean Madory, *Santa Ana Community College*; Anthony Truong, *California State University, Fullerton*; Basma Jibrael, *California State University, Fullerton*; Stephen Gonzalez, *California State University, Fullerton* and Niroshika Keppetipola, *California State University, Fullerton*

Abstract: Polypyrimidine Tract Binding Proteins, PTBP1 and PTBP2, belong to a family of RNA binding proteins that function to regulate alternative splicing. PTBP1 and PTBP2 can bind to CU rich elements within the premature mRNA to promote or inhibit splice site selection. PTBP1 is expressed in nearly all tissues but is absent in neurons while PTBP2 is expressed almost exclusively in neurons. Problems with alternative splicing can lead to the production of aberrant proteins and result in neurodegenerative diseases. PTBP1 and PTBP2 share 74% sequence identity and are similar in domain arrangement. These proteins regulate over-lapping and distinct sets of target exons. Notably, differences in expression patterns and splicing activity play a critical role for neuronal differentiation and maturation. How these two proteins can exert different tissue specific splicing outcomes remains unknown. Recent mass spectrometry studies have revealed that PTBP2 is phosphorylated at a greater number of residues than PTBP1 in the unstructured N-terminal and linker regions. Thus, the hypothesis underlying this study is that phosphorylation of PTBP2 N-terminal and linker regions dictates its neuronal specific splicing activity. To test this, we have generated PTBP1-PTBP2 chimeras. The constructs were tested for protein expression in mouse neuro 2A cells via Western Blot. Our results highlight the chimeras are well expressed. We are currently investigating their splicing activity using a reporter minigene that contains a test exon differentially regulated by PTBP1 and PTBP2. The results from this study will determine the role of the N-terminal and linker regions in PTPB2 neuronal splicing regulation.

FRI - 302 Structural Investigation into a Natural DNA Polymerase with Unnatural Reverse Transcriptase Activity

Discipline: Life Sciences
Subdiscipline: Biochemistry

Roman Meza*, *University of California, Irvine*; Nicholas Chim, *University of California, Irvine* and John Chaput, *University of California, Irvine*

Abstract: Replicative DNA polymerases are responsible for replicating the genomes of living organisms. *Geobacillus stearothermophilus* DNA polymerase I (Bst DNAP-I) was recently shown to reverse transcribe threose nucleic acid (TNA) back into DNA[1]. Composed of a four-carbon threose sugar rather than the normal five-carbon deoxyribose sugar found in DNA, TNA is structurally distinct from naturally occurring genetic polymers. Hence, the unique reverse transcription ability of Bst DNAP-I warrants further investigation. To that end, we employ X-ray crystallography to capture structural snapshots of Bst's mechanism to recognize non-cognate TNA templates and catalyze DNA reverse transcription. The objective of this study is to work toward elucidating the closed ternary structure within the mechanistic pathway where Bst DNAP-I is bound to a TNA template/DNA primer duplex and an incoming triphosphate. Three Bst DNAP-I mutants (i.e., D329A, D598A, and D329A/D598A), previously shown to be critical in obtaining closed ternary structures of the natural system, were expressed and purified using an established protocol[2]. Following purification, crystallization screens were setup and the most promising crystallization conditions were optimized. Bst D598A crystal structures from two crystallization conditions reveal a novel intermediate conformation, which provides further structural insight into the mechanism required to facilitate TNA reverse transcription.

FRI - 303 Characterization of Two Redundant Proteins Involved in Chemotaxis

Discipline: Life Sciences
Subdiscipline: Biochemistry

Rawan Elaksher*, *New Mexico State University*; Sierra Strebe, *New Mexico State University*; LaPorsha Campbell, *New Mexico State University*; Inoka Menikpurage, *New Mexico State University* and Paola Mera, *New Mexico State University*

Abstract: Chemotaxis allows bacteria to adapt to change rapidly by moving to chemically favorable environments and avoiding unfavorable environments (Eisenbach *et al*., 2000). *In Caulobactor crescentus*, the gene *cagA* is found near genes that control chemotaxis; however, its function is unknown. Our hypothesis is that the protein encoded by *cagA* is involved in chemotaxis. We found a second gene, *cagA1,* which has an identical sequence to *cagA* but it localizes elsewhere in the genome. Using the server TMHMM. v. 2.0 we showed that CagA and CagA1 proteins were predicted to be membrane bound. We confirmed this prediction using fluorescent tags to determine the subcellular localization of CagA and CagA1. The identification of the second copy of CagA protein allowed us to analyze redundancy in function. I used genetic engineering and double recombination techniques to delete *cagA* from a *ΔcagA1* strain and *cagA* from the wildtype. I was able to confirm the deletions using colony PCR. Using growth curves and chemotaxis assays, which I optimized, I tested for viability and motility. Our preliminary results illustrate that CagA and CagA1 are not essential for viability; however, our motility assays suggest that these proteins are involved in different types of motility. Future directions include determining whether the proteins localize on the inner or outer membrane and whether they are involved in biofilm formation. Understanding the function and phenotype of these proteins will be beneficial to better understand chemotaxis and their correlation to how bacteria colonizes their host.

FRI - 304 Overexpression of Insulin-like Growth Factor Binding Protein 1 (IGFBP-1) in Breast Cancer Cells Results in Tamoxifen Resistance and Hyperactive MAPK and ERK Signaling

Discipline: Life Sciences
Subdiscipline: Biochemistry

Janel Sowers*, *New Mexico State University*; Yan Zheng, *New Mexico State University* and Kevin D. Houston, *New Mexico State University*

Abstract: Tamoxifen is a selective estrogen receptor modulator, being used as a treatment for breast cancers that express estrogen receptor alpha. Previous research has shown that tamoxifen sensitivity in breast cancer cells is, in part, via activation of G protein-coupled estrogen receptor 1 (GPER1) which mediates the accumulation of the insulin-like growth factor binding protein 1 (IGFBP-1) and inhibits IGF-1-dependent cell signaling. Within five to ten years of using this treatment, patients often become resistant to tamoxifen. The molecular mechanisms causing this resistance are not well known. It has been shown that the epidermal growth factor receptor (EGFR) is hyperactive in tamoxifen-resistant cells, resulting in MAPK pathway (Ras-Raf-MEK-ERK) activation. We hypothesized IGFBP-1 accumulation is a key component for the development of tamoxifen resistance. To test this hypothesis, estrogen-receptor-alpha-positive breast cancer cells that overexpressed IGFBP-1 were developed and the ability of tamoxifen to decrease cell viability was determined. Similar to tamoxifen resistant cells, there was no decrease in cell viability in breast cancer cells that were engineered to overexpress IGFBP-1. Immunoblot analysis revealed hyperphosphorylated MAPK in both the IGFBP-1-overexpressing and tamoxifen-resistant cells. Inhibition of the ERK-mediated signal transduction pathway using a small molecule inhibitor resulted in a significant decrease in cell viability in IGFBP-1-overexpressing and tamoxifen-resistant cells after co-treatment with tamoxifen. These data suggest the overexpression of IGFBP-1 leads to tamoxifen resistance, and this resistance depends on dysregulated ERK signaling. Future work will determine if the tamoxifen-induced IGFBP-3 similarly participates in the development of tamoxifen resistance in breast cancer cells.

FRI - 305 Roles of Zip8 and Zip14 Transporters in Myogenesis

Discipline: Life Sciences
Subdiscipline: Biochemistry

Shellaina Gordon*, *University of Massachusetts Medical School*; Katherine Vest, *University of Cincinnati* and Teresita Padilla-Benavides, *University of Massachusetts Medical School*

Abstract: Transition metals like manganese (Mn) are co-factors to enzymes and act as second messengers in cell signaling. Studies on the molecular mechanisms by which Mn contributes to development focus on its role as co-factor to mitochondrial enzyme superoxide dismutase 2 (Sod2). Mn also participates in protein glycosylation and during bone and neural development. Our laboratory investigates the biological relevance of Mn in the differentiation of skeletal muscle cells. During myogenesis, mitochondrial synthesis increases including the expression of Sod2, which protects against oxidative stress. Our lab has shown that gene and protein levels of Zip8 and Zip14, two membrane Zn/Mn/Fe/Cd transporters, increase during differentiation of C2C12 immortalized mouse myoblasts. We hypothesized that these transporters may contribute to the acquisition of Mn during myogenesis and the metallation of Sod2. To determine the roles of Zip8, Zip14, and Mn during myogenesis we used shRNA to knockdown these transporters in primary myoblasts. We found that Zip8 knockdown myoblasts presented a proliferation defect and were unable to differentiate, shown by the expression of muscle-specific differentiation markers and cell morphology. Zip14 knockdown myoblasts behaved similarly to control cells. Whole cell metal content analyses showed a significant reduction of Mn and Zn in the Zip8 knockdown. A decrease in Sod2 activity was observed. Mn supplementation in the culture media failed to recover the proliferation defect. This work contributes to the limited literature related to Mn biology in myogenesis and provides a foundation for future efforts to understand Mn in other differentiation and disease models.

FRI - 306 Comparison of Alpha-2-Macroglobulins from Swine and Humans and Their Copper Binding

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alejandra Garcia*, *California State University, Fullerton*; Maria Linder, *California State University, Fullerton*; Cameron Marzvaan, *California State University, Fullerton*; Enrico Falcone, *University of Strasbourg* and Peter Faller, *University of Strasbourg*

Abstract: Alpha-2-macroglobulin (a2M), a member of the macroglobulin family of blood plasma proteins, has functions ranging from trapping proteases to transporting cytokines and growth factors. Some years ago, we determined that a2M was also an important blood carrier of copper for uptake by cells; but the details of its binding to copper remained unclear. In the current studies we purified a2M from volunteer human plasma as well as from that of pigs, to further investigate the nature of copper binding. The procedure developed for human a2M was applied: PEG 8000 fractionation and Zn(II)-immobilized metal affinity chromatography. The resulting samples were separated in large pore size exclusion chromatography (Sephacryl S300). Human a2M eluted as one large peak (MW of ~740 kDa), with a much smaller peak ~400 kDa. By SDS-PAGE, both peaks showed the expected 180 kDa subunit band, indicating that most of the human a2M was a tetramer. The sample purified from Yorkshire pig plasma eluted as a ~360 kDa protein, suggesting a dimer. But SDS-PAGE revealed a single subunit of ~70 kDa. Preliminary data obtained by EPR gave similar but not identical profiles for the two proteins, with 2 binding sites, the main one with Cu(II) atoms bound to three Ns and one O. Mass spectrometry revealed the pig protein to be hemopexin, a heme scavenger. As pigs are unusual in not having a form of albumin that transports copper, we are now conducting further studies on hemopexin as an alternative copper carrier in the blood.

FRI - 307 Searching for the Spike Domain of the Human Astrovirus Virginia 1 Capsid Protein

Discipline: Life Sciences
Subdiscipline: Biochemistry

Kevin Delgado-Cunningham*, *Department of Biomolecular Engineering, University of California Santa Cruz*; Jordan Ford, *Department of Biomolecular Engineering, University of California Santa Cruz*; Lena Meyer, *Department of Biomolecular Engineering, University of California Santa Cruz* and Rebecca DuBois, *Department of Biomolecular Engineering, University of California Santa Cruz*

Abstract: Human astrovirus Virginia 1 (*Mamastrovirus 9*) has been associated with acute encephalitis in immunocompromised patients since 2010. Its capsid protein is highly divergent from that of the classical human astroviruses (*Mamastrovirus 1*) outside of a conserved N terminal core domain. As such, a VA1 homolog of the spike domain of the classical human astrovirus capsid protein, which elicits neutralizing antibodies, has yet to be identified. Identification and recombinant production of such a domain would provide an opportunity to determine neutralizing epitopes on the VA1 capsid. We seek to identify a stable expression construct within the capsid protein of human astrovirus VA1, excluding the conserved core domain. A series of expression constructs is being screened for stability after recombinant production in *E.coli*. Initial purifications of soluble protein are carried out by TALON metal affinity chromatography, while proteins expressed as inclusion body aggregates are purified by ion exchange chromatography after refolding. A final purification is carried out by gel filtration chromatography in each case. Constructs which, after purification is complete, show negligible aggregation by gel filtration chromatography and remain soluble are considered stable. Test expressions of all constructs have yielded inclusion body aggregates. Screening for successful refolding conditions has begun. It is expected that buffer conditions compatible with stability will be found for one of the constructs. Identification of a stable expression construct will provide evidence of a spike domain in the capsid protein of human astrovirus VA1, and enable its antigenic characterization.

FRI - 308 Canine Ceruloplasmin As a Multimeric Complex – but What Is It Composed of?

Discipline: Life Sciences
Subdiscipline: Biochemistry

Yasmine Alam*, *California State University, Fullerton* and Maria Linder, *California State University, Fullerton*

Abstract: Copper is an essential trace element found in all living organisms, though it is toxic in excess amounts. Dogs are peculiar in copper metabolism, as they have a tendency to develop copper overload in their liver. We have previously discovered that the main copper binding protein, ceruloplasmin (Cp), in canine blood plasma behaves like a larger protein in size exclusion chromatography (SEC). Thus, we hypothesized that it is aggregating to itself, or binding to some other protein(s). Our lab has shown that high concentrations of potassium phosphate (300mM, pH 6.8) dissociate the presumed Cp complex. Similar concentrations of NaCl did not cause dissociation. Initial evaluation of stained SDS-PAGE bands suggested no other protein was eluting with the same pattern as Cp in SEC. This is consistent with the concept that Cp was not binding another protein but aggregating. However, new gels and densitometry are underway to confirm whether Cp is circulating as a heteromeric complex. Coimmunoprecipitation studies were inconclusive due to problematic antibodies. The results suggest that canine ceruloplasmin may be circulating as a homomeric protein. By investigating Cp and the factors that contribute to normal copper homeostasis in mammals, methods for eliminating copper toxicosis can be identified.

FRI - 309 Insights into Two Paralog Phosphorylated Proteins, PTBP1 and PTBP2 and Its Role in Alternative Splicing.

Discipline: Life Sciences
Subdiscipline: Biochemistry

Stephen Gonzalez*, *California State University, Fullerton* and Niroshika Keppetipola, *California State University, Fullerton*

Abstract: Alternative splicing plays an important role in gene regulation in higher eukaryotes. Cis-regulatory elements on a pre-mRNA work together with corresponding trans-acting factors to either promote or silence splicing of regulated exons. Misregulation of alternative splicing causes neurodegenerative diseases such as Alzheimer's disease, muscular dystrophy, and ovarian cancer. Thus, a detailed mechanistic understanding of the process may provide targets for rational drug design for these splicing related diseases. One of the trans-acting factors in controlling splicing patterns in pre-mRNA is a family of RNA binding proteins known as the Polypyrimidine Tract Binding Proteins, PTBP1 and PTBP2. PTBP1 and PTBP2 share 74% sequence identity and similar domain organization: four RNA Recognition Motifs (RRMs) that are joined via three linker regions and one N-terminal region. PTBP1 and PTBP2 primarily act as splicing suppressors for regulated exons. We recently discovered that PTBP1 and PTBP2 are phosphorylated at different residues over the entire length of the two proteins. To address whether differences in phosphorylation play a role in the different splicing activities of PTBP1 and PTBP2, we are generating PTBP1-PTBP2 hybrid proteins by 2-step PCR. We have amplified the corresponding regions of PTBP1 and PTBP2 successfully and are now in the process of generating the hybrid DNA construct. The generated construct will be cloned into a mammalian expression vector and assayed in vivo for protein expression and splicing activity.

FRI - 310 Elucidating the Role of a Divergent Heme Oxygenase in Organelle Biogenesis in the Malaria Parasite

Discipline: Life Sciences
Subdiscipline: Biochemistry

Celine Slam*, *University of Utah*; Amanda Mixon, *University of Utah* and Paul Sigala, *University of Utah*

Abstract: Malaria is a devastating disease with an estimated 500,000 deaths annually. Malaria is caused by single-cell, eukaryotic *Plasmodium* parasites that infect and grow inside human red blood cells. Parasites have developed many unique molecular adaptations to survive in the heme-rich environment of erythrocytes, with many unusual proteins of unknown function. We identified a divergent heme-oxygenase homolog (PfHO) in the *Plasmodium* genome that binds heme but has lost heme-oxygenase activity. PfHO is targeted to the parasite apicoplast, which is a chloroplast-like organelle with a small genome that houses core metabolic pathways. Prior data shows that PfHO binds DNA in a heme-dependent manner and is essential for transcribing the apicoplast genome into RNA. We hypothesize that the essential function of PfHO is to bind apicoplast DNA and recruit RNA polymerase to initiate transcription. We propose that PfHO binds heme that accumulates due to parasite digestion of hemoglobin, causing PfHO to dissociate from DNA and thereby turn off apicoplast transcription in mature parasites. To test this model, we are using *E. coli* bacteria to express and purify wildtype PfHO and mutant variants expected to alter heme-binding affinity and thus modulate DNA affinity. We will test the effects of these mutations using *in vitro* heme and DNA-binding assays. We will then express these PfHO variants in parasites to test if they rescue lethal knock-down of endogenous PfHO. These studies will test the importance of heme-binding for PfHO's essential function and thereby unravel a critical feature of its non-canonical role in apicoplast genome transcription.

FRI - 311 Assembly of Membrane Nanodiscs and Incorporation Fo EGFR and RON Receptors

Discipline: Life Sciences
Subdiscipline: Biochemistry

Aubrey Gibson*, *University of New Mexico*; Diane S. Lidke, *University of New Mexico*; Mara P. Steinkamp, *University of New Mexico*; Carolina Franco-Nitta, *University of New Mexico* and Rachel Grattan, *University of New Mexico*

Abstract: Cell communication involves a complex network of signaling proteins which generate essential responses such as maintaining homeostasis and cell proliferation. To understand the effect that a particular receptor has on a cell, it is necessary to determine the molecular mechanisms underlying the signaling process. Two membrane receptor tyrosine kinases of particular interest in the field of cancer biology are epidermal growth factor receptor (EGFR) and recepteur d'origine nantais (RON). These receptors are overexpressed in several cancer types and are activated via crosstalk even in the presence of receptor-specific inhibitors. However, the mechanisms allowing for this crosstalk are not yet understood. We hypothesize that RON is a substrate for EGFR and that crosstalk occurs at the plasma membrane through direct receptor interactions.

Our *in vitro* test system involves embedding these proteins into nanodiscs. Nanodiscs are lipid bilayers surrounded by a belt-protein that provide a model of the plasma membrane. Nanodiscs allow for the isolation of proteins of interest while providing a native-like lipid environment. We have generated full-length RON and EGFR proteins as well as protein fragments consisting of transmembrane and kinase domains to determine whether these receptors can interact in the absence of extracellular components. Ongoing investigations will involve analyzing nanodisc assembly and protein incorporation by western blotting and electron microscopy. *In vitro* kinase assays will also be used to determine whether EGFR can directly phosphorylate RON. Results of this study may benefit carcinogenesis investigations and possibly aid in development of new treatments targeting EGFR and RON proteins.

FRI - 312 Identifying Post-Translational Modifications of Antigen 85B Secretion in *Mycobacterium Tuberculosis*

Discipline: Life Sciences
Subdiscipline: Biochemistry

James Chang*, *University of Central Florida*; Carolina Mehaffy, *Colorado State University* and Karen Dobos, *Colorado State University*

Abstract: Of all infectious diseases, tuberculosis (TB) is the leading cause of death. Mycobacterium tuberculosis (Mtb), the bacteria causing TB, is especially harmful because it can survive in alveolar macrophages. The protein complex antigen 85 (A, B, C) is a major factor secreted by Mtb, that allows the bacteria to bind to fibronectin within the esophagus. If we can identify the structural differences between the native and recombinant protein, we can replicate the same immunogenic effect the native protein creates. We believe that prior to secretion the protein is decorated with post-translational modifications (PTMs) unique to native 85B.The scope of this project is **to identify and locate PTMs in native Antigen 85B in order to mimic these modifications in the recombinant protein**. We suspect that the Ag85B undergoes PTM phosphorylation in Mtb.Thus, we will aim to detect phosphorylation on Ag85B by using an orbitrap direct infusion and by performing functional assays using an alkaline phosphatase reaction. If phosphorylation exists, the alkaline phosphatase would make the native act the same way as the recombinant in the immunoassay. We expect equal activity on the recombinant indirect ELISA plate compared to the native plate due to the lack of PTMs on the protein surface. This approach utilizes top-down and bottom-up proteomics, as well as immunoassays, to get a holistic view of the PTMs. This is key for the protein's role in antigen detection diagnostics and development in prophylactic vaccine systems. This study focuses on the phosphorylation event, however, other PTMs may be involved.

FRI - 313 Optimization of Recombinant Mammalian and Fish Drug Transporter Expression in Escherichia coli

Discipline: Life Sciences
Subdiscipline: Biochemistry

anthony vega*, *University of California, Davis* and Sascha Nicklisch, *University of California, Davis*

Abstract: ABC-type drug transporters are key players in regulating uptake efflux of drugs and environmental chemicals in all organisms. Understanding the detailed structure-function relationships of these transport proteins is important to better predict the elimination pathways of drugs and environmental chemicals on an organismal, cellular, and molecular level. In this study, we will clone and express the major drug transporter P-glycoprotein (aka MDR1) from yellowfin tuna, mouse and human in commercially available E. coli expression plasmids and strains and select the best strain/plasmid combination for optimal growth, protein yield and drug transporter activity. Both the selected E. coli expression strains and plasmids are genetically modified to express membrane proteins from different organisms in the bacteria while preventing degradation or toxic overexpression of the target membrane proteins. Protein expression and yield will be monitored using optical density (OD) measurements and SDS-gel electrophoresis and Western blotting. Purification will be carried out using Immobilized Metal Affinity Chromatography (IMAC) and size exclusion (SE) Fast Protein Liquid Chromatography (FPLC). The purity of the protein will be further qualified using LC mass spectrometry. The optimization strategy includes utilizing different plasmids and strains for successful transformation and expression, incubation time, and finally column selection for purification.

FRI - 314 The Mechanisms of Catalytic Regulation of Isocitrate Dehydrogenase 1 (IDH1)

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alexandra Strom*, *San Diego State University*; Christal Sohl, *San Diego State University*; Vinnie Widjaja, *San Diego State University*; Lucas Luna, *San Diego State University*; Dahra Pucher, *University of Southern California*; Tin Duc Nguyen, *University of California, San Diego*; Diego Avellaneda Matteo, *San Diego State University* and An Hoang, *San Diego State University*

Abstract: Isocitrate dehydrogenase 1 (IDH1) catalyzes the conversion of isocitrate to α-ketoglutarate in the presence of NADP+ as a coenzyme. Tumorigenic IDH1 mutants gain the ability to catalyze a NADPH-dependent neomorphic reaction of converting α-ketoglutarate to the oncometabolite D-2-hydroxyglutarate, which drive brain cancer, acute myeloid leukemia, and chondrosarcoma. However, further studies of IDH1 are required to fully understand the mechanisms behind its regulation. Post-translational modifications (PTMs), which include acetylation, represent one effective means of protein regulation. Here we hypothesize that IDH1 acetylation results in decreased catalytic efficiency. To test this hypothesis, we performed kinetic studies on a lysine to glutamine IDH1 mutant that mimics acetylation (K224Q). We report a decreased rate of isocitrate to α-ketoglutarate conversion in this mutant when compared to wild type IDH1. We also show that treatment with wild type IDH1 with acetylCoA similarly decreases activity. These studies suggest that acetylation may be an important PTM for regulating IDH1 activity, helping us to understand pathways relevant to IDH1 activity.

FRI - 315 Toward the Reconstitution and Characterization of Telomeric Nucleosomes

Discipline: Life Sciences
Subdiscipline: Biochemistry

Aldrex Munsayac*, *University of California, Santa Cruz*; Terren Chang, *University of California, Santa Cruz*; Liam Tran, *University of California, Santa Cruz* and Michael Stone, *University of California, Santa Cruz*

Abstract: Eukaryotic chromosomes are capped by repetitive DNA sequences called telomeres which guard the genome against unwanted DNA repair. In cancer, proper telomere function is disrupted, and targeting these structures shows great therapeutic promise. Despite much effort dedicated to understanding the functional role telomeres play in genome protection, the mechanism in which telomeres achieve this protection remains largely unknown, and has thus hindered the discovery of drugs designed to target them. To function, telomeres adopt a compacted protected state with the aid of the general DNA binding protein complex known as the nucleosome core particle alongside telomere-specific binding proteins. During processes such as DNA replication, this compacted state must be remodeled into an open and accessible conformation. However, the precise molecular mechanisms that regulate this interconversion remains unknown. Central to this question is understanding how the nucleosome core particle binds and wraps telomeric DNA. Here, we lay the groundwork necessary to conduct single-molecule experiments designed to directly detect and quantitatively analyze the dynamical behavior of telomeric nucleosomes. We have generated a library of telomere sequences of varying length by exploiting the intrinsic instability of repetitive sequences during bacterial replication. Using these sequences, we have successfully reconstituted telomeric nucleosomes and aim to characterize their dynamics in the absence and presence of telomere-binding proteins using single-molecule fluorescence resonance energy transfer. Understanding the dynamical behavior of telomeric nucleosomes will provide mechanistic insight into how telomeres transition from protected to unprotected states and aid in the discovery of therapeutics designed to disrupt these processes.

FRI - 316 Molecular Mechanisms of Mutant Isocitrate Dehydrogenase 1 Catalysis

Discipline: Life Sciences
Subdiscipline: Biochemistry

Giovanni Quichocho*, *San Diego State University*; Ruth Xu, *San Diego State University*; Lucas Luna, *San Diego State University*; Diego Avellaneda Matteo, *San Diego State University*; Michelle Scott, *San Diego State University*; Jeon Erik Fonbon, *San Diego State University* and Christal Sohl, *San Diego State University*

Abstract: Brain tumor mortality rate >60% within 5 years of diagnosis. Isocitrate dehydrogenase 1 (IDH1) mutations drive >70% of low-grade gliomas and secondary glioblastomas. IDH1 catalyzes $NADP^+$-dependent oxidative decarboxylation of isocitrate to α-ketoglutarate (α-KG). IDH1 mutations result in neomorphic activity, oncometabolite formation, NADPH-dependent reduction of α-KG to D-2-hydroxyglutarate (D2HG). The most common mutations occur at the catalytic-site residue 132, where arginine (R132) is typically replaced by histidine (R132H). We previously characterized tumor-relevant mutants at residue 132, showing wide catalytic diversity. To better understand mechanisms of catalysis, we will expand our characterization of IDH1 by observing additional catalytic-site mutants. Based on previous data with R132H/L, we hypothesize R132Y/I, having similar structures respectively, promotes similar neomorphic catalytic activity. R132P will have little to no catalytic activity, from disruption of local secondary structure. R132H/M259A, L120A/R132H, and L120V/R132H mutants will produce little change in activity . To test this hypothesis, we generated cDNA-constructs, heterologously expressed and purified R132I, R132P, R132Y, R132H/M259A, L120A/R132H, and L120V/R132H from *E. coli* to determine effects on neomorphic activity. Kinetic assays were performed to determine mutant neomorphic reaction rates. We found R132I most efficient in catalyzing neomorphic activity followed by R132Y, and R132P. R132H/M259A, L120A/R132H, and L120V/R132H produced little to no neomorphic activity. By replacing catalytic-site residues with a wide range of amino acids, and studying catalytic efficiency of each mutation, we will be able to discover the molecular mechanisms that facilitate neomorphic activity and inform drug design for selective mutant-IDH1 inhibitors effective against a wide range of tumor-relevant mutants.

FRI - 317 Deciphering the Role of CK1δ Phosphorylation of Clock within Mammalian Molecular Clock Mechanism

Discipline: Life Sciences
Subdiscipline: Biochemistry

Sara Ponce*, *Gavilan Community College*; Megan Torgrimson, *University of California, Santa Cruz*; Jennifer Fribourgh, *University of California, Santa Cruz* and Carrie Partch, *Department of Chemistry and Biochemistry, UC Santa Cruz*

Abstract: The mammalian molecular clock mechanism is comprised of dynamic proteins that make a transcription/translation feedback loop (TTFL) in our cells, oscillating between an activation and a repressive complex coinciding with earth's 24-hour solar day. The clock mechanism regulates important parts of our physiology including metabolism and DNA damage repair. Psychiatric and physiological disorders have been correlated to molecular clock disruptions. Based on compelling evidence, we postulate that Casein kinase 1δ (CK1δ) phosphorylates the CLOCK subunit of the major transcription factor, CLOCK:BMAL1, within this TTFL. We hypothesize that phosphorylation will disrupt CLOCK's ability to dimerize to its heterodimeric partner, BMAL1. Disruption of dimerization between the transcription factor subunits could play a significant role in the oscillation between the activation and repressive complexes. We will first investigate whether CK1δ phosphorylates a particular serine on CLOCK conforming to its consensus motif. Upon confirmation of phosphorylation, potential consequences on protein binding interactions will be examined with biochemical assays. PCR site-directed mutagenesis will be used to introduce a phosphomimetic mutation in place of the serine of interest. After expression of the mutated protein in *E. coli*, the CLOCK mutant will be isolated and purified using affinity and size exclusion chromatography. The mutant's binding affinity for other clock proteins will be examined with binding assays including bio-layer interferometry. Exploring the role of this phosphorylation will lead to a deeper understanding of the mammalian clock mechanism as a whole. This knowledge can provide insight into future therapeutic innovations for clock related disorders.

FRI - 318 Characterization of a Novel Model of Head and Neck Cancer Pain in Mice

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Christina Dias*, *MD Anderson Cancer Center* and Geoffroy Laumet, *MD Anderson Cancer Center*

Abstract: Head and neck cancer patients are subject to debilitating, chronic pain. However, these patients rarely receive adequate pain treatment due to our limited knowledge of the mechanisms underlying this pain. Animal models are used to analyze these mechanisms as pain cannot be modeled *in vitro*, due to its sensory and emotional nature. Our objective was to establish a model of head and neck cancer pain to further test potential drug interventions. We hypothesized that injecting tumor cells would induce pain and inflammation in the spinal cord. We induced head and neck cancer by injecting epithelial cells that stably express viral oncogenes (mEERL cells) into mice. Pain hypersensitivity was measured with the von-Frey Dixon method. Spontaneous pain was assessed with the Mouse Grimace Scale. To evaluate inflammation, we isolated and reverse transcribed spinal cord RNA. Gene expression of cytokine and glial cell markers was measured by quantitative polymerase chain reaction. The gene expression was normalized by two housekeeping genes. Pain hypersensitivity developed within days of the mEERl cell injection, but before the tumor was palpable. Spontaneous pain was present on day 15. Interleukin-1β (*Il1b*), Toll-Like Receptor 4 (*Tlr4*), and NFκB Inhibitor-α (*Nfkbia*) were upregulated in the spinal cords of tumor-bearing mice compared to controls. We showed the development of pain in a murine model of head and neck cancer for the first time. The data indicate an activation of the IL-1, TLR4, and NFκB signaling pathways. Targeting these pathways may offer a therapeutic opportunity to alleviate head and neck cancer pain.

FRI - 319 Batseq Reconstructs B and T Cell Receptors in Human Gastric Cancer from Single-Cell Rna-Sequencing Data

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Kelly Chang*, *University of California, Berkeley*; Jinmiao Chen, *Singapore Immunology Network* and Xiaomeng Zhang, *Singapore Immunology Network*

Abstract: The field of single-cell research is rapidly evolving as scientists realize the value of such data. Single-cell RNA-sequencing (scRNA-seq) may be utilized to further the understanding of the adaptive immune system - more specifically, to enhance knowledge on the diversity and specificity of B cell receptors (BCR) and T cell receptors (TCR). Various labs have created separate computational methods to reconstruct BCR and/or TCR sequences with scRNA-seq data. We focus on five commonly used methodologies - BASIC (1), TraCeR (2), BraCeR (3), VDJPuzzle2 (4), MiXCR (5) - found in the literature that assemble antigen-specific receptor sequences. We compare the difficulty of installation, time efficiency, and reconstruction productivity among the five softwares using our own in-house scRNA-seq data obtained from a patient diagnosed with gastric cancer. Taking into account the pros and cons of each method, we developed a web based software called BaTSeq, which integrates the five softwares so that it is easy enough for any person - regardless of their background in programming - to reconstruct BCR and TCR nucleotide sequences. BaTSeq has demonstrated to be an effective tool for reconstructing BCR and TCR sequences from scRNA-seq data. Application of BaTSeq to in-house data revealed clonal expansion of CD8 T cells in gastric cancer, potentially leading to novel T cell therapy development.

FRI - 321 Secondary Tumor Formation Following Treatment with DNA-Alkylating Agent Temozolomide for High-Grade Glioblastoma in Mice

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Cherish Coleman*, *University of Detroit Mercy*; Susan Irtenkauf, *Henry Ford Hospital*; Tamia Waller, *University of Detroit Mercy* and Ana deCarvalho, *Henry Ford Hospital*

Abstract: Temozolomide (TMZ) is a DNA-alkylating agent used for the treatment of glioblastoma (GBM) patients. Response to TMZ-inflicted DNA damage include DNA repair, cell death, or the accumulation of mutations, which could lead to cancer. GBM patient-derived xenografts (PDX) were developed by implanting tumor cells into the brains of immunocompromised mice to study TMZ sensitivity. GBM PDX lines that responded to 40 mg/kg/day in 21-day cycles of TMZ treatment survived longer, but surprisingly developed lung tumors 3-5 month after treatment. For confirmation, three mouse strains were treated with TMZ and observed for symptoms of tumor development. TMZ treatment led to lung tumors in nude mice, thymus and/or lung tumors in severe combined immunodeficiency (SCID) mice and in C57 immunocompetent mice. No tumors were observed in control treated mice. The goals of this study were to determine baseline expression of DNA repair genes in mouse tissues potentially exposed to TMZ and to characterize the tumors through the expression of tissue specific markers. Tissue was collected from mouse normal and cancerous lung and thymus, used for DNA and RNA extraction, and for culturing cells. Total RNA underwent reverse transcription. The resulting cDNA was used to determine gene expression qualitatively through endpoint polymerase chain reaction (PCR) and quantitatively through real time PCR (qPCR). Gene expression results support that all tumors in SCID mice originate in the thymus, and that DNA repair genes are upregulated in lung tumors relative to normal lung tissue in nude mice. TMZ-mediated tumorigenicity has implications for pre-clinical and clinical studies.

FRI - 322 Assessing Tertiary Lymphoid Structures in Mouse Mammary Metastasis Models to Predict Immunotherapy Efficacy

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Elvelyn Fernandez*, *Georgetown University*; Alana Welm, *University of Utah* and Alicia Lai, *University of Utah*

Abstract: Metastasis is the leading cause of death in nearly all cancer types. Immunotherapy emerged as a new era of cancer treatment, however, a majority of patients do not respond to the therapy. One feature known for immunotherapy resistance is the lack of lymphocyte infiltration, by which lymphocytes, especially tumor-fighting cytotoxic T lymphocytes (CTLs), are absent in the tumor area. Strategies to improve lymphocyte infiltration or understand how cancer cells compromise the immune system would advance our knowledge to further improve treatment efficacy.

The receptor tyrosine kinase Ron has been shown to promote metastasis by suppressing CTL activity. Pharmaceutical or genetic depletion of Ron restores the antitumor response. Tertiary lymphoid structures (TLS) are sites that generate and regulate antitumor defenses implemented by immune cells such as T lymphocytes, B lymphocytes, and dendritic cells. Formation of TLS has been shown in several cancer types and correlates to the increased presence of intratumor immune cells. We hypothesized that the presence of TLS could potentially lead to more favorable antitumor responses following Ron inhibition. Using our mouse mammary metastasis model, breast cancer cells were injected intravenously into wild type and Ron knock-out (TK) mice. Tumors from mouse lungs, a metastatic site for breast cancer, are being assessed for the presence of TLS. Through immunohistochemistry, TLS presence is assessed by staining for T and B lymphocytes in paraffin sections of lung metastases. We expect TK mice with the presence of TLS to have greater levels of an antitumor response.

FRI - 323 Catecholamine-Induced DNA Damage in Ovarian Cancer Cells

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Arelis Acevedo*, *University of Puerto Rico* and Edu Suarez, *University of Puerto Rico*

Abstract: Ovarian cancer is the fifth leading cause of mortality among women, responsible for 5% of all cancer deaths in women in the USA. Remarkable evidence exists of the relationship between the activation of the sympathetic nervous system and cancer progression. Furthermore, recent data suggest that adrenergic signaling alters genetic integrity of cancer cells by damaging the DNA and/or influencing the DNA Damage Response and Repair pathways. Additionally, previous data suggest that increased adrenergic stimulation from stress released catecholamines can lead to genomic instability in ovarian cancer cells. Therefore, we hypothesized that increased adrenergic activity will promote formation of significant levels of DNA damage. To assess the extent of damage after catecholamine exposure, we determined p-H2AX (sensitive marker for double-stranded DNA damage) expression by immunofluorescence analyses in SCOV3 and other ovarian cancer cell lines. Alongside, Neutral Comet Assays were performed to assess double-stranded DNA damage after catecholamine exposure. SKOV3 cells that were exposed to epinephrine and norepinephrine at 1h and 24h displayed increased expression of p-H2AX. Moreover, immunofluorescence analyses for p-H2AX in SVOV3 and OV90 showed increased foci formation when compared to the control group. In addition, Neutral Comet Assay analyses in catecholamine-treated SKOV3 and COV362 cells displayed higher levels of double-stranded DNA breaks in comparison to untreated cells. Lastly, to determine if DNA damage is due to adrenergic stimuli, cells were pretreated with propranolol (non-specific β-blocker) and results showed a significant reduction in DNA damage levels. These results suggest that catecholamines can induce double-stranded DNA damage in ovarian cancer cells.

FRI - 324 Exploring the Synergy of Gnaq and YAP in a Zebrafish Uveal Melanoma Model

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Nicole Zambrana Garcia*, *University of Puerto Rico, Rio Piedras*; Grace Phelps, *Massachusetts Institute of Technology* and Jacqueline Lees, *Massachusetts Institute of Technology*

Abstract:

Uveal melanoma (UM) is the most common adult primary malignancy of the eye. UM is associated with activation of oncogene GNAQ/11, which signals to YAP and others. Unlike most cancers, UM rarely has mutations in the p53 pathway. Our lab has established a zebrafish UM model through activated GNAQ, but melanoma only occurs in the context of p53 loss. We've recently discovered when GNAQ and YAP are co-expressed in a p53WT background, zebrafish can develop melanoma; suggesting GNAQ and YAP may have a synergistic role in UM. We hypothesize that a downstream signaling arm to GNAQ synergizes with YAP causing tumorigenesis. This project has two goals: (1) explore the synergy of GNAQ and YAP in p53WT zebrafish and (2) determine if these genes synergize in mammalian melanocytes. First, we've performed immunohistochemistry on zebrafish melanomas expressing GNAQ+YAP to determine activation of known downstream GNAQ signaling pathways such as pERK, pFAK, and pAkt. Additionally, we've utilized a melanocyte lineage-specific GFP reporter to show zebrafish GNAQ+YAP embryos have significantly more melanocyte lineage cells than wildtype embryos. Also, we've used inhibitors against different GNAQ pathway arms on GNAQ+YAP embryos to determine which leads to a decrease of melanocyte lineage cells. Preliminary data show ERK, FAK and YAP inhibitors don't decrease the number of GNAQ+YAP cells, suggesting other downstream GNAQ pathway genes are responsible for the synergy. Second, we've established a GNAQ+YAP mammalian cell line and will perform proliferation assays. In conclusion, other GNAQ pathways genes may be responsible for the synergistic activity of GNAQ+YAP.

FRI - 325 Ketorolac Treatment Reduces Pro-Tumorigenic Cytokines in Ascites Samples from Ovarian Cancer Patients

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Avantika Krishna*, *University of Maryland Baltimore County*; Melanie Rivera, *University of New Mexico Health Sciences Center*; Sarah Adams, *University of New Mexico Health Sciences Center*; Laurie G. Hudson, *University of New Mexico College of Pharmacy* and Angela Wandinger-Ness, *University of New Mexico Health Sciences Center*

Abstract: Ovarian cancer has one of the highest gynecologic malignancy case fatality rates. Only 10-15% of patients successfully respond to therapy, the remaining go through relapse or persistence of disease. Our group has been studying the dual activities of the enantiomeric, non-steroidal anti-inflammatory drug ketorolac with S-ketorolac being a COX1/COX2 inhibitor given for pain relief and R-ketorolac acting as a previously unrecognized Rac1 and Cdc42 GTPase inhibitor. Our retrospective study shows a statistically significant increase in ovarian cancer patient survival after a single dose of ketorolac. Inflammatory cytokines promote ovarian carcinoma growth and suppress immune responsiveness, prompting my hypothesis that the ascites of patients treated with ketorolac will have a significant decrease in inflammatory cytokine levels, aiding in the prevention of tumor proliferation and angiogenesis. Pilot studies showed a decrease in IL-6, IL-8, and IL-10 cytokines in patient ascites following ketorolac. To identify the full range of cytokines present in the ovarian epithelial environment a Proteome Profiler Human Cytokine Array Kit was used on a human ascites sample and OVCAR3 cells treated with ketorolac, paclitaxel and no treatment. A total of 19 cytokines were identified, MIF and CXCL12 were present in both the OVCAR3 and ascites samples. A cytometric bead array tested the cytokines in the ascites of patients before and 6 hours post-ketorolac looking specifically at the pro-inflammatory and pro-angiogenic cytokines; IL-6, IL-10, VEGF, and G-CSF. Results indicate, a decrease in pro-tumorigenic cytokines post-ketorolac, providing greater understanding of the potential for ketorolac use as a targeted cancer therapeutic.

FRI - 327 Therapeutic Vulnerability Associated with Treatment-Resistant Prostate Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Chayanne Solorzano*, *University of Houston*; Damian Young, *Baylor College of Medicine* and Prasanna Kandel Kandel, *Baylor College of Medicine*

Abstract: Prostate Cancer (PCa) is the second leading cause of cancer death in males and the National Cancer Institute estimates ~32,000 males die yearly from PCa in the U.S. PCa has a higher rate of incidence and is more aggressive in African American (AA) males over other populations. PCa tumor growth, progression, and metastasis are often dependent on male hormones such as androgens that bind to the androgen receptor (AR), a nuclear receptor that activates many downstream genes that promote PCa progression. Thus, a common treatment is to reduce

androgen production or inhibit AR function. However, PCa can relapse into a more aggressive form that is less dependent on AR signaling and resistant to existing anti-AR therapies. Interestingly, another transcription factor called TLX/NR2E1 is over-expressed in treatment-resistant PCa (TRPCa). TLX is an oncogene that builds resistance to hormone therapy by regulating AR expression and activity. The overarching goal of our research is to interrogate the oncogenic role of TLX, model TLX function and discover novel therapies for TRPCa. Based on immunoblotting, we discovered two-fold increase in TLX expression in some TRPCa cells. Encouraged by this preliminary finding, we are examining the relationship between TLX and PCa resistance. To test TLX sensitivity, we are performing siRNA knockdown studies and cell viability assays. Furthermore, we will determine the TLX status in primary tumor cells taken from AA patients with treatment refractory PCa. New therapies could be discovered by targeting TLX for TRPCa allowing us to close the gap in this cancer health disparity.

FRI - 328 Abberant Splicing As Biomarkers in Cancer Cell Lines Sensitized to Drugs That Target Splicing Regulators

Discipline: Life Sciences
Subdiscipline: Genetics

Carmelle Catamura*, *University of California, Santa Cruz* and Angela Brooks, *Department of Biomolecular Engineering, University of California, Santa Cruz*

Abstract: RNA splicing is a molecular process that occurs in eukaryotes in which pre-mRNA is transformed into mature mRNA through the incision of the non-coding sections of a gene and then joining the coding sections together. Alternative splicing is a process in which a single gene sequence codes for various protein isoforms using different combinations of exons. Dysregulated splicing, however, has been shown to influence sensitivity to certain drugs in some cancer cell line and mouse models. The main purpose of this study was to determine the correlation of a cell line's outlier splicing to its drug sensitivity. Our hypothesis is that high levels of aberrant splicing in untreated cancer cells would be predictive of more sensitivity when treated with a drug that is a known splicing modulator. To address our hypothesis, we used a computational program called JuncBASE to identify alternative splicing events from RNA sequencing data for 924 cancer cell lines. I performed an analysis on the JuncBASE data wherein I used an interquartile range and a magnitude threshold to detect outliers. I studied the Spearman and Pearson correlation of a cell line's outlier splicing and its sensitivity to treatment with splicing modulator drugs. To identify other drugs that might be more effective in cell lines with splicing alterations, I performed the same analysis to pharmacological data from the Broad Institute Cancer Cell Line Encyclopedia. My findings suggest that high-levels of aberrant splicing in cancerous hematopoietic and lymphoid tissue constitute a negative correlation with Palbociclib, a cyclin-dependent kinase inhibitor.

FRI - 329 The Genetic Basis of Divergence in Immune Defense between *Drosophila* Species

Discipline: Life Sciences
Subdiscipline: Genetics

Mariaelena Nabors*, *University of Kansas* and Robert Unckless, *University of Kansas*

Abstract: There is ample evidence for rapid evolution of genes involved in immune defense in many species. However, specific examples that connect genetic and phenotypic divergence between species in the ability to fight diseases are relatively rare. This is important because it is presumed that this rapid evolutionary divergence is due to a host-pathogen arms race, but there is little direct evidence that this is true. Our work aimed to understand the molecular basis of divergence in immune defense and determine the extent to which fast evolving genes lead to this phenotypic divergence. To determine phenotypic divergence in immune defense, we performed systemic infections on *Drosophila simulans* and *Drosophila mauritiana,* and measured survival five days post infection. Interestingly, we found the species with greater resistance depended on the pathogen used. To better understand the evolution of immune defense between species, we performed interspecific genetic mapping to determine genomic regions associated with the divergence in immune defense between species. We tested for variation in immune defense within and between *D. mauritiana* and *D. simulans*. We then used a backcross design (hybrid males are infertile) through females to map this divergence in response to both pathogens to the chromosome, and performed RNA-seq to identify potential candidate genes. To confirm promising candidate genes' roles in immune defense, we used CRISPR/Cas9 to move alleles from one species to the other. This study on interspecific divergence in immune defense is among the first of its kind and will provide an exciting new approach to comparative immunology.

FRI - 330 Comparative Transcriptomics between *Steinernema Carpocapsae* Females and Males and *Caenorhabditis Elegans* Hermaphrodites and Males

Discipline: Life Sciences
Subdiscipline: Genetics

Isaryhia Rodriguez*, *University of California, Irvine*; Lorrayne Serra, *University of California, Irvine*; Bryan Rodriguez, *University of California, Irvine*; Cassandra McGill, *University of California, Irvine* and Ali Mortazavi, *University of California, Irvine*

Abstract: Entomopathogenic nematodes (EPNs) are parasitic nematodes that can efficiently kill insects, with *Steinernema carpocapsae* being the most studied EPN. Although *Steinernematids* have been widely studied for insect infection and mutualism and their commercial applications are already established, little is known about the patterns of gene expression in heads and tails of infective juveniles (IJs) and adults or how these compare to expression in the model organism *C. elegans*. Comparisons between *Steinernema* and *Caenorhabditis* demonstrate morphological similarities such as shape and morphology of the body, mouth cavity, pharynx and digestive system, although *C. elegans* is hermaphroditic while *S. carpocapsae* is gonochoristic, i.e. has males and females. While males of both *S. carpocapsae* and *C. elegans* have an additional set of neurons in the lower tail region that control mating behavior, the tail morphology is also very distinct. We hypothesize that there is a core set of sex-specific genes that are co-expressed in both *S. carpocapsae* and *C. elegans* adult sexes in a region-specific manner. We performed a comparative analysis between heads and tails of *S. carpocapsae* and *C. elegans* IJs/dauers as well as male, female/hermaphrodite adults using single-worm RNA-seq. We found that male tails of *S. carpocapsae* have similar gene expression to *C. elegans* male tails. *C. elegans* hermaphrodites also share similar gene expression to *S. carpocapsae* females. This is one of the first comparative transcriptomic analyses of body parts between distantly related species of nematodes and provides insights into both the highly conserved and genetically distinctive characteristics of both species.

FRI - 331 Dissecting the Relationship between a QTL for Intravenous Self-Administration of Cocaine and *Fam53b* in Mice

Discipline: Life Sciences
Subdiscipline: Genetics

Christian Monroy Hernandez*, *The Jackson Laboratory*; Jason Bubier, *The Jackson Laboratory*; Ryan Logan, *University of Pittsburgh*; Leona Gagnon, *The Jackson Laboratory*; Rainy Dodd, *The Jackson Laboratory*; Rick Maser, *The Jackson Laboratory*; Price Dickson, *The Jackson Laboratory* and Elissa Chesler, *The Jackson Laboratory*

Abstract: Cocaine addiction is a major public health issue affecting millions of people worldwide. Increasing our understanding of the biological processes regulating this disorder is crucial to effectively treat it. Mouse models enable the use of powerful genetic and behavioral assays and tools, allowing us to gain valuable insight into the biological underpinnings of cocaine addiction. One of these tools is the intravenous self-administration paradigm (IVSA), considered the gold-standard in preclinical volitional drug use research. In a previous study, the cocaine IVSA paradigm was used on the C57BL/6J X DBA/2J (BXD) recombinant inbred (RI) mice panel. This lead to the identification of a series of genome-wide significant quantitative trait loci (QTL) associated with several IVSA behavioral phenotypes. A *trans* expression QTL (eQTL) for *Fam53b* mapped to the same region as one of the behavioral QTLs, on chromosome 11; *Fam53b* has been identified as a risk gene for cocaine dependence in a human genome-wide association study (GWAS). In this study, we used mice from the BXD RI panel with relevant recombination events at the chromosome 11 QTL to narrow the interval of interest, and

prioritize between the two strong candidate genes: *Cyfip2* and *Hnrnph1*. Furthermore, we also used CRISPR/Cas9 to create *Fam53b* knockout mice, which will be used in future cocaine response phenotyping experiments. This work will position us to continue exploring the relationship between the IVSA QTL and *Fam53b* in mice, which in turn will help us further understand the role of *Fam53b* in human cocaine dependence.

FRI - 400 Impact of a Prenatal Stress Management Intervention on Infant Cortisol and the Moderating Effect of Mothers' Pregnancy Anxiety

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Angelica Flameno*, *California State University Long Beach* and Guido Urizar, *California State University Long Beach*

Abstract: Altered cortisol patterns in infants have been associated with increased risk for chronic diseases later in life such as diabetes, high blood pressure, and cardiovascular disease. Therefore, stress management interventions for mothers are needed to test whether they may have a positive influence on infants' cortisol levels. The current study examined whether low-income mothers randomized to a cognitive behavioral stress management (CBSM) intervention during pregnancy (*n*=55) had infants with more normative cortisol patterns at three months postpartum compared to an attention control (AC) group (*n*=45) and whether these outcomes were influenced by mothers' level of pregnancy anxiety. Mothers' pregnancy anxiety (Prenatal Anxiety Scale) was assessed at baseline. They were then randomized to either an eight-week CBSM intervention where they were taught coping skills to manage stress, or an AC group where they received printed materials on health information over the same eight-week period. A stratified randomization procedure was used to ensure equal numbers of low and high pregnancy anxiety mothers in each randomization group. At three months postpartum, mothers were instructed to collect two saliva samples from their infants on one collection day. Regression analyses revealed that infants of mothers randomized to CBSM group had a larger decline in cortisol throughout the day (steeper diurnal slope) compared to infant of mothers in the AC group; however, this was only true for women with low pregnancy anxiety (R^2=.07, b= 2.35, *p* <.05). These results suggest that prenatal CBSM interventions are potentially effective in regulating infant cortisol patterns.

FRI - 401 Literally Supernatural: Pathways from Religious Commitment to Theological Defensiveness

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

karenza Shepherd*, *Southern Nazarene University* and Anna Harper, *Southern Nazarene University*

Abstract: The purpose of this research was to investigate the relationships between a person's religious commitment and his or her theological orientation. This study investigated two factors that may play a role in the extent to which religious faith serves a security function: belief in the supernatural (Jong, 2012), and a literal interpretation of faith (Duriez, Dezutter, Neyrinck & Hutsebaut, 2007). The university student participants were recruited from two Christian liberal arts universities in the Midwest. Adult participants were recruited via social media and the data from 487 participants were analyzed. The mean age of the participants was 24 (SD =8.9). The majority of participants were White (79.3 %), female (73%), and Christian (90.3%). Most participants had completed some college or associate's degree (63.7%). Participants completed an online survey which included the Religious Commitment Inventory (Worthington et al., 2012), Supernatural Belief Scale (Jong 2012), Orthodoxy (Literal Interpretation) subscale of the Post Critical Belief Scale (Durie et al.,2007), and Defensive Theology Scale (Beck, 2004). Supernatural belief and literal interpretation fully mediated the relationship between religious commitment and theological defensiveness. Assessing multiple dimensions of religious experience is important and helpful to know when working with people in religious settings and with people who have diverse religious beliefs.

FRI - 402 The Role of Acculturative Stress and Mental Health Symptoms Based on Generation Status during Pregnancy in Child Impulsivity

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Jennifer Figueroa*, *California State University San Marcos* and Kimberly D'Anna-Hernandez, *California State University San Marcos*

Abstract: The fetal programming hypothesis suggests that in utero stress may alter development and behavior in children. Impulsivity is an early life behavior often used as a predictor of higher level risk-taking and low academic achievement later in life. As the Mexican population grows, acculturative stress, the stress of adapting to a new culture, becomes a relevant risk factor for perinatal mental health outcomes and may be associated with programming of impulsive behavior. This study aims to address if levels of acculturative stress and maternal mental health symptoms (depression and anxiety) experienced by Mexican American women are associated with child impulsivity. This study also looks at the role of generation status (N=35) in acculturative stress and mental health symptoms when looking at impulsivity. Participants (N=49) completed questionnaires addressing cultural factors and mental health. Impulsivity was assessed using the snack delay episode from the Laboratory Temperament Battery Assessment. Results indicated that acculturative stress was not related to impulsivity (*B*=.000, *SE*=.015, *t*=0.23, *p*=.982). Anxiety did not predict impulsivity (*B*=0.21, *SE*=0.13, *t*=1.639, p=.108). Depression also did not predict impulsivity (*B*=.008, *SE*=0.14, *t*=.576, *p*=.567). A significant relationship was found between anxiety and impulsivity when moderated by generation status (*R*= .4296, *SE*=.0757, *t*=-2.4011, *p*=0.225). Mothers with low generation status and increasing anxiety were more likely to have children with higher impulsivity. This may be due to difficulties of being the first to adapt to a new country of residence with limited social support. Further research should investigate other factors that might be associated with child impulsivity.

FRI - 403 Habituation to an Aversive Olfactory Cue

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Gerardo Sandoval*, *California State University, Fullerton*; Christopher Campbell, *California State University, Fullerton*; Anjum Hussain, *California State University, Fullerton*; Allison R Moulton, *California State University, Fullerton*; Jenan Husain, *California State University, Fullerton*; Justis C Barcelona, *California State University, Fullerton*; Kate T Tanaka, *California State University, Fullerton*; Tim Sechang, *California State University, Fullerton*; Victoria Mallipudi, *California State University, Fullerton* and Adam Roberts, *California State University, Fullerton*

Abstract: The zebrafish model system has great potential to provide valuable insights into the neural basis of behavior due to biological advantages (i.e., translucency) and an extensive set of molecular tools (i.e., optical reporters of neural activity). Despite these great advantages, very little effort has been made to apply this model system to understand learning and memory either at a synaptic or systems-level. Towards this goal, we are searching for simple forms of memory, such as habituation, where an animal learns to not respond to innocuous and repeated stimuli. Therefore, we searched for, and may have found, a form of memory that is elicited by repeated applications of the odorant cadaverine. Cadaverine, an aversive odorant, elicits increased locomotion; repeated applications of it result in habituation of the locomotor response. Further, we have recorded from brain areas that respond to cadaverine to identify the neural circuits that mediate this form of learning.

FRI - 404 Familismo and Language Brokering Experiences Predict Impulsiveness Among High-Achieving Latinx College Students

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Sergio A. Ruvalcaba*, *Department of Cognitive Science, Pomona College* and Guadalupe A. Bacio, *Departments of Psychology and Chicana/o-Latina/o Studies, Pomona College*

Abstract: Immigrant families to the United States often rely on their children's linguistic and cultural proficiencies to navigate their new society (i.e., language brokering). The literature suggests that those who engage in language brokering (LB) endorse a sense of family obligation, a facet of familismo. Family obligation had been found to reduce dimensions of impulsiveness (e.g., risk taking) among Latinx adolescents. This is critical, as impulsiveness entails tendencies to engage in risky maladaptive decision-making that may lead to substance use initiation and risky sexual behaviors. An interplay of familismo, LB experiences, and impulsiveness has yet to be explored, particularly in college students. The current study seeks to investigate if endorsement of familismo—as well as its facets (i.e. support, obligation, and referent)—and LB experiences predict impulsiveness. This study analyzed data from 160 Latinx college students from private liberal arts institutions in Southern California who completed a series of self-report measures on language brokering experiences, familismo, and impulsiveness. Multiple regression analyses revealed that familismo, gender, and LB experiences significantly predicted lack of careful thinking and spontaneous behavior. Further analyses revealed that familial reference and support, but not obligation, guided these relations. Implications for these findings suggest that beliefs regarding family alignment and support may influence decision-making among college students. Additionally, these findings highlight the importance in recognizing and sustaining a dynamic understanding the interplay of several inter- and intra-personal factors when contextualizing the well-being of Latinx young adults.

FRI - 405 A Tale of Two Nations: Perceptions of Psychological Distress in the United States and Costa Rica

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Alyssa Vaughan*, *Southern Nazarene University* and Anna Harper, *Southern Nazarene University*

Abstract: The purpose of this study was to measure differences in the experiences of psychological distress between Americans and Costa Ricans, as well as differences in the perceived acceptability of the Kessler-10 (K-10), a scale designed to measure psychological distress. Although cross-cultural studies have revealed differences in rates of psychological distress, it has been argued that these differences may stem from the use of scales that are not fit for cross-cultural adoption (Dardas, Silva, Noonan, & Simmons, 2018; Kirmayer, 2001).

Given that the K-10 scale incorporates individualistic assumptions, it was hypothesized that Costa Ricans would report lower levels of psychological distress compared to Americans. Furthermore, it was expected that Costa Ricans and Americans would differ in their interpretation of the K-10 items and their perceptions of the scale's acceptability. Finally, it was hypothesized that differences in attitudes regarding individualism and collectivism would be associated with differences in psychological distress and perceived acceptability of the K-10 items.

University students and community adults (N= 159) completed the K-10, Individualism and Collectivism Scale, Acceptability of K-10 Questionnaire, and demographic questions. On average, Costa Ricans reported lower levels of psychological distress and lower perceived acceptability of the K10, compared to Americans. Horizontal individualistic attitudes were negatively correlated with psychological distress scores and acceptability scores, while vertical individualistic attitudes were positively correlated with psychological distress and perceived acceptability.

These findings highlight the importance of assessing the perceived acceptability of psychological constructs before interpreting the results of measures, particularly in settings impacting health diagnosis and treatment.

FRI - 406 An Evaluation of the Effectiveness of Mandated Financial Disclosure Forms

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Natalie R. Verdiguel*, *University of Central Florida*; Xiaoqing Wan, *University of Central Florida* and Nichole R. Lighthall, *University of Central Florida*

Abstract: Form CRS (Client Relationship Summary) is a document mandated by the Securities and Exchange Commission to explain the differences between a broker-dealer and an investment adviser. Previous research has shown most Americans do not understand the difference between the two, and thus cannot make informed decisions about which service best suits their needs. Upon its release, the document drew concerns about whether it would be an effective intervention or further add to paper piles. Past studies on the effects of mandated disclosures had found them to be mostly ineffective. While previous research assessed investors' belief about the effectiveness of Form CRS, no study to date has assessed the forms' objective effectiveness, operationalized as a meaningful change in comprehension and in preference-consistent decisions (PCD). We hypothesized that Form CRS will be ineffective in assisting investors in making informed decisions. In the current study, 615 Mechanical Turk participants were given Form CRS, and were asked to make hypothetical choices between the two services described. Comprehension is assessed by a novel test developed for this study. PCD is operationalized as the consistency of stated preferences and hypothetical choices. Two paired sample t-tests were performed on participants' comprehension and preference consistent decision pre- and post- intervention. Comprehension improved significantly after intervention, but PCD did not. While Form CRS achieved one of its intended purposes by improving comprehension, it fell short of improving decision quality. Our future analysis will assess which populations benefit most from Form CRS by assessing cognitive, age-related, and socio-economic variables.

FRI - 407 How Important Is Expressing Fraction Understanding Consistently across Speech, Gesture, Action and Drawings?

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Christian Palaguachi*, *Northeastern Illinois University*; Yeo Eun (Grace) Yun, *Northeastern Illinois University*; Steven Montalvo, *Northeastern Illinois University*; Ashley Lebron-Vazquez, *University of Illinois, Urbana-Champaign*; Breckie Church, *Northeastern Illinois University*; Shereen Oca Beilstein, *University of Illinois, Urbana-Champaign* and Michelle Perry, *University of Illinois, Urbana-Champaign*

Abstract: The United States is ranked 38th out of 71 countries in the mathematical portion of the PISA. Cognitive barriers in numerical development have prevented many from entering STEM fields, such as students from low SES and minorities. One math concept that is particularly difficult to master is fraction magnitude. Theory suggests that mathematical understanding is reflected in the ability to represent a concept across multiple expressive verbal and nonverbal modalities: *speech, gesture/action,* and *drawings*. Research suggests that the correct understanding of fractions is indicated by whether children understand that fractions are equal parts related to a whole. However, few have examined how children's understanding of fractions is manifested in multiple expressive representations. In this study, we examined 26 video-recorded interviews of children ages 7-10 years explaining their understanding of a particular fraction: *1/4*. Some children were then given the opportunity to express their understanding of fractions through a variety of verbal (speech) and nonverbal (gesture/action and drawings) modalities. Using a standard assessment, we classified children with either high- or low-fraction understanding. We found that children classified as having *high-fraction understanding* were able to express correct fraction ideas consistently across all three expressive modalities. Children with low-fraction understanding failed to expressed correct ideas across modalities; expressing incorrect ideas in some while correct ideas in other modalities. This study provides support that in order to help children understand fractions, teachers need to find a way to enforce the integration of fraction concepts across multiple expressive representations.

FRI - 408 Speech Gesture Mismatch in Fraction Understanding May Reflect Knowledge in Transition

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Steven Montalvo*, *Northeastern Illinois University*; Yeo Eun (Grace) Yun, *Northeastern Illinois University*; Christian Palaguachi, *Northeastern Illinois University*; Ashley Lebron-Vazquez, *University of Illinois, Urbana-Champaign*; Breckie Church, *Northeastern Illinois University*; Shereen Oca Beilstein, *University of Illinois, Urbana-Champaign* and Michelle Perry, *University of Illinois, Urbana-Champaign*

Abstract: Previous studies on mathematical learning have looked at how conceptual understanding can be conveyed differently between verbal and nonverbal expression (a speech-gesture mismatch). Production of *nonverbal correct* ideas that children produce along with *verbal incorrect* ideas has been shown to index transitional understanding and *readiness to learn*. However, this has not been explored in fraction learning. This present research attempted to identify this pattern with children who are learning about fraction magnitudes. We hypothesized that some children convey correct understanding, *but only through nonverbal expression*, and that this nonverbal expression does not indicate fully advanced comprehension. Video-recorded interviews were conducted with children ages 7-10 to assess their understanding of fractions. While verbalizing, they spontaneously used gesture to express fraction ideas. We then examined whether correct fraction understanding *was only conveyed nonverbally* or was *conveyed both verbally and nonverbally*. We tested children's prior knowledge of fractions using a 10-item standardized test. Preliminary analysis found that 60% of our sample expressed correct understanding in both speech and gesture (correct matchers), while 40% conveyed correct understanding only through nonverbal expression (expressing incorrect understanding in speech; mismatchers). Correct matchers scored an average of 8.67 correct while mismatchers scored an average of 2.75. Results suggest that some children display inconsistency in their fraction understanding across verbal and nonverbal expressions; correct understanding being expressed only nonverbally. Speech-gesture mismatches may signal that a child is in transition towards acquiring correct fraction understanding as has been shown in prior research.

FRI - 410 Free Memory Screening As a Strategy for Hispanic Recruitment in Dementia Research

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Amanda Calcetas*, *University of California, San Diego*; Kimberly Lopez, *University of California, San Diego*; Cynthia Avalos, *University of California, San Diego*; David Salmon, *University of California, San Diego* and Hector Gonzalez, *University of California, San Diego*

Abstract: Meeting recruitment and enrollment objectives for Hispanic populations has been a continuing struggle for clinical researchers. Many obstacles hinder enrollment of potential participants such as degree of interest, awareness of resources, and unwillingness to participate in study procedures. To gain a better perspective of and adapt to these challenges, we will assess what proportion of the Hispanic community that participates in memory screening events express interest in research. The present study will examine the demographic of the last 2 years of recruitment events and factors that play a role in study participation. Memory screenings occur on an ongoing basis throughout the year at community-based centers. Undergraduate students and psychometrists from the Shiley-Marcos Alzheimer's Disease Center visit these centers and administer the Consortium to Establish a Registry for Alzheimer's Disease (CERAD) and the Mini-Mental State Exam (MMSE). Staff also reviews screening results, determined from appropriate test normative data, with participants and provides information regarding research studies to those interested. So far, 222 participants were screened at off-site memory screening events over the course of 2018 and 2019. We hope to assess the most frequent reason individuals decline to enroll in research studies as well as pinpoint other obstacles Hispanic populations may face with research involvement. Overall, these memory screening day events are an opportunity to inform individuals about AD, learn about their concerns and attitudes towards research, and potentially recruit them into ongoing research projects.

FRI - 411 The Relationship between Stressors and Depression Among Latino Sexual Minority Men

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

David Rivera*, *San Diego State University* and Aaron Blashill, *San Diego State University*

Abstract: Childhood sexual abuse (CSA), intimate partner violence (IPV), and internalized homophobia (IH) are common stressors experienced by sexual minority men (SMM) associated with depression. Latino SMM who experience various types of stressors may experience greater depression as a result of their potential additive effect. The current study aimed to examine the association between experienced stressors and depression among Latino SMM. Participants were 151 Latino SMM aged 18-29 residing in the San Diego County. The PHQ-8 was used to measure depression. The HITS Screening Tool was used to measure IPV. The SIHS Public Identification as Gay subscale was used to measure IH. Two items were used to assess for CSA. Separate binary variables were computed for the PHQ-8, HITS, IPV, SIH subscale, and CSA items using their respective cut scores. Stressors were measured using the sum of binary variables: HITS, CSA, and SIHS. A logistic regression was conducted using stressors as the predictor variable and binary PHQ-8 as the criterion variable. Results revealed a significant model fit (χ^2 = 4.736, p = .030, Nagelkerke R^2 = .041). Greater stressor scores were significantly associated with greater odds of major depression (B = .432, Wald = 4.562, OR = 1.54 [95% CI 1.04, 2.29], p = .033). Experiencing various types of stressors may be a risk factor for greater depression among Latino SMM. Clinicians may wish to assess for history of various types of stressors to identify Latino SMM who may be at an elevated risk for depression.

FRI - 412 Significance of White Matter Hyperintensities in Alzheimer's Disease

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Da Yeoun Moon*, *San Diego State University* and Laura Zahodne, *University of Michigan-Ann Arbor*

Abstract: White matter hyperintensities (WMH) are lesions in the white matter assumed to be of vascular origin. Highly prevalent in brains of non-demented elderly individuals, past studies have linked WMH with increased risk of stroke, cognitive decline, and mortality. This review aimed to summarize the current state of literature on the contribution of WMH to Alzheimer's disease (AD) etiology, and examine differential regional effects. WMH are visualized as an increased signal intensity on T2-weighted fluid attenuation inversion recovery (FLAIR) scans. Quantification of WMH can be achieved using visual rating, semi-automated methods, or fully automated methods. The clinical contribution of WMH to AD pathology has been examined via different study designs (e.g., cross-sectional, longitudinal) in different populations (e.g., older adults with and without dementia). Current literature supports a potential role for WMH in clinical AD, evidenced by significantly greater WMH burden in AD, particularly in parietal and periventricular regions. Although the literature is limited, there is research supporting interactive relationship between WMH and AD biomarkers. There are limitations of existing studies such as inconsistent operationalization of WMH, heterogeneous AD diagnostic criteria, and lack of representative and diverse samples. Furthermore, studies vary in inclusion of relevant covariates, such as vascular risk factors. Future researchers should consider tracking progression of WMH in high-risk AD populations, incorporating standardized measures of relevant covariates.

FRI - 413 Characterization of the Effects of Systemically Increasing Dopamine, Serotonin, and Noradrenaline Levels on the Valuation of Reward Vs. Avoidance

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Jonté Roberts*, *University of Colorado Denver*; Oniza Chaman, *University of Colorado Denver* and Erik Oleson, *University of Colorado Denver*

Abstract: Optimal behavior and overall survival require obtaining highly-valued outcomes from our environment. These action-outcome situations are often driven by either the pursuit of reward or the avoidance of harm. The three primary monoamine neurotransmitter systems that modulate such motivated behaviors are dopamine (DA), serotonin (5-HT), and noradrenaline (NA). Of these, the mesolimbic DA system is generally considered to be a reward pathway. However, it is becoming increasingly evident that DA release events also process and influence aversively-motivated behavior. Combining operant behavior with a behavioral economic framework to model behavioral changes in response to increasing price (i.e., lever responses/outcome magnitude), we recently demonstrated that DA release events represent avoidance value and modify the price rats will pay to avoid electrical foot-shock. Using a similar approach, my current project will perform a broader characterization of the primary ascending monoamine systems in the valuation of reward vs. avoidance. We will pharmacologically target these systems using the selective reuptake inhibitors GBR-12909, fluoxetine, and desipramine for DA, 5-HT, and NA respectively. Based on our previous findings and the existing literature, we predict; GBR-12909 will increase reward and avoidance valuation, fluoxetine will increase avoidance value but decrease reward value, and desipramine will decrease avoidance value without affecting reward. Investigating whether these pathways produce distinct effects on reward vs. avoidance valuation will provide novel insight into how the brain controls these fundamental aspects of behavior. The implications of this work may also advance our understanding of major psychiatric conditions such as depression and drug addiction.

FRI - 414 Role of the Endocannabinoid System in the Lateral Habenula on Cognitive Flexibility

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Grace Lim*, *Washington State University* and Ryan McLaughlin, *Washington State University*

Abstract: Over 350 million people are affected by major depression on a global scale according to the World Health Organization with an increasing economic impact of over $210 billion annually with a growth of 21.5% since 2005. The ability to switch behaviors or strategies when faced with chronic stress is an important determinant to the susceptibility and longevity of depression within people, also referred to as cognitive flexibility. The objective of this proposed study is to analyze the effects of the endogenous cannabinoid (ECB) system on cognitive flexibility through the lateral habenula. Cannula implant surgeries will be conducted on rats to input antagonist or agonist drugs into the brain. Behavioral tests will be conducted on rats to examine whether these manipulations will promote or deter cognitive flexibility.

FRI - 415 Amantadine Confers Significant Motor and Cognitive Benefits after Experimental Brain Trauma

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Adaora Okigbo*, *University of Pittsburgh*; Brittany Royes, *University of Pittsburgh*; Corina Bondi, *Safar Center for Resuscitation Research*; Jeffrey Cheng, *University of Pittsburgh Physical Medicine & Rehabilitation Safar Center for Resuscitation Research University of Pittsburgh* and Anthony Kline, *UPMC Children's Hospital of Pittsburgh Safar Center for Resuscitation Research*

Abstract: Several pharmacotherapies have been evaluated after experimental traumatic brain injury (TBI). Amantadine (AMT) has shown potential for clinical efficacy, but the few studies on its effectiveness have been mixed. One possibility for the diverse effects is that suboptimal dosing, due to the evaluation of only one dose, is often evaluated. Therefore, the goal of the current study was to conduct a dose response of AMT after TBI to determine an optimal behavioral benefit. Isoflurane-anesthetized adult male rats received either a controlled cortical impact of moderate severity or sham injury and then were randomly assigned to receive once daily intraperitoneally injections of AMT (10, 20, or 40 mg/kg) or saline vehicle (VEH, 1 mL/kg) commencing 24 hours after injury for 19 days. Motor and cognitive function were assessed on post-operative days 1-5 and 14-19, respectively. There were no statistical differences among the sham groups treated with AMT or VEH so the data were pooled. AMT (20 mg/kg) facilitated beam-balance recovery and spatial learning compared to VEH-treated controls ($p < 0.05$). No other doses of AMT were effective. These results indicate that dosing should be carefully considered when assessing the effects of pharmacotherapies after TBI, such that potential benefits are not unwillingly missed.

FRI - 416 Repurposing of N-Acetylcysteine: Determining the Effects of N-Acetylcysteine Following Chronic Unpredictable Stress in Zebrafish (*Danio rerio)*

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Emma DiPasquo*, *Indiana University Northwest* and Maureen Rutherford, *Indiana University Northwest*

Abstract: Although there have been drastic advancements in the understanding of the pathophysiology of anxiety disorders, current pharmacological treatments are limited in efficacy and sometimes induce serious side effects. Dysfunction of physiological stress responses may trigger or heighten the development of neuropsychiatric disorders, specifically anxiety. There is considerable data implicating glutamate in the pathophysiology of anxiety disorders, but there are no current treatment options for anxiety that specifically target the glutamatergic system. To better understand anxiety disorders and develop effective treatments for these conditions, it is important to understand the glutamatergic regulation of physiological stress responses. N-acetylcysteine (NAC) is a glutathione precursor which modulates glutamatergic transmission and shows promise as a treatment for anxiety disorders. However, it is unknown whether the clinical usefulness of the drug is due to regulation of stress hormones. The zebrafish exhibits translational relevance to humans regarding neurochemistry and brain structure, including an evolutionary conserved stress hormone response. Zebrafish in this study were exposed to chronic unpredictable stress for one week and either treated with or without NAC during that week. Behavioral responses in the light-dark test and cortisol levels were measured and compared to non-stressed controls. We hypothesized that chronic unpredictable stress will increase anxiety-like behavior and decrease levels of whole-body cortisol. We expected a reduction in anxiety-like behavior and a normalization of whole-body cortisol levels when zebrafish were treated chronically with NAC following chronic unpredictable stress in zebrafish.

FRI - 417 Familism and Self-Efficacy of Mexican-American Women in a Weight-Loss Intervention

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Lesley Guareña*, *University of California San Diego* and Becky Marquez, *University of California San Diego*

Abstract: Culture influences all aspects of daily life, including dietary and physical activity behaviors. Specifically, Mexican culture values familism, or the cultural tendency in which individuals prioritize the needs of the family unit as opposed to personal needs (Lugo Steidel & Conteras, 2003). Self-efficacy refers to an individual's sense of confidence in relation to their ability to engage in physical activity and dietary changes necessary for weight loss. This research study assessed acculturation, familism, and self-efficacy in relation to weight-management behaviors in Mexican or Mexican-American adult mothers and daughters over the course of a 16-week weight-loss program. Participants completed a series of self-report psychosocial measures assessing acculturation, familism and self-efficacy prior to and following the intervention. Results demonstrated a significantly higher level of acculturation for daughters in comparison to mothers before the intervention, but no significant differences in familism prior to the intervention, nor a significant difference of self-efficacy post-intervention. In addition, the relationship between familism and self-efficacy was not statistically significant, however, the data trend suggests a positive relationship between both factors. These findings suggest that weight-loss interventions should assess and address cultural factors such as familism and acculturation as they are not homogenous amongst Mexican-American females in the US, and could potentially influence attitudes toward weight management behaviors. Further investigating these cultural factors with a larger sample size could yield more conclusive results for informing culturally salient weight-loss interventions in this at-risk population.

FRI - 418 Exploring the Pathway Model Connecting Water and Education Using Conditional Probability Analysis

Discipline: Psychology & Social Sciences

Subdiscipline: Other Psychology & Social Sciences

Elijah Vela*, *New Mexico State University*; Margie Vela, *New Mexico State University* and Paul Gutierrez, *New Mexico State University*

Abstract: Many communities along the US- Mexico border lack infrastructure to deliver treated, potable water to its community members. In this study quasi-youth participatory action research was used to examine the connection between lack of access to piped water, educational attainment, and access to healthcare, as described in “Determining Pathways and Connections Between Access to Water and High School Noncompletion Rates for Communities Along the U.S.–Mexico Border” (Vela et al., 2018). This study uses conditional probability analysis to examine the relationship between the significant variables, identified through a chi-square test of association, and the respondents’ source of drinking water. The results suggest that certain common behaviors displayed by the community members can be inferred from the source of their drinking water. This information is useful for informing future policy decisions at the school level, for improving educational programs, and the state level and federal level, for improving federal programs.

Vela, M. R., Lind, S. R., & Paul, G. H. (2018). Determining Pathways and Connections Between Access to Water and High School Noncompletion Rates for Communities Along the U.S.–Mexico Border. Journal of Social Change, 10(1), 105-117. *https://doi.org/10.5590/JOSC*

FRI - 419 The Impact of Race and Gender on Potential Jurors Willingness to Discard a Recanted Confession

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Jade Moore*, *California Lutheran University*; Amanda ElBassiouny, *California Lutheran University* and Julie Kuehnel, *California Lutheran University*

Abstract: Determining if the criminal justice system is fair or biased toward certain race-ethnicities and genders is a pressing issue in today’s legal system. This research will be examining the impact of the defendant’s race-ethnicity and gender on a potential juror’s willingness to discard a confession that has been recanted by a defendant. It is hypothesized that potential jurors are more likely to discard a confession recanted by a woman versus a male and a Caucasian versus Black or Hispanic individuals. It is expected that the race-ethnicity and gender of a defendant will interact to influence the willingness of a potential juror to disregard a confession recanted by a defendant. Participants will read a vignette describing a situation where a defendant who is either male or female and either Caucasian, Black, or Hispanic, had confessed to a crime during interrogation, but later has recanted that confession. After reading the vignette the participants will respond to a survey which will determine if the participant is willing to discard the confession, as well as if the participant would still find the defendant guilty. After responding to these questions’ participants will rank how confident they are with their decisions. As false confessions are a reality in a legal system which has shown controversial levels of justice, possibly resulting in wrongful convictions, it is imperative that we understand how gender and race-ethnicity may bias potential jurors for or against a defendant who has recanted a confession (Scheck, Neufeld, & Dwyer, 2000).

FRI - 420 Undergraduate Students “Graduate” in Self-Efficacy in the Postgraduate School Application Process

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Aliaa Eldabli*, *Aurora University*; Meaghan Rowe-Johnson, *Aurora University* and Stephanie I.C. Mata-Gamboa, *Aurora University*

Abstract: Applying to graduate school requires a plethora of tasks, including creating a résumé, obtaining letters of recommendation, completing standardized tests, preparing for interviews, and writing a personal statement. Knowledge of these tasks can be limited. For example, past research has found that minorities, first-generation students, and women may not have access to pertinent information about the postgraduate application process due to lack of campus resources and/or informants, or socioeconomic barriers (Ramirez, 2011). To counteract these barriers, examine how students evaluate their own preparation for this process, and to close this gap of knowledge for undergraduate students, we hypothesized that curriculum intervention that provides in-depth information on the previously-mentioned tasks would increase undergraduate students' self-efficacy in the postgraduate school application process. Curriculum interventions were based on Social Cognitive Career Theory, and a Postgraduate School Application Self-Efficacy Scale was curated and distributed to undergraduate students at a Midwest university during their attendance to four “Applying to Graduate School” workshops. Pre- and post-test scores suggested that there was an increased trend in self-efficacy levels amongst students after attendance to workshops on the graduate school search (Pre-Test $M = 58.71$, $SD = 16.76$; Post-Test $M = 73.60$, $SD = 6.80$), résumé construction (Pre-Test $M = 30.90$, $SD = 10.29$; Post-Test $M = 39.67$, $SD = 5.43$), and GRE preparation (Pre-Test $M = 26.25$, $SD = 5.68$; Post-Test $M = 32.00$, $SD = 4.08$). Future research is necessary to explore what specific factors influence undergraduate students’ abilities to ascend in higher education.

FRI - 421 The Role of Objective and Subjective Social Status Disparities on Anxiety Amongfreshmen Dormitory Roommates: The Moderating Role of University Belonging

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Lucy Gonzalez*, *California State University, Northridge*; Karina Barragan, *California State University, Northridge* and Yolanda Vasquez-Salgado, *California State University Northridge*

Abstract: Research has demonstrated the importance of social status (SS) on college students’ mental health (Salami & Walker, 2014; Eisenberg et al., 2010). The purpose of our study was to extend prior work by examining whether objective and subjective SS disparities among dormitory roommates relate to anxiety experienced during the first year of college. We also examined whether these relations would be moderated by university belonging. We hypothesized that subjective measures of SS disparities, particularly, those that involved a comparison between one’s perceived SS to that of one’s roommate, would be stronger predictors of anxiety than objective measures. We explored whether the strength of these relations varied depending on whether one had high or low university belonging. Participants completed an online survey at the end of their first year in college ($N = 76$, $M_{age} = 18.68$). All lived in a dormitory where at least one roommate was a first-generation college student. Our results indicated that objective and subjective SS disparities significantly related to anxiety (r’s: .24 to .33, $p < .05$). In addition, when examined by university belonging, among those with low belonging, parental education, a control variable, was the only predictor of anxiety ($b = -.12$, $p = .001$). However, among those with high belonging, subjective SS disparities was the strongest predictor ($b = .15$, $p = .03$). These findings suggest that objective and subjective SS disparities among dormitory roommates impact the mental health of students during the college transition and university belonging determines the extent of these relations.

FRI - 422 The Relationship between *Respeto* and Family Functioning Among the Latinx Millennial Generation

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Jennifer Rufino*, *Pomona College*; Jesus A Valencia Medina, *Pomona College*; Jennifer Aminta Acevedo, *Pomona College Department of Psychology* and Guadalupe Bacio, *Departments of Psychology and Chicana/o-Latina/o Studies, Pomona College*

Abstract: Studies suggest that the traditional Latinx cultural value of *respeto* (i.e., the expectation for family members to show deference and obedience to elders) is associated with higher family cohesion and lower family conflict. However, gender differences remain unclear. This study examined the relationship between *respeto* and family functioning among Latinx young adults by gender. To this end, we conducted a secondary analysis of a 2017 study on Latinx millennials, ages 18-35. Participants completed a series of validated scales of *respeto* and family functioning. We predicted that Latinos would endorse lower levels of *respeto* compared to Latinas and this differing levels of *respeto* would result in contrasting correlations between *respeto* and family functioning subscales (i.e., cohesion and conflict). An

independent samples t-test showed that participants significantly differed in *respeto* by gender. Contrary to predictions, Latinos reported higher levels of *respeto* on average compared to Latinas. As expected, *respeto* was positively correlated with cohesion across gender. However, *respeto* was positively correlated with family conflict for women, but not men. Findings suggest that there are gender differences in Latinx endorsement of *respeto* among Latinx young adults and its relation to family functioning. Particularly, *respeto* among millennial Latinas did not decrease family conflict. This could potentially be explained by traditional gender roles, negative aspects of *marianismo*, and the concept of feminism. Further research is necessary to understand whether and how the transmission of traditional values and expectations to Latinx younger family members may impact them differently based on their gender.

FRI - 423 Swiping to Relieve Stress? Understanding Tinder Use Among Undergraduates

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Zamzam Hufane*, *Washington State University* and Alexander Spradlin, *Washington State University*

Abstract: Mobile online dating applications have become popular among young adults seeking romantic partners, physical intimacy, and friendship. Tinder more specifically has quickly become one of the most popular mobile dating application used to meet people within the same proximity. To date, however, only a handful of studies have examined the types of people using Tinder, their reasons for doing so, and the role of negative affect in this relationship. Using a large sample of undergraduates at a major US university, the purpose of the present study is to investigate the role that stress and stress management play in driving Tinder use. Participants will complete multiple online self-report questionnaires regarding their frequency and quantity of Tinder use, their Tinder use motives, their Big 5 personality traits, and their levels of stress, depression, and anxiety. *We hypothesize that people with higher levels of stress over the past week will also be more motivated to use Tinder to cope with that stress, leading to overall greater Tinder usage. We also hypothesize that this relationship will be moderated by the personality trait of neuroticism, such that those with higher levels of neuroticism will show a stronger indirect effect of stress on Tinder use via coping motives.* These hypothesis will help us further investigate how validation on dating applications associate with stress and if the relationship between stress and dating app usage is moderated by specific motives. These findings will help us gain a better perspective on the popularity/use of Tinder amongst emerging young adults.

FRI - 424 Exploring the Pathway Model Connecting Water and Education in West Texas Colonias Using Quasi-Youth Participatory Action Research; A Mixed Methods Approach

Discipline: Psychology & Social Sciences
Subdiscipline: Sociology

Riva Silver*, *New Mexico State University*; Margie Vela, *New Mexico State University* and Paul Gutierrez, *New Mexico State University*

Abstract: Water is a critical resource for households and communities, and affects a broad range of “quality of life” standards. This study explores the connection between water infrastructure and high school graduation rates in West Texas Colonias through quasi-Youth Participatory Action Research. Using photographs and narratives submitted by students at a West Texas high school, the researchers in this study identified and examined common infrastructure issues found in Colonias along the U.S. Mexico border. The researchers repeatedly analyzed the student submissions to categorize the severity of water infrastructure issues in this West Texas Colonia, building on The Pathway Model Connecting Water and Education (Vela et. al., 2018), established previously. The student’s qualitative data and results identify and correspond to the The Pathway Diagram, suggesting that improved water infrastructure increases quality of life and education which promotes higher highschool graduation rates.

FRI - 425 Analyzing the Impact of Professional Development on Peer-Led Learning Groups in Reducing Transfer Student Attrition in a Large Enrollment Introductory Biology Class

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Tamara Montes*, *University of Alabama at Birmingham*; Samiksha Raut, *University of Alabama at Birmingham*; James Boyett, *University of Alabama at Birmingham*; Sebastian Schormann, *University of Alabama at Birmingham*; David Verhine, *University of Alabama at Birmingham* and Gabrielle Richards, *University of Alabama at Birmingham*

Abstract: National calls for undergraduate education reform have prompted the need towards active engagement practices in the classroom. Utilizing active-learning practices help to decrease the attrition in Science, Technology, Engineering and Mathematics (STEM) gateway courses. Furthermore, peer-learning groups have been recognized to play a critical role in implementing active-learning practices in the classroom and beyond. Very few studies to date have explored the impact of these peer-led sessions in the light of pedagogical training imparted to them and also how these sessions impact the performance of the transfer student population. A mixed methods approach (n=30) will be utilized to assess the efficacy of this professional training and how it impacts the class performance of the transfer student population. We hope that findings from this study will enable us to make a recommendation to other educators on training their learning assistants in evidence-based practices as an effective way to reduce transfer student STEM attrition from gateway courses like freshman introductory biology classes.

FRI - 426 Designing a Water Meter to Track Water Consumption in Real Time to Visualize Water Usage

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Sheri Marzan*, *University of Hawaiʻi: Kapiʻolani Community College* and Aaron Hanai, *Kapiolani Community College*

Abstract: The University of Hawaʻi’ system’s goal is to be a “net-zero” energy by 2035, but does not currently consider water conservation as part of the plan. Hawaiʻi gets drinking water from underground aquifers, due to growing populations, the lack water conservation efforts can make communities susceptible to water droughts Conserving our water starts with understanding how much water is being used and for what purpose. Current water meters focus on detecting appliance failure in water systems, but are cost prohibitive and do not track usage overtime. The objective is to build a cost-efficient water monitor that records water from specific water sources onto a website to gather water consumption data at Kapiʻolani Community College. The device utilizes a flow meter that is attached to a faucet and operated by an Arduino microcontroller that is connected to a Raspberry Pi computer. The Arduino is programmed to constantly measure the amount of water going through the meter, and the data is sent to the Pi that then uploads the information to a server that can be accessed by on a website via NodeRED. Tests were run to confirm that the flow meter is accurately collecting water flow and uploaded in real time.Currently, the website tracks the hourly water consumption of one lab sink and compiles the data over months. Tracking this data over time is necessary in order to develop a more specific plan to conserve water looking at its usage. Future work involves installing more meters understand water consumption on campus.

FRI - 428 What’s in a Story: Bridging Indigenous and Western Science in the Eel River Watershed

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Leslie Hutchins*, *UC Berkeley* and Allison O'Dowd, *Humboldt State University*

Abstract: Watershed management throughout California commonly leaves out perspectives from tribal communities. The Eel River basin, the third largest in the State of California, is exemplary of this paradigm. The Upper Mainstem of the Eel is host to the Potter Valley Project, a pair of dams that divert a significant portion of water flow from the Eel River, which has significantly impacted the livelihoods of tribal members belonging to the Round Valley Indian Tribes (RVIT). A total of twenty microfilms housed at the Bancroft Library Archives were analyzed. The microfilms contained oral histories and stories collected from tribal elders in the Round Valley during the 1930s. Any content within the microfilms related to the Eel River, salmonids, or hydrology was scanned and transcribed. Interpretations of the knowledge found within stories were then completed by the author and tribal elders. Transcribed stories, their interpretation, and excerpts from Western science stream ecology journal articles, were then analyzed for common themes. A total of 11 stories and their interpretations were found to have significant overlap (75% of the stories content) with an excerpt from at least one Western science journal article. Instances of knowledge from Indigenous science and Western science exceeded one another, such as species life history traits. From these results, a conceptual framework highlighting how bio-cultural management could take place in the Eel River watershed was created. The results of this study highlight the depth of ecological knowledge resource managers could gain by integrating all perspectives in a watershed.

FRI - 429 Optimizing the PCR Clean-up Method for 18s Amplicons Generated from Phytoplankton Samples Collected in Bellingham Bay

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Tamisha Yazzie*, *Northwest Indian College*; Rachael Mallon, *Northwest Indian College* and Rachel Arnold, *Northwest Indian College*

Abstract: Phytoplankton are the building blocks for the marine food web. These ecosystems are dynamic as they vary on multiple time scales and are influenced by many physical parameters. A massive reproduction of phytoplankton (bloom) can be instigated by natural biological processes and have been occurring with greater frequency with an increase in anthropogenic influence. Some blooms are known as harmful algal blooms (HABs), which have deleterious effects on the larger ecosystem and have been more frequent in recent years due to climate change and/or human influence.

HABs greatly affect the marine ecosystem of the Pacific Northwest; Native communities rely on the marine ecosystem and the effects of HABs (closures of shellfish hatcheries, fisheries, and traditional gathering grounds) have a significant impact on Coastal tribes of Washington State. These culturally and ecologically relevant marine food webs are heavily influenced by the dynamic nature of phytoplankton populations, which warrants frequent monitoring. To describe the community structure of phytoplankton in Bellingham Bay, water samples were collected weekly from the surface and a depth of 24m at the Se'lhaem Buoy. The small ribosomal subunit (a marker gene for species, 18S) was amplified using PCR. The primary goal of this study is to compare the effectiveness of PCR clean-up kit (Qiagen) to a bead clean-up (Ampure XP) method. Samples were collected in duplicate to compare the quantity and quality of PCR amplicons following the cleaning process. Optimizing PCR clean-up provides a more efficient protocol for future projects and more accurate sequence reads for downstream analysis.

FRI - 434 The Impact of Environmental Cues on Anadromous Fish Passage through the Island Farm Weir Fish Ladder

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Candace Narvaez*, *Pennsylvania State University* and Olaf Jensen, *Rutgers University*

Abstract: Mid-Atlantic populations of River herring and American shad have declined precipitously in recent years. With over 1,700 dams in New Jersey, barriers to spawning migration are one of the most significant impediments to the restoration of river herring and shad populations in the state. American shad and River herring serve as ecologically important prey species for large-mouthed bass, catfish, striped bass, small-mouthed bass, trout, and salmon. This study aims to determine the effects of human impediments on anadromous fish spawning migration in the Raritan River by examining various environmental cues. Temperature data, passage times through the Island Farm Weir Fish Passage, and water discharge data will be analyzed using an R programming package. Correlation between temperature and average species passage rates, water discharge and average species passage rates, temperature and presence of anadromous fish species, and discharge and anadromous fish species will be investigated using various statistical analysis methods. We expect that rising annual temperatures will have the greatest impact on the timing of anadromous fish spawning migration while high discharge rates may impact movement through the fish ladder. Furthermore, we expect that water discharge will not impact migration. Warming temperatures could result in changes in temporal and spatial distributions for anadromous fish thus causing shifts in the timing of spawning migration. These changes could potentially disrupt critical predator-prey interactions and impact economically and ecologically significant fishery stocks.

FRI - 500 Uncoding Comparable Morphologies: Using Molecular Identification to Test a Morphological Key for Two important Marine Sportfishes

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Allyson C. Sawkins*, *Scripps Institution of Oceanography, University of California, San Diego*; Erica T. Jarvis Mason, *Scripps Institution of Oceanography, University of California, San Diego*; Andrew R. Thompson, *National Oceanic and Atmospheric Administration* and Brice X. Semmens, *Scripps Institution of Oceanography, University of California, San Diego*

Abstract: Barred Sand Bass (*Paralabrax nebulifer*) and Kelp Bass (*Paralabrax clathratus*), together ranked as one of the most important recreational fisheries in southern California for nearly half a century, but dramatic decreases in catch since 2003 have led to investigations into the cause of their decline. Fish larvae data are often used to glean insight into the population dynamics of a species by providing information on adult population sizes and good and bad recruitment years. However, these data are not available to the species level for the basses because the larvae are difficult to morphologically identify. In this study we will test whether a "morphological key" can be configured using a combination of morphology and molecular identification (genetics) on a subset of California Cooperative Oceanic Fisheries Investigations (CalCOFI) ichthyoplankton samples collected in southern California over the past 67 years. CalCOFI samples prior to 1997 are preserved in formalin (DNA-degrading) rather than ethanol; thus prohibiting genetic testing. Using ethanol-preserved samples collected post-1996 and morphometric data on individual larva, we will test whether specific morphological characteristics are key diagnostics for each bass species. If successful, the morphological key could then be applied to the formalin-preserved samples (1951-1996), allowing better resolution in morphology-based species assignment without the need for expensive and lab intensive DNA techniques. Ultimately, species resolution of the CalCOFI samples will allow us to leverage 67-years of *Paralabrax* larvae abundance to better understand the population dynamics of these important gamefishes.

FRI - 501 Does Shading By Cordgrass Reduce Heat Stress in Ribbed Mussels in a Local Salt Marsh?

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Asia Watson*, *Georgia Southern University*; Jody Erber, *Georgia Southern University* and Sophie George, *Georgia Southern University*

Abstract: Rising temperatures and increasing drought frequency in the South Eastern United States is affecting marsh health. Recent studies indicate that in the presence of ribbed mussels, *Geukensia demissa*, salt marsh recovery can take as little as 10 years versus 100 years without them. Less is known on how these mussels are responding to increasing temperatures. Mussels can form very large aggregates (mounds) at the base of cordgrass (*Spartina alterniflora)* stems. We hypothesize that mussel temperatures will be lower and their abundance higher on mounds with tall cordgrass and in the middle than at the edge of these mounds where cordgrass may be absent. Eight large mounds, four with cordgrass height ≤ 40cm (less shade) and four with cordgrass ≥ 60cm (shaded) were flagged in the mid-zone of a saltmarsh at Tybee Island, Georgia. Mussel abundance and mussel temperatures were monitored in the middle and edge of each mound. Results revealed significantly higher mussel abundance on mounds with tall cordgrass (100-173 mussels/mound) than on those with short cordgrass (51-132 mussels/mound). Mussels living at the edge of mounds had significantly higher temperatures regardless of whether mounds were shaded or less shaded. Mussel temperatures were significantly lower for those living in the middle of mounds with shade than those at the edge of mounds with less shade. This study reveals the importance of cordgrass in providing shade and reducing possible heat stress in ribbed mussels.

FRI - 502 Water Column Ocean Acidification Along the California Coast and Biological Impacts Using Case-Bling Model

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Treasure Warren*, *University of California, Davis*; Brendan Carter, *University of Washington*; Adrienne Sutton, *National Oceanic and Atmospheric Administration* and Sophie Chu, *National Oceanic and Atmospheric Administration*

Abstract: The ocean absorbs CO_2 from the atmosphere, resulting in a decrease in pH known as ocean acidification (OA). A decrease in aragonite saturation state (Ωarag), due to OA, makes larval *Mytilus californianus* shells fragile and susceptible to crushing. The threshold of Ωarag was found to be 1.8 for eight-day old larvae by Gaylord et al. 2011. If ocean acidification continues at projected rates, resulting in a decrease of 0.008 Ωarag per year, *Mytilus californianus* larvae will be susceptible at all depths by 2027. This study focuses on the relationship of pH and Ωarag to OA at the California Current Ecosystem (CCE2) mooring site, using the California State Estimate (CASE-BLING) Model. Discrete bottle dissolved inorganic carbon and total alkalinity data, from CalCOFI rosette bottles, were used to calculate pH and Ωarag using CO2Sys. These calculations were compared to the CASE-BLING model data using Bartlett's Test. P-values of 7.17×10^{-7} and 0.243 for the surface and sub-surface output, respectively, show no difference statistically between the bottle data and the model output. A twenty-year projection of the model output resulted in an Ωarag decrease below the crushing threshold, during April through July, for larvae at all depths. The threshold is surpassed for all larvae below fifty meters for the entire year. If ocean acidification continues at these projected rates, the decrease in Ωarag will negatively affect the *Mytilus californianus* population, making it hard to survive larval stages in the next twenty years.

FRI - 503 Ice Melt, Low Salinity Events, Variation in Larval Form, and Particle Capture in *Pisaster Ochraceus* (Asteroidea) Larvae

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Sophie George, *Georgia Southern University* and Eric Navarro*, *Washington State University*

Abstract: This is the first study to document the possible effects of low salinity waters on particle capture by echinoderm larvae. In recent years, low salinity events characterized by high temperatures (18-23°C) and low salinity waters (20-22‰), have increased in the Salish Sea, a semi-enclosed estuary in the Pacific Northwest. We hypothesized that because seastars are stenohaline osmocomformers, their larvae will be unable to capitalize on high phytoplankton abundance associated with low salinity events. We also hypothesized a strong link between salinity–induced morphological changes and larval feeding. To address these hypotheses, low salinity events were simulated in the laboratory. Five salinity treatments with seven larval ages were tested for the seastar *Pisaster ochraceus*. For all trials, larvae were fed the alga *Isochrysis galbana*. Surprisingly, *Pisaster* larvae regardless of age captured algal particles in low salinity waters at similar rates and in some cases, higher rates than the controls. However, *Pisaster* larvae captured very few particles when returned to 30‰ after a low salinity event. Principal component analysis revealed that salinity-induced morphological changes did not always have a negative effect on larval feeding. Due to the ability to vary their morphology, larvae may be able to feed effectively in the water column regardless of varying environmental conditions (salinity and temperature) in the Salish Sea. However, continuous interruption of larval feeding by low salinity events could be deleterious. Larval development could be prolonged for months exposing them to increased risk of predation.

FRI - 504 The Implications of *ATP7B* in Cellular Proliferation of Hepatocellular Carcinoma

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Hai Pham*, *University of Houston*; Clavia Ruth Wooton-Kee, *Baylor College of Medicine* and David Moore, *Baylor College of Medicine*

Abstract: Wilson's disease (WD) is an autosomal recessive disorder disrupting copper metabolism, resulting in clinical symptoms of steatosis, cirrhosis, and hepatic inflammation. WD is caused by an overload of free copper resulting from a loss-of-function mutation in ATP7B, the gene that encodes for copper-transporting ATPase (ATP7B) found primarily in the liver and brain. We utilized Atp7b-/- mice as a model due to its stable and controlled environmental and genetic factors. We previously demonstrated that Atp7b-/- mice have hepatic nuclear receptor function in LRH-1, RXR, FXR, and HNF4α is decreased. There were additional protection from diet-induced obesity with improved insulin and glucose tolerance, and resulting in irregular hepatic growth. Our goal was to investigate the implications of ATP7B and Wilson's disease in the development of hepatic malignancies. We hypothesized that the clinical symptoms of the Atp7b-/- knockout mice overlap with the cellular proliferation and inflammation profile of mouse models with hepatocellular carcinoma (HCC). Immunohistochemical analysis and in vitro characterization of its omics will provide more information on the relationship between HCC and WD, and help with developing future therapeutic options by providing insight about possible downstream targets from nuclear receptors.

FRI - 505 To be or Not to be Virulent: A *Vibrio Parahaemolyticus* Story

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Reavelyn Pray*, *Texas A&M Corpus Christi*; Danial Nasr Azadani, *Texas A&M Corpus Christi*; Hailey Wallgren, *Texas A&M Corpus Christi*; Daniele Provenzano, *University of Texas Rio Grande Valley* and Jeffrey W. Turner, *Texas A&M University-Corpus Christi*

Abstract: Vibrio parahaemolyticus is a Gram-negative bacterium that occurs naturally in marine environments and flourishes in warmer seasons. It is the leading cause of seafood related gastroenteritis worldwide. Its occurrence is on the rise due to increasing water temperatures brought about by climate change. As ocean temperatures rise, the distribution of the bacterium and the number of V. parahaemolyticus infections is expected to increase, posing a serious threat to food security. Preliminary data suggests that some pandemic O3:K6 strains vary in their ability to survive cold storage conditions that would be typical of post oyster harvest. To investigate factors affecting cold tolerance, a collection of 850 clinical and environmental V. parahaemolyticus isolates, will be assayed by PCR for the presence of the pandemic-specific open reading frame orf8 as well as genes related to cold tolerance e.g., the cold-shock transcriptional regulator cspA. Strains having distinct cold-shock gene content will then be assayed for cold tolerance in a traditional culture-based experiment. We hypothesize that strains unable to survive cold storage conditions will be underrepresented among clinical isolates.

FRI - 506 The Effect of Decomposition on Nitrogen Fixation Associated with *Codium Fragile* Off the Coast of Santa Catalina Island

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Sarah Ortiz*, *Barnard College of Columbia University*; Yubin Raut, *University of Southern California* and Douglas Capone, *University of Southern California*

Abstract: Nitrogen fixation is the process carried out by a specialized group of prokaryotes, referred to as diazotrophs, which use the nitrogenase enzyme to convert atmospheric dinitrogen gas, N_2, into biologically available ammonia, NH_3. This is an important ocean process as it provides biologically available nitrogen to marine organisms, including macroalgae, thus supporting the conversion of CO_2 into organic matter which is eventually sequestered in the deep ocean. While nitrogen fixation associated with living *Codium fragile* is well studied, little is known regarding the effects of decomposition on this crucial process. This study investigated nitrogen fixation associated with living and decomposing *C. fragile* by assessing nitrogenase activity via the acetylene reduction method using gas chromatography with flame-ionization detection. Previous studies have shown that the middle stages of the decomposition of *Sargassum* and *Macrocystis pyrifera* result in increased nitrogen fixation rates by their associated diazotrophs. Similarly, preliminary results from this study show that *C. fragile* decomposition results in increased nitrogen fixation rates. Furthermore, this study investigated the effects of light concentration on nitrogenase activity and higher dark nitrogen fixation rates relative to light incubations suggest the importance of heterotrophic nitrogen fixation in these diazotrophic associations. Lastly, sodium molybdate inhibition assays were used to assess the relevance of sulfate reducers within the diazotrophic community associated with degrading *C. fragile*. These results shed insight into the role of nitrogen fixation during macroalgal decomposition and may have important implications for the farming of macroalgae as diazotrophic associations could potentially help alleviate nitrogen limitation for macroalgae.

FRI - 507 The Awakening of a Symbiotic Coral: Physiological and Metabolic Changes in the Transition from Night to Day

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Lasair Ni Chochlain*, *The Pennsylvania State University*; Tomás López Londoño, *The Pennsylvania State University* and Roberto Iglesias-Prieto, *The Pennsylvania State University*

Abstract: Symbiotic coral associate with photosynthetic algae forming a mutualistic relationship between the animal host and the symbionts. These symbiotic algae provide the majority of the metabolic energy that the corals require to live and calcify, creating reefs. At night, in the absence of light, both the animal and the algae respire, depleting the oxygen environment inside the coral. But during the day, the algae perform photosynthesis, which saturates the coral tissues with oxygen. Much research has been done to understand the metabolic interactions between the symbionts and the coral host. However, the metabolic changes that take place specifically during the transition from night to day are not fully understood. Preliminary results show that when corals are first exposed to gradually increasing light levels after being dark-acclimated for an extended period of time, the rate at which they evolve oxygen varies. We will measure the changes in the respiration rate for algae cultures and for corals when they are brought to a hypoxic condition and then exposed to gradually increasing light levels by measuring oxygen evolution and chlorophyll fluorescence as an approach to identify changes in the photochemical efficiency of photosystem II. The respiration rate is an indicator of the metabolic reactions occurring so by this approach, we want to gain an understanding of the changes that take place in the transition from hypoxic conditions at night to hyperoxic conditions during the day.

FRI - 508 Microbial Food Web Dynamics of the Gorda Ridge Hydrothermal Vent System

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Erica Herrera*, *Woods Hole Oceanographic Institution*; Sarah K. Hu, *Woods Hole Oceanographic Institution* and Julie Huber, *Woods Hole Oceanographic Institution*

Abstract: Microbial communities play an essential role in nutrient cycling that occurs within marine systems. Mechanisms by which energy transfer occurs between chemosynthetic prokaryotes residing in deep-sea hydrothermal vent ecosystems and higher trophic level organisms are poorly characterized. To better understand the food web dynamics occurring within these communities, grazing experiments were conducted using fluorescently labeled prey (FLP) analogs on water samples collected from the Gorda Ridge hydrothermal vent system, located off the southern coast of Oregon. Tracking the amount of FLP consumed over a 36-hour period in samples collected from the vent, plume, and background seawater of the vent system provides insight into predation occurring at the base of the food web. Grazing rates calculated from these experiments will provide better understanding as to how carbon is cycled within these communities and the role that chemosynthetic organisms play in energy production in the larger ocean system.

FRI - 509 Characterization of Marine Microbial Succession Along the California Coast

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Malia Machado*, *Cabrillo College*; Michael Kempnich, *University of California, Santa Cruz* and Marilou Sison-Mangus, *University of California, Santa Cruz*

Abstract: Bacteria play an important role in the breakdown and cycling of organic nutrients in ocean systems. Changes in microbial abundance and community composition are related to environmental factors such as temperature, nutrient availability, biological productivity, and ocean currents, and affect the health of other marine organisms including phytoplankton. Bacteria are known to interact with phytoplankton in a myriad of ways. These interactions are currently poorly understood, but crucial to determining ocean community dynamics. Here we aim to investigate the dynamics of picophytoplankton and bacterial communities at various times of the year and correlate them with existing environmental metadata. The abundance of bacteria and picophytoplankton were determined through imaging flow-cytometry using SYBR-green staining. Our initial data shows that picophytoplankton have a peak biomass in the late winter seasons while bacteria are most abundant in the summer seasons. These results suggest that picophytoplankton and bacteria thrive at different times of the year due to the different ways they source their energy and nutrients and how they are being controlled by top-down (physical and nutrients) and bottom-up effects (primary productivity). This data, combined with 16S relative abundance data from next-gen sequencing, will allow a deeper understanding of the changes in marine microbial communities through time. By continuing to examine the specific bacteria present during peak seasons of phytoplankton productivity, we will be able to further understand the role of bacteria-phytoplankton interactions in marine environments.

FRI - 510 Where Fish Live and Why: Variation in Fine-Scale Habitat Associations of Vermilion Rockfish (*Sebastes miniatus*) and Canary Rockfish (*Sebastes pinniger*) with Latitude Along the California Coastline

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Marisa Thompson*, *California State University, Monterey Bay* and James Lindholm, *Institute for Applied Marine Ecology at California State University, Monterey Bay*

Abstract: Understanding fish-habitat interactions is a fundamental component of sound fisheries management, particularly in the assessment of deepwater fish stocks and spatial management strategies. While in recent years remotely operated vehicle (ROV) technologies have made it possible to explore these fish-habitat interactions, no known studies have compared the response of sister-species rockfishes to habitat specificity at fine scales (<1 m) across a broad latitudinal range. The objective of this study is to investigate microhabitat utilization of two commercially important demersal species, Vermilion rockfish, *Sebastes miniatus*, and Canary rockfish, *Sebastes pinniger*, along the California coastline ranging from Pt. Arena to La Jolla Cove. Data on both species' microhabitat utilization, including substrate type, total length, and behavioral response, were extracted from ROV video using non-overlapping video quadrats. Our results to-date from data collected off Bodega Head in northern California demonstrate an ontogenetic shift in Canary rockfish microhabitat utilization. Evidence suggests that juvenile rockfish (10-15 cm) primarily associate with soft sediment and are observed holding station on the seafloor, while larger sub-adults (20-30 cm) generally associate with hard substrate and are found holding station or actively swimming more frequently in the water column. Implications of this research may enhance quantitative assessments of habitat complexity and rockfish stocks to assist state and federal fishery managers.

FRI - 511 Modeling the Distribution of Bottlenose Dolphins (*Tursiops truncatus*) in the Chesapeake Bay As a Function of Environmental Factors

Discipline: Life Sciences

Subdiscipline: Marine Sciences

Lauren Rodriguez*, *Michigan State University*; Helen Bailey, *University of Maryland Center for Environmental Science*; Jamie Testa, *University of Maryland Center for Environmental Science* and Amber Fandel, *University of Maryland Center for Environmental Science*

Abstract: Bottlenose dolphins (*Tursiops truncatus*) are wide-ranging marine mammals that live in both open-ocean habitats as well as coastal areas. Little is known about their seasonal occurrence within highly urbanized regions such as the Chesapeake Bay, U.S.A. The goal of this study was to determine the spatial and temporal distribution of bottlenose dolphins in the Chesapeake Bay using geospatial and statistical modeling techniques. Two years of observational dolphin sighting data from a citizen-science initiative, Chesapeake DolphinWatch, was mapped using ArcGIS 10.5 to visually characterize dolphin occurrence. Sightings were then integrated with fisheries and water quality data to identify factors influencing dolphin occurrence in this area. We found a distinct seasonal occurrence pattern with dolphins being most commonly sighted from May through August. Using a generalized additive model, the probability of dolphin presence was found to be significantly impacted by environmental variables.These results provide a better understanding of the geographical distribution and annual movements of bottlenose dolphins in the Chesapeake Bay. The direct relationship documented between dolphin presence, prey availability, and environmental conditions can be used to support conservation efforts and inform population management.

FRI - 512 Presence Vs. Absence: The Reintegration of an *Umu Kai*

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Shor Williams*, *Hawaii Institute of Marine Biology* and Frederick Reppun, *Hawaii Institute of Marine Biology*

Abstract: *Umu kai* are a type of fish trap that was widely used until the mid 20th century in the Hawaiian Islands as a way for kūpuna (elders) to catch fish in shallow waters close to shore. These submarine structures are stacks of rocks that act as shelters for juvenile fish, which in turn attract larger fish. The current study investigated the effect of *umu kai* on fish abundance and species diversity in two different nearshore environments on Oʻahu, Hawaiʻi. We constructed six *umu* in total: threie in the stream and estuary that run along the north side of Heʻeia fishpond (a tidally-flushed, estuarine Hawaiian fishpond), and another three on the fringing reef along the outside of the fishpond wall. We used visual assessments and two netting techniques to collect fish species and abundance data. The netted fish were measured (length and weight) to establish the size-mass distribution of each species present. Data was collected at experiment sites before and after the *umu* were installed, and at six control sites (no *umu*) adjacent to the *umu*. An underwater camera was also deployed at two *umu* to record the behavior of fish associated with the structure. In addition to increases in fish abundance, at least three species of fish were observed at the *umu kai* that were not documented at control sites. This data is useful in informing how this traditional method of fish aggregation can be used to supplement fish survey techniques and also be reincorporated into community subsistence strategies.

FRI - 513 Assessment of *Ferocactus Gatesii P*opulations in Bahia De Los Angeles Using Manual Collection and UAVs

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Ilana Rivera Larrea*, *University of San Diego* and Drew Talley, *University of San Diego*

Abstract: Bahia de los Angeles is an archipelago consisting of 16 islands with diverse cactus populations (West 2002). Restricted to a subset of these small islands is an endemic cactus, the Bahía de los Ángeles biznaga (*Ferocactus gatesii*). Despite its rarity, and loss of individuals due to illegal harvesting, there have been no quantitative surveys of this population, and little is known about their recruitment or ecology (West 2002). **The goal of this study is to assess the *F. gatesii*populations in Bahia de los Angeles using both terrestrial and Unmanned Aerial Vehicle (UAV) methodologies, to assess the accuracy and effectiveness of UAV census for this species.** From a total of 16 islands in Bahia de los Angeles, a subset of three islands were selected for this study. Dronedeploy was used to capture images, stitch them together, and form a high-resolution image of the island. These images were used to identify individual *F. gatesii,* and each was measured ("trunk" diameter) and assessed for reproductive status (flowers). The same parameters were collected on the ground. Surveyors walked the entirety of the islands and identified individual cactus. All parameters collected through field work were compared to those collected using UAVs. Preliminary analysis shows the UAV can correctly identify 100% of *F. gatesii*greater than 18 cm in diameter, while also identifying reproductive status. This suggests that, for monitoring adult populations of this threatened endemic, UAV surveys provide a rapid and effective method, but that there may be limitations in identifying newly-recruited individuals.

FRI - 514 Sunlight and Microbial Effects on Dissolved Organic Carbon in Tundra Ponds Near Utqiagvik, Alaska

Discipline: Life Sciences
Subdiscipline: Environmental Science

Christopher Sandoval*, *Universtiy of Texas at El Paso*; Christy Adame, *University of Texas at El Paso* and Vanessa L. Lougheed, *University of Texas at El Paso*

Abstract: Because of the rising temperatures in the Arctic, we are seeing permafrost thaw at a rate not seen before. Due to these increased rates of thaw, carbon contained within the permafrost, sometimes older than 10,000 years, is being released into our modern atmosphere, including aquatic environments. This thawing causes Dissolved Organic Carbon (DOC) to be flushed from soils which are than oxidized to CO2 by sunlight and microbes, which is then released into the atmosphere. We completed an experiment examining how light and microbes affect carbon transformation in wetland ponds, rivers and nearshore lagoons near Utqiagvik, Alaska. Filtered samples were incubated in Whirl-Paks® with and without a native or exotic microbial inoculum, in light and dark conditions. Samples were incubated for a period of 5 days in a cold room kept at 14°C, equipped with a metal halide bulb (17,600 lux). Dark samples were wrapped in tin foil away from halide bulb to avoid overheating. Changes in dissolved oxygen (DO), dissolved organic carbon (DOC) and spectral properties of the organic matter (C440, SUVA254, spectral ratio) were monitored. Preliminary results from a reference pond (IBP-C) and a thermokarst pond (TK3), which has experienced a greater rate of thaw and slumping than the reference site, indicate that light increased the lability of DOC relative to the dark control, and native innocula were better able to transform photodegraded DOC relative to non-native innocula. Additional sites will be added to the analyses to see if these trends hold across multiple habitats and dates.

FRI - 515 Assessing the Impacts of Environmental Sound on the Abundance and Size of Coenobita Clypeatus

Discipline: Life Sciences
Subdiscipline: Environmental Science

Paola Negrón-Moreno*, *University of Puerto Rico at Cayey*; Ana Gonzalez, *University of Puerto Rico at Cayey*; Francisco J. Torres, *University of Puerto Rico at Cayey* and María I. de Jesús-Burgos, *University of Puerto Rico at Cayey*

Abstract: Anthropogenic noise is recognized as a global environmental stressor. Studies suggest that noise can alter animal behaviors related to reproduction, resource assessment, and decision making. Anthropogenic noise particularly affects the natural soundscape of littoral ecosystems due to tourism and residential development. *Coenobita clypeatus* is a species abundant in the littoral zones of tropical and subtropical regions. Although the detrimental impacts of noise on animal behaviors are known, no one has analyzed the impact of environmental sound on *C. clypeatus'* abundance and size. We hypothesize that high levels of environmental sound will affect *C. clypeatus'* population description. We used a transect methodology to profile animals in beaches of Puerto Rico, including natural reserves and highly visited beaches. The environmental sound was measured during different time points in the field. Preliminary results suggest that *C. clypeatus* is more abundant and displays bigger size and longer major chela in the natural reserves in comparison to highly visited beaches ($p<0.0001$). Analyses of the soundscape suggest a significant difference in

environmental sound, with natural reserves displaying lower sound measurements in comparison to highly visited beaches (p=0.003). A larger difference was found when rush hour was analyzed (p=0.0006). Our data suggest that high levels of environmental sound may cause detrimental effects on *C. clypeatus*, causing a reduction in animal numbers and/or smaller animals. Further studies assessing the impact of sound production on the littoral zone are needed. A better understanding of the impact of environmental sound on littoral organisms can promote the regulation of noise production.

FRI - 516 Restoring Eastern Redcedar Encroached Watersheds to Prairie or Switchgrass

Discipline: Life Sciences
Subdiscipline: Environmental Science

Rainee DeRoin*, *Oklahoma state university* and Chris Zou, *Oklahoma State University*

Abstract: Eastern redcedar represents a modern-day challenge to Oklahoma as it has encroached approximately eight million acres of land. This conversion is detrimental to the ecological and economic value of the land, reducing ecosystem water provisioning in particular. Eastern redcedar trees consume more water such that less is available for municipal and agricultural uses as well as ecological stream flows. Currently, efforts to reduce eastern redcedar encroachment have been unsuccessful; however, studies have shown eastern redcedar biomass to be a potential ethanol feedstock for the state. The purpose of this study is to compare eastern redcedar removal and replacement with native prairie or planted switchgrass on surface runoff, sediment yield, and biomass production. More specifically, this study monitors surface runoff and sediment yield of encroached eastern redcedar, harvested eastern redcedar, cultivated switchgrass, and native prairie using experimental watersheds (5-10 acres in size). Preliminary analysis shows that removal of eastern redcedar increased water yield by 4-5 fold. Growing switchgrass produced more biomass than restoration to native prairie, but water yield did not differ between the two. Sediment concentrations from encroached eastern redcedar watersheds were higher compared to native prairie watersheds. After harvest, previously encroached watersheds initially experienced an increase in sediment yield due to soil disturbance. After switchgrass and native vegetation re-established, sediment yields declined. These results indicate that water yield and biomass production can be increased by converting eastern redcedar woodlands to switchgrass for use as dedicated biofuel feedstock.

FRI - 517 Juvenile Coho Salmon Habitat Use on the Klamath River

Discipline: Life Sciences
Subdiscipline: Environmental Science

Nicholas Chischilly*, *Fort Lewis College*; Darren Ward, *Humboldt State University* and Max Ramos, *Humboldt State University*

Abstract: The Klamath River is the second largest river in California and was once the third largest producer of salmon on the West Coast. For more than 50 years, dams on the Klamath River have isolated historic salmon habitats in the upper watershed. Removal of four major dams on the Klamath River is scheduled to begin in the year 2020. Our research gathered baseline data prior to the project to help determine how the trout populations currently living above the dams will be affected by the return of salmon by evaluating their use of habitat. We investigated the habitat use of two influential species (Coho Salmon and Rainbow Trout) when they are juveniles, comparing streams where the species currently live together to streams above the dams where trout currently live without salmon. We conducted habitat surveys as well as snorkel surveys in tributaries to the Klamath River, above and below Iron Gate Dam. Preliminary results have showed us that Coho and Rainbow juveniles remain consistent with behavior recorded in academic literature below the dam. This suggests that Rainbow populations above the dam will be heavily affected by this dam removal project, and the return of the salmon species including Coho Salmon.

FRI - 518 Biochar Application Improves Growth Rates of Washington Apple Trees

Discipline: Life Sciences
Subdiscipline: Environmental Science

Jose Figueroa Orduño*, *Heritage University*; Xavier Martinez, *Heritage University*; Alexander Martinez, *Heritage University*; Paige Delp, *Heritage University* and Jessica Black, *Heritage University*

Abstract: 58% of all apple production in the United States occurs in Washington State. Yakima County, a semi-arid region, leads the state in apple production. Recent studies have found that the addition of biochar, a byproduct of pyrolysis, to soil can increase fertility and mitigate effects of climate-change in water-stressed regions. We investigated the effects of biochar in soil of a newly planted orchard for 10 weeks. We hypothesized that biochar will increase both apple yield and growth rate. Three biochar treatment groups consisted of 0.5%, 1%, and 2% application by weight were applied to the Wildfire™ Gala apple cultivar. A fourth treatment group consisted of previously applied slash pile material. The control consisted of no applied biochar. All treatment groups contained three replicates; 15 plots in total. Trunk diameter and soil samples were collected every two weeks. Approximately 48 days after planting, the 2% application treatment group average trunk diameter was significantly greater than the control group (one-way ANOVA, p = 0.00068). This trend continued into the following two weeks. However, by the end of 10 weeks, no significant differences between treatments were observed. Our study results suggested that, for a critical period, the addition of biochar applied at a concentration of 2% by weight increased growth rates of the Wildfire™ Gala apple cultivar. This implies greater resilience during peak heat temperatures in June and July. The application of biochar in apple orchards of the Yakima Valley shows promise to give crops an early start.

FRI - 519 Assessing Biochar As a Soil Amendment in Bell Pepper Production in a Water Stressed Region of Washington State

Discipline: Life Sciences
Subdiscipline: Environmental Science

Alexander Martinez*, *Heritage University*; Xavier Martinez, *Heritage University* and Jessica Black, *Heritage University*

Abstract: The United States is the fifth largest producer of bell peppers globally, producing 1.6 billion pounds. Bell pepper production is a $642 million dollar industry in the U.S. In the Yakima Valley of Washington State, bell peppers are one of many valuable crops produced. Biochar is a product pyrolysis and has historically been utilized as a soil amendment. Recent studies on biochar suggest that it is capable of aiding in nutrient retention and soil moisture retention, both of which can lead to increased crop production and plant growth. We hypothesize that the addition of biochar will significantly increase bell pepper *Capsicum annuum* growth. Two biochar treatment groups, 0.5% and 1% application by weight, were applied to plots within a bell pepper field. The control group consisted of no applied biochar. Each biochar treatment group consisted of three plots; the control group consisted of six plots. Each plot consisted of 48 plants. Observed metrics included flower count, fruit yield, and plant diameter. Preliminary results suggest that the application of biochar increased average bell pepper plant diameter between 6.5% and 8.1% greater than the control group. Furthermore, our results suggest that greater application rates of biochar lead to greater plant growth. Our research findings suggest that biochar may be useful for increasing the productivity of bell pepper and other similar crops in the Yakima Valley.

FRI - 520 Study of *Coenobita Clypeatus* Shell Utilization in Selected Beaches of Puerto Rico, Caribbean Island

Discipline: Life Sciences
Subdiscipline: Environmental Science

Ana D. González-Colón*, *University of Puerto Rico at Cayey*; Paola Negrón-Moreno, *University of Puerto Rico at Cayey*; Francisco J. Torres, *University of Puerto Rico at Cayey* and María I. de Jesús-Burgos, *University of Puerto Rico at Cayey*

Abstract: *Coenobita clypeatus* is a land hermit crab, playing significant roles in coastal ecosystems like seed dispenser and scavenger contributing to the food chain. *C. clypeatus'* survival and growth in natural environments depends upon the acquisition of empty gastropod shells like shelters to protect their fragile abdominal region from abrasion, desiccation, and predation. Thus, shell availability and accurate selection are crucial for

hermit crab life. Although, hermit crab shell utilization patterns have been studied in several locations, there are no recent studies analyzing the shell utilization of *C. clypeatus* in the Caribbean. Therefore, we investigated the shell utilization pattern of *C. clypeatus* in selected beaches of Puerto Rico. The analyses of the gastropod shell used by *C. clypeatus* were carried out using the transepts methodology. We collected 732 animals and described the occupied gastropod shells. Data demonstrate that *C. clypeatus* in the visited beaches utilized *Astraea tuber* (23%), *Nerita tessellata* (9.3%), *Turbo castanea* (8.1%), *Bulimulus guadalupensis* and *Tectarius muricatus* (7.6%) shells, like major shelters. We also detected a strong correlation between major chela and shell orifice (r=0.98). Common occupied shells by *C. clypeatus* display conical shapes and oval apertures. These facts suggest the animal's ability to choose and/or the availability of a suitable shell for the animal's body size. This study provides a better and current description of *C. clypeatus* shell utilization pattern in the Caribbean. Further analyses need to be conducted to establish if the shell utilization pattern observed is mediated by the animal's preferences and/or by shell availability.

FRI - 521 Microplastic Concentrations in Surface Seawater of the Monterey Bay National Marine Sanctuary

Discipline: Life Sciences
Subdiscipline: Environmental Science

Lauren Kashiwabara*, *California State University Monterey Bay*; Matthew Savoca, *Hopkins Marine Station, Stanford University*; Marissa DeVogelaere, *University of Portland*; Chad King, *Monterey Bay National Marine Sanctuary, National Oceanic and Atmospheric Administration* and Jeremy Goldbogen, *Hopkins Marine Station, Stanford University*

Abstract: Microplastics, small pieces of plastic (<5mm), are the most common type of marine debris. Nearly 1000 marine species ingest microplastics, and the effects on the food web and ecosystem is of increasing concern. This has implications for the Monterey Bay National Marine Sanctuary (MBNMS) because of the sanctuary's mandate to understand and protect this area of national significance. The vertical distribution (5-1000m) of microplastics within the bay has been recently reported, finding the highest concentrations (15 particles m^{-3}) at 200m depth, with higher concentrations of microplastics in offshore samples as compared to nearshore samples (Choy et al., 2019). To contribute to the limited research concerning microplastics in the MBNMS, we sought to understand the concentrations of microplastics surface seawater samples. In the summers of 2017 and 2018, we collected surface water samples using a manta trawl net (355mm mesh size) from two nearshore locations (Santa Cruz Boardwalk and Marina Sewage Outfall) and two offshore locations (Sur Ridge and Davidson Seamount) within the MBNMS. To isolate and extract synthetic material from our samples, we developed a process of density separation, chemical digestion, and vacuum filtration. We then used epifluorescence microscopy and ImageJ software to quantify the number of microplastics per cubic liter of seawater. To link the polymer type of our a subset of our samples to their plastic source, we used Fourier-transform infrared spectroscopy (FT-IR). Our results will provide vital baseline information on the extent of microplastic pollution in the surface waters of the MBNMS at nearshore and offshore locations.

FRI - 522 Projecting Extremes in California Current Acidification

Discipline: Life Sciences
Subdiscipline: Environmental Science

Gabriela Cazares*, *Massachusetts Institute of Technology* and Nicole Lovenduski, *University of Colorado Boulder*

Abstract: With the substantial use of fossil fuels as a source of energy, the concentration of carbon dioxide in the atmosphere has increased significantly. Much of this anthropogenic carbon has been absorbed into the ocean, forcing a series of chemical reactions that culminates in the acidification of the ocean. The acidification of the ocean causes the decrease in carbonate ion concentration, creating an undersaturated system that increases susceptibility to shell dissolution. Modeling studies of the California Current system have projected drastic and rising acidification levels in this region of the ocean within the following century, implying a stressful future for all members of the system's food web and the fishing industry. For this project, we looked at the projected changes in the frequency of acidification events on a monthly basis from 1920 through 2100 in the California Current system and analyzed seasonal trends using saturation depth data from the Community Earth System Model Large Ensemble (CESM-LE). A case study of the CCE1 and CCE2 buoys was done to test the accuracy of the CESM-LE projections. Our results demonstrated how the frequency of acidification events is expected to rise much quicker than initially hypothesized, and how undersaturated water levels are rising to depths these have historically never reached before.

FRI - 523 Low-Cost Portable Air Sensors Are a Useful Tool for Assessing Fine Scale Exposure to Particulate Matter Pollution in Peru.

Discipline: Life Sciences
Subdiscipline: Environmental Science

Brigitte Solorzano*, *Mount Saint Mary's University*; Cynthia Amador, *Mount Saint Mary's University* and Adriane Jones, *Mount Saint Mary's University*

Abstract: The AirCasting Airbeam 2 air sensor is an inexpensive, easy-to-use, portable device that provides instant measurements of particulate matter (PM) pollution in one's surroundings. Reliable and immediate data can raise awareness about air pollution and associated health concerns. From July 31, to August 8, 2018, we travelled to Peru, and used the Airbeam 2 air sensor to measure PMs in the 10, 2.5 and 1 micrometer size class. We asked the questions 1) Do the values reported by the portable sensors agree with fixed sensors installed by health organizations? And 2) Can low cost portable air sensors be used to measure patterns of PM pollution over short timescales? The urban regions of Lima and Cusco experience elevated levels of PM 2.5. Data from the portable sensors ranged from 20 to 40 μg/m3 with short-term increases of up to 80 μg/m3. These were in agreement with the data reported by stationary sensors at the US embassy in Lima that ranged from 20 to 60 μg/m3. These levels exceed the WHO limits for PM 2.5 of 10 μg/m3 over 24 hours. The rural regions of Quillabamba, Santa Teresa, and the Andes Mountains exhibited low PM 2.5 values, with readings less than 25 μg/m3 and fluctuations that reflect short-term events like traffic. Portable air sensors can be useful and accurate tools to assess local fine-scale exposure to air pollution, specifically in regions where air pollution is a public health concern and where instantaneous air quality information is scarce.

FRI - 524 Testing for Water and Sediment Contamination in the Monterey Peninsula and Salinas Watershed for Select Persistent Organic Pollutants

Discipline: Life Sciences
Subdiscipline: Environmental Science

Samantha Champ*, *Monterey Peninsula College*; Thomas Greathouse, *College of Alameda*; Erin Stanfield, *California State University, Monterey Bay* and Arlene Haffa, *California State University, Monterey Bay*

Abstract: Triclosan, a broad spectrum antibacterial and antifungal agent, and bifenthrin, a pyrethrin insecticide are both known to be highly toxic to freshwater aquatic life. These chemicals enter the environment through wastewater and agricultural runoff from the highly productive Salinas Valley. The goal of this study is to determine if there are detectable amounts of triclosan and bifenthrin at various points and depths along the Salinas River, in Elkhorn Slough Marine Estuary and in samples of influent and effluent wastewater. Surface water samples, sediment samples at water line, sediment samples in the body of water, as well as influent and effluent water samples will be collected for analysis. All liquid samples will be extracted and concentrated using C18 solid-phase extraction (SPE). Sediment samples will be exposed to an organic solvent, agitated, filtered and then put through SPE columns. Spectrophotometric determination of both triclosan and bifenthrin is employed after the concentrated solutions are treated with a diazonium ion solution and an enzyme solution, respectively. It's anticipated sediments will have a higher triclosan and bifenthrin value than water samples. Triclosan concentrations in wastewater will probably be higher than in environmental samples, the inverse relationship is anticipated for bifenthrin. A better understanding of the types of chemicals accumulating, or running through the waterways, into the local watersheds as a result of human interference can help with future research in this area and current studies looking into common pollutants both in California and elsewhere.

FRI - 525 Assessing the Ability of Herbicide Sorption By Char-like Material

Discipline: Life Sciences
Subdiscipline: Environmental Science

Andrea Saavedra*, *Northeastern Illinois University*; Javier Gonzalez, *USDA-ARS National Soil Erosion Research Lab* and Laura Sanders, *Northeastern Illinois University*

Abstract: Atrazine is the second most used herbicide in the U.S. Midwest for weed control in corn. Although the recommended management practices, e.g. buffer zones and recommended application rates, are implemented during the atrazine applications in the U.S. Midwest, the off-site transport of this herbicide from agricultural fields to near waterways is still observed. Additional conservation practices, including contaminant removal structures with target-specific media are needed to improve water quality. This media should be cheap, easily accessible, and efficient to remove the desire contaminant. This study investigates the efficiency of hardwood charcoal, to remove atrazine in solution at the lab scale using the kinetic and the batch sorption approaches. For the kinetic sorption study, 1 mg L-1 of atrazine solution and hardwood charcoal was shaken from 1 to 24 h. For the batch sorption experiment, atrazine solution (concentrations ranging from 0.01 to 5 mg L-1) /hardwood charcoal was shaken for 24 h; then, the supernatant was decanted; and a sequential desorption was performed to the sorbed atrazine using a solution of 0.01 M CaCl2 and 50% methanol solution. Three replicates were used per each time (kinetics) and concentration (batch), including the control (no hardwood charcoal). After shaking in each approach, the atrazine in equilibrium was determined by liquid chromatography with mass detection and the amount of atrazine sorbed by the hardwood charcoal was calculated by difference. The results of this study will help to evaluate a cheap and easily available media that can be used in contaminant removal structures.

FRI - 526 Diversification within a Matrix and Its Influence on Pollinator Community Composition in Monocultures, Polycultures, and Urban Gardens

Discipline: Life Sciences
Subdiscipline: Environmental Science

Gisel DeLaCerda*, *University of California, Berkeley* and Aidee Guzman, *UC Berkeley*

Abstract: Pollinators provide an important ecosystem service in urban garden and agricultural matrixes. The California Central Valley hosts a range of land use types along an urban to agricultural gradient, including many community gardens within an urban landscape. Landscape fragmentation and land conversion are known to reduce pollinator species richness and abundance, but previous studies suggest that management practices that promote crop diversity have a positive impact on pollinator community inter-species richness and abundance. Relatively little information is known regarding intra-species genetic diversity within and between matrixes in a mixed landscape. For this study, we sampled pollinators using netting and kill-jars along 10 m transects from twelve different farms among three different matrixes within the Central Valley - monoculture farms, polyculture farms, and urban gardens. This presentation will report measurements of genetic diversity via PCR methods. Our hypothesis is that pollinators found within urban gardens will have higher levels of genetic diversity and species richness due to the increased biodiversity within the nutritional landscape. Likewise, we predict to find greater pollinator biodiversity on polyculture farms compared to monoculture farms. With these results, we hope to determine whether pollinator-friendly management within given matrixes will promote genetic diversity among pollinator species, as this should be considered as part of management decisions.

FRI - 527 Fecal Bacteria in Whatcom County Creeks

Discipline: Life Sciences
Subdiscipline: Environmental Science

Yakaiyastai Gorman*, *Northwest Indian College* and Karlee Cooper, *Northwest Indian College*

Abstract: Clean water is essential to all. In Whatcom County, Washington, we are a community of advocacy for a healthy, clean environment. Our landscape has changed from pacific lowland forest and prairie to agricultural land for dairy and produce. This change has added sources of Coliform bacteria that can contaminate tribal shellfish beds. We assume riparian vegetation filters Coliform from agricultural runoff prior to entering waterways. If a stream is filled with vegetation, wood, or organic debris it will slow the water, which creates a microhabitat for bacterial predators. Our hypothesis is that open streams without well-developed riparian vegetation will be sources of bacteria, while streams with developed riparian vegetation will be bacterial sinks. We will be using the standard MI membrane filtration method developed by the EPA to determine the bacterial quantity. Sampling from two structure types of streams, open and riparian, we will quantify the density of *Escherichia coli* and total coliform bacteria upstream and downstream of agricultural runoff. The importance of this research is to inform best practices for minimizing bacteria that adversely impacts tribal shellfish beds and how optimizing agricultural areas of Whatcom County could reduce contamination.

FRI - 528 Temperature Profile of O'ahu's Highest Mountain

Discipline: Geoscience
Subdiscipline: Earth Science

Toby York*, *Honolulu Community College* and John DeLay, *Honolulu Community College*

Abstract: Mt. Ka'ala, the highest mountain on the island of O'ahu and the summit of the Wai'anae mountain range. The Wai'anae mountain range is leeward of the trade wind flow relative to O'ahu's other main mountain range, the Ko'olau, and experiences drier conditions as a result of a rain shadow effect. However, because the summit of Mt. Ka'ala is at a higher elevation it creates additional orographic uplift, so the upland forest is frequently immersed in clouds. The summit area biological community is a Tropical Montane Cloud Forest (TMCF) dominated by native species, including a number of rare and endangered endemics such as native tree snails likely sensitive to temperature. Ongoing water balance research at the summit suggests that cloud water interception which is subject to the lifting condensation level, is an important component of the mountain's water balance. Adiabatic lapse rates are critical to determining lifting condensation levels, but these are currently unknown for the area. The temperature profile will also be helpful for interpretation of isotopic ratio measurements currently being collected from precipitation along an elevation gradient along the mountain slopes. In order to determine the adiabatic lapse rate, temperature stations were deployed at 100-meter elevation intervals. Preliminary data indicates adiabatic lapse rates of about 6° per 1000 meters, similar to those recorded on the island of Hawai'i. The adiabatic temperature profile of Mt. Ka'ala is relevant for precipitation studies, species management, and provides a baseline with regards to atmospheric warming.

FRI - 529 Detecting Surface Melt Events on the West Antarctic Ice Sheet Via Passive Microwave Sensors

Discipline: Geoscience
Subdiscipline: Earth Science

Emma Robertson*, *University of Massachusetts Amherst* and Dan Lubin, *Scripps Institution of Oceanography, UC San Diego*

Abstract: Warming ocean temperatures underneath coastal ice shelves have been the primary driver of volume loss from West Antarctic ice shelves. Surface melt is a lesser understood phenomenon and occurs sporadically over lower elevations of the West Antarctic Ice Sheet (WAIS). The Pine Island and Thwaites glaciers of Western Antarctica are two of Antarctica's most vulnerable to retreat and volume loss. Decline in ice shelf volume has significant consequences for the stability of the WAIS and global sea-level rise. We investigated episodes of summer surface melt over a period of thirty years (1987-2017) using Special Sensor Microwave Imager (SSMI and SSMI/S) data provided by the National Snow and Ice Data Center. We computed cold-season averages at each grid cell to determine threshold values using the 19 GHz horizontal channels at 6.25 km resolution from the MEaSUREs Calibrated Enhanced-Resolution Passive Microwave Daily EASE-Grid 2.0 Brightness Temperature ESDR data set. A

brightness temperature(T_b) above the threshold value indicated the occurrence of a melt event. High-resolution Image-derived Grounding and Hydrostatic Lines for the Antarctic Ice Sheet were used to determine grounding lines for the Pine Island and Thwaites glacier study area. Preliminary analysis of brightness temperature data and satellite imagery observations has revealed that the current West Antarctic climate allows for the sporadic occurrence of extensive melt events. Additional analysis will determine the physical processes that contribute to these melt events. Further research is necessary to improve understanding of melt events and develop models to predict future episodes.

FRI - 530 Quantifying Chukchi Polynya Occurrence Using Passive Microwave and Local Observational Data

Discipline: Geoscience
Subdiscipline: Earth Science

Kitrea Pacifica L. M. Takata-Glushkoff*, *Bowdoin College* and Angela C. Bliss, *Oregon State University*

Abstract: Arctic sea ice dynamics and thermodynamics are critical to understand due to their feedbacks on regional and global atmospheric and oceanographic processes. Polynyas are areas where sea ice periodically thins or opens to reveal an ocean-atmosphere interface. The Barrow Coastal Polynya and the Chukchi Polynya, found in the Northeastern Chukchi Sea off the Alaskan coast, have widespread implications as they impact sea ice hunting practices, and foster the survival of a diversity of marine animals. They also have the potential to affect moisture and heat flux, warming local temperature.

We develop a database of the timing and duration of Barrow Coastal Polynya and Chukchi Polynya events between November 1 and May 31, for the years 2002 through 2019 using 12.5 km resolution satellite passive microwave data from the Japan Aerospace Exploration Agency's Advanced Microwave Scanning Radiometer (AMSR-E/AMSR-2) sensors. An automated system identifies polynya events based on annual time series of total water percent over each polynya's domain area. Polynya timing and duration are verified with sea ice concentration maps and ground truthed using local Iñupiat observational data out of Utqiagvik, Alaska. This database of polynya events reveals interannual variability in the timing and frequency of the Barrow Coastal Polynya and Chukchi Polynya in response to synoptic scale wind forcing. By accurately quantifying these polynya events, we lay the groundwork for further understanding the impacts of polynyas on regional wintertime atmospheric moisture and heat flux.

FRI - 531 Assessing California's Seismic Risk:Simulating Earthquake Scenarios on the San Andreas Fault System during a 100-Year Earthquake Drought

Discipline: Geoscience
Subdiscipline: Earth Science

Suzie Duran*, *Pasadena City College*; Gabriela Noriega, *Southern California Earthquake Center (SCEC) at USC* and Tomas Jordan, *Southern California Earthquake Center*

Abstract: The San Andreas Fault System is experiencing an earthquake drought which is a period of 100-years where earthquake events of M7.0+ have not occurred on the Northern and Southern Section of the San Andreas. As an intern at the Southern California Earthquake Center in the Hazard and Risk Visualization team member we analyzed two large historical earthquakes: 1) Northern California, San Francisco's MW 7.9 which occurred in 1906 and 2) Southern California, Fort Tejon MW 7.9 which occurred in 1857. Both events were estimated to have produced losses ranging in millions of dollars, equivalent to billions in 2018. Using FEMA's hazard and risk assessment program, HAZUS, we were able to acquire data by analyzing 100+ simulated earthquake events using a physics-based model, Rate-State earthQuake Simulator (RSQSim), Eclipse, and SCEC-VDO(Virtual Display of Objects). By integrating these programs we were able to display casualty and economic losses. Earthquakes cannot be predicted, but we use models to forecast potential impacts at various times of the day. If an earthquake > MW 7.5 were to take place on the San Andreas fault, the public would not be able to respond appropriately due to the current earthquake drought that has desensitized people to seismic risk. By forecasting events using a 2-million year catalog we have found that if a large magnitude event were to take place, similar to those of 1857 and 1906, the hazard and risk implications due to growth in population and dense infrastructure would be significantly greater.

FRI - 532 Visualizing Groundwater Resources to Promote Source Water Protection in the Kachemak Bay Region

Discipline: Geoscience
Subdiscipline: Earth Science

Analyssa Hernandez*, *Texas A&M University - Kingsville*; Nina Garfield, *National Oceanic and Atmospheric Administration-National Ocean Service*; Coowe Walker, *Kachemak Bay National Estuarine Research Reserve* and Mark Rains, *University of South Florida*

Abstract: As the population grows within the Kenai Peninsula, concerns with aggregate mining sites in the area have risen as they have the potential to harm ecosystems supporting salmon, a major economic and cultural resource to Alaska. One aspect proven to contribute greatly to stream productivity in salmon-bearing streams is groundwater, which discharges to streams and contributes to streamflow, modulates stream temperatures, and delivers nutrients that support the stream food webs that help juvenile salmon thrive. To consider how aggregate mining sites may disturb groundwater flows, existing well log data was used to visualize the locations and depths of shallow water-bearing formations. Out of the 818 well data logs available, 84 were within the study area of Anchor Point, near the highest concentration of existing or planned aggregate mining sites. Using ESRI products, the top-most water-bearing formation was interpolated across the study area and compared to the locations and depths of existing and planned aggregate mining sites, indicating where groundwater resources appear to be the most vulnerable. Results allow the visual interpretation of the proximity of aggregate mining sites to aquifers and the associated risks to that groundwater, such as enhanced evaporation, heating, or the introduction of contaminants. This information can be used to assist in land use planning, permitting, policy decisions, and habitat protection and will be conveyed via a story map that will include details needed to achieve source-water protection.

FRI - 533 Visualizing California's Seismic Drought: Analyzing Simulated Earthquakes on the San Andreas Fault System

Discipline: Geoscience
Subdiscipline: Geology

Stephanie Soto*, *University of Puerto Rico - Mayaguez Campus* and Gabriela Noriega, *Southern California Earthquake Center*

Abstract: Throughout the history of earthquakes in California, the state has suffered destructive events causing the loss of lives and billions of dollars. As part of the 2019 Undergraduate Studies in Earthquake Information Technology research challenge, the Hazard and Risk Visualization team performed a hazard risk assessment from simulated earthquake scenarios on the San Andreas Fault system similar to the 1857 Mw7.9 Fort Tejon Earthquake and 1906 Mw7.8 San Francisco Earthquakes in California. This study was conducted using a 2-million-year catalog of simulated earthquakes produced by Rate-State EarthQuake Simulator (RSQSim), a physics-based model. We identified 120 events that impacted California, similar to the 1857 and 1906 earthquakes, using events M7+ within a 100-year period. Using the Open Seismic Hazard Analysis and Eclipse software, we generated ShakeMaps that were analyzed in HAZUS, FEMA's risk assessment model. We conducted spatial analysis to calculate the overall casualties counts and economic losses for each scenario. We utilized the 2010 US Census data to visualize and understand seismic risk per county. Using SCEC-VDO (Virtual Display of Objects) and GIS software (i.e. ArcMap and AGOL) we were able to create maps to educate the public on seismic risk for real and simulated earthquakes. We calculated earthquake probabilities and annualized losses in Northern and Southern California to compare damages. Based on our analysis, events in Northern California generated higher losses. These estimates present an alarming concern for the state of California which can be used to improve emergency planning and mitigation efforts.

FRI - 534 Calibration of the Foraminiferal Carbonate Clumped Isotope Paleothermometer

Discipline: Geoscience
Subdiscipline: Other Geoscience

Ingrid Maradiaga*, *University of California, Los Angeles*; Alexandra Valencia Villa, *University of Wisconsin Madison*; Randon Flores, *University of California, Los Angeles*; Christian Blair, *University of California, Los Angeles*; Sena Tay, *Savannah State University*; Naarai Hernandez, *Santa Monica College*; Maxence Guillermic, *University of California, Los Angeles*; Ixchal Gonzalez-Trujillo, *Santa Monica College* and Aradhna Tripati, *University of California, Los Angeles*

Abstract: The assessment of past ocean temperatures is crucial to the investigation and mitigation of global climate change. Clumped isotope thermometry is a relatively new geochemical proxy that can be used to estimate past ocean temperatures based on the chemical chemistry of foraminiferal carbonate shells. This technique relies on the temperature dependence of the abundance of ^{13}C- ^{18}O bonds formed during carbonate calcification. The goal of this study is to develop a clumped isotope calibration for foraminifera by comparing isotope ratios with oxygen isotope-estimates of calcification temperatures and modern ocean water temperatures. We obtained three foraminiferal sample sets comprised of ten species of modern planktonic foraminifera. These foraminifera where collected from 19 sites around the world by extractions of oceanic drill core-top sediments. We measured our samples through a gas-source isotope ratio mass spectrometer, which resulted in calcification temperatures ranging from 2.96 °C to 30.1 °C. The relationship between these foraminiferal Δ_{47} measurements and independently determined calcification temperatures was shown through a linear regression. This calibration of the foraminiferal clumped isotope thermometer will improve through an assessment of the potential effects of carbonate dissolution at depth on Δ_{47}measurements. These results can then be used for current climate model research through application of past temperature reconstructions and carbon cycle patterns.

FRI - 535 Impacts of Land Use and Landscape Position in Denitrification Rates during Spring Snowmelt Period

Discipline: Geoscience
Subdiscipline: Other Geoscience

Pamela Garcia*, *University of Puerto Rico, Mayaguez Campus* and Brittany Lancellotti, *University of Vermont*

Abstract: Spring snowmelt is an important period for nutrient fluxes throughout the watershed and has considerable impacts on water quality. Riparian zones protect hydrological systems from nutrient runoff (Dandie et al., 2011). Denitrification is an important process for reducing nitrogen (N) inputs to riparian zones, which can in turn reduce N loading to streams and rivers. However, if the denitrification process does not go to completion, greenhouse gases (GHG), such as nitrous oxide (N_2O), can be emitted to the atmosphere. This research compares denitrification rates across different landscape positions (upland and wetland) within two types of riparian buffers (agricultural and forested) during the spring snowmelt period in Vermont, USA.

The main focus of this research is understanding how denitrification rates vary within these sites and across these landscape positions. These results will help build a better understanding of how physical soil conditions affect denitrification, which has important impacts on nutrient export and GHG emissions to the atmosphere. We will pair continuous data on physical soil conditions (i.e. volumetric water content, oxygen availability (O_2) and temperature) with denitrification rates and soil N_2O fluxes. With these data, we can detect fluctuations in denitrification rates throughout the snowmelt period and look for relationships between physical soil conditions, soil denitrification rates, and N_2O fluxes. We expect to find that periods with higher soil wetness and less O_2 will result in higher denitrification rates and less GHG fluxes. Final results at the end of the summer will confirm or deny this hypothesis.

FRI - 536 Extracting Ingredients and Recipe Steps within Chemical Documents with Natural Language Processing

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Erick Saenz-Gardea*, *Kansas State University* and William Hsu, *Kansas State University*

Abstract: As our world becomes enhanced by the digital age, the amount of data can be, at times, overwhelming. To combat this, we have begun to use machine learning algorithms and text mining techniques to help us understand all of this readily available information. This work uses machine learning and Natural Language Processing to identify ingredients and recipe containing sentences within manufactured material documents. Utilizing this technology, text documents in the STEM field can be transformed into meaningful values that a computer can interpret and understand. One of our goals is to assist future scholars in their research by cutting down the amount of time needed to analyze and re-analyze an entire paper. The features highlighted here are Part-Of-Speech tagging, Named Entity Recognition, measurements, and Wikification possibilities. Once these features are extracted, we then manually annotate text documents to train the Naïve Bayes Classifier. Our initial results indicate that we have favorable precision of true positives at the cost of a low recall rate. Current research is focused on eliminating the abundance of false positives to improve these values. In addition to this, we have not found a correlation between the number of Wikification possibilities and recipe containing sentences. The ultimate goal for this project is to present step-by-step instructions for the recipe with no additional resources and also providing alternative known recipes with source articles.

FRI - 537 A Data-Driven Approach to Transparency in Political Ads on Social Media

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Elizaveta Atalig*, *Wesleyan University* and Saray Shai, *Wesleyan University*

Abstract: The number of political ads deployed on social media within the United States is increasing tremendously, making the issue of transparency ever more important in our democracy. Companies such as Facebook, Twitter, and Google are attempting to make ads on their platform transparent to the users by collecting information from the groups creating the ads on their platforms. The funding source for each advertisement has to be revealed upon its creation; however, there is the suspicion that funding entities utilize several names to help hide their goals. In this study, we are conducting a large-scale analysis of data extracted from the Facebook API, consisting of political ads run between November 2015 and December 2018. Our goal is to identify ads that appear to be different and supported by different funders but are actually similar in their creative body, and therefore might be part of organized campaigns by a single source. With millions of unique ads, the naïve approach of comparing the text in every pair is not feasible. Instead, we explore various implementations of Locality Sensitive Hashing, where ads are represented numerically and are then compared by their corresponding numbers, making the method scalable for large datasets. We then construct a network of pairwise connections and detect clusters of tightly connected funders based on their ad similarity. Ultimately, by looking at ad behavior through a data-focused perspective we can disrupt efforts of funders to manipulate public opinion and provide an efficient check on political ads shown on social media.

FRI - 538 Creating a Large Cyberbullying Dataset from Multiple Sources to Improve the Accuracy of Cyberbullying Classifications

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Obsmara Ulloa*, *Northeastern Illinois University*; Jorge Garcia, *Northeastern Illinois University*; Mirna Salem, *Northeastern Illinois University*; Christopher Gomez, *Northeastern Illinois University*; Rachel F. Adler, *Northeastern Illinois University*; Francisco Iacobelli, *Northeastern Illinois University* and Rachel Trana, *Northeastern Illinois University*

Abstract: Due to the far-reaching effects of online social networks, cyberbullying is more difficult to control than traditional bullying. Automatic detection of bullying messages can help. However, systems attempting this are usually catered to specific platforms due to the difficulty of collecting and unifying corpora from a variety of sources. Considering this, our research goals are twofold. First, we are developing an extensive corpus of cyberbullying text by unifying existing datasets from sources which include *Ask.fm, Instagram, Formspring*, and *Twitter* in addition to a corpus of text from *Twitter* that we manually labeled. Second, we will develop a tool that social networking sites can use to accurately identify and classify text as cyberbullying. To accomplish these goals, we created Python scripts to gather and combine existing cyberbullying datasets that were largely not standardized in their format and content, in order to create a single, large, and more complete dataset for machine learning algorithms to learn from and for researchers to explore. We extracted key features, like posted comments, labels indicating the presence of cyberbullying, and additional relevant factors such as the username, timestamp, and other demographic data. During this research we will also develop a proof-of-concept application, using machine learning, where users can submit text to have it classified as bullying or not. Additionally, users will be able to agree or disagree with the classification, thus contributing to the corpus. Our work's larger impact is to minimize the amount of cyberbullying on social networking sites.

FRI - 539 Discovery of AF9 Yeats Domain Inhibitors through Structure- and Ligand-Based Virtual Screening

Discipline: Computer & Information Sciences
Subdiscipline: Other Computer and Information Sciences

Ibrahima Doukoure*, *City College of New York* and Yoel Rodriguez, *HOSTOS COMMUNITY COLLEGE*

Abstract: The YEATS (Yaf9, ENL, AF9, Taf14, and Sas5) domain is found in a variety of nuclear complexes with molecular functions ranging from chromatin remodeling and histone modification to transcription, regulation and DNA repair. Among the YEATS family proteins AF9 has been shown to play an important role in potentiating inflammatory gene expression. Recently, it has been reported that the AF9 YEATS domain recognizes preferentially crotonyl-lysine over acetyl-lysine at all three major histone H3 lysine acylation sites (i.e., H3K9|18|27). Dysfunction of the AF9 YEATS domain has been linked to human disease, mainly cancer. Thus, small-molecule modulators capable of disrupting the interaction between the AF9 YEATS domain and histone lysine acylation are of great interest. To identify these small molecules, computer-assisted tools were used in this study. First, a ligand-based search using a hit compound discovered in our group (MS0129775) helped find ~2,000 compounds by screening the eMolecules lead-like database (~6 millions compounds). This initial step was realized using the following software: ROCS3.2.2.26 to conduct the screening and VIDA4.4.0.46 to visualize the top-ranked molecules. Next, a structure- based search was conducted using OEDOCKING3.2.0.26. The selected ~2,000 compounds from the ligand-based search were docked against the binding site of the AF9 YEATS domain. The Tanimoto scoring function and visual inspection were used to prioritize ~100 compounds for purchase availability. The selected ligands could be used to better understand the function of the AF9 YEATS domain in gene transcriptional regulation and ultimately as a therapeutic target in cancer treatment.

FRI - 600 Investigating the Parameters Responsible for tRNA Gene Evolution

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Vanessa Garcia*, *California State University Monterey Bay*; Bryan Thornlow, *University of California Santa Cruz* and Russell Corbett-Detig, *University of California Santa Cruz*

Abstract: Transfer RNA (tRNA) genes encode essential components of translation and are ubiquitous across all domains of life. However, the forces governing their evolution remain poorly understood. Primate genomes contain hundreds of tRNA genes, and because many of these genes are exactly identical in their nucleotide sequences, the tRNA gene family likely exhibits some degree of functional redundancy. Moreover, tRNA genes have remarkable transcription rates, leading to an increase in mutation rate via transcription associated mutagenesis (TAM). tRNA genes are a probable source of disease and fitness costs in human populations due to their high contribution to mutational load in the human genome. The strong deleterious effects of mutations to tRNA genes, combined with an elevated mutation rate, may explain their conservation in primate genomes at high copy-numbers. To investigate this, we have developed a tRNA gene simulator, including a Python interface allowing the user specification of numerous important parameters. Our user-friendly software will be integral to insights on the interplay between genetic redundancy and mutation rate in duplicate gene families, and estimating the parameters governing the evolution of tRNA genes in primate populations.

FRI - 601 Bioinformatic Prediction of Pathways Mediating Neuropathy and Neuropathic Pain in Hispanic and African-American Rheumatoid Arthritis Patients

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

John François*, *ohn Jay College of Criminal Justice, City University of New York* and Lissette Delgado-cruzata, *ohn Jay College of Criminal Justice, City University of New York*

Abstract: MicroRNAs (miRNAs) are a special subgroup of non-coding RNAs which prevent the expression of genes at the post-transcriptional level by binding to complementary mRNA transcripts repressing protein production and targeting the mRNA for degradation. As a result, miRNAs might inhibit multiple mRNAs and are often involved in regulating more than one cellular pathway. Recent studies have shown that miRNAs play a key role in the pathogenesis of rheumatoid arthritis (RA) and other autoimmune diseases. We hypothesize miRNAs mediate neuropathy and neuropathic pain pathways in this disease in African-American and Hispanic RA. To investigate this, we recruited twenty-seven African-American and Hispanic RA patients into a pilot study and measured levels of 800 miRNAs in serum circulating extracellular vesicles using Nanostring nCounter miRNA Expression Panel and analyzed using nSolver Analysis Software. We found that levels of *miR-223-3p* and *miR-16-5p* correlate positively with clinical measures of neuropathic pain: ID pain and the Toronto Clinical Neuropathy Score (TCNS), respectively (Pearson Coeff.ID Pain=0.556, p=0.014 and Pearson Coeff.TCNS= 0.5, p=0.02). We carried out a bioinformatic analysis to predict the targets of the identified miRNAs by using the online database, miRDB. We identified 1,485 gene targets with predicted scores in the range of 60-100. With these targets, we conducted a gene ontology analysis using the Database for Annotation, Visualization and Integrated Discovery (DAVID) and identified the neurotrophin signaling pathway (p=1.00 x 10-4) as a possible important mechanism in RA in this population.

FRI - 602 Cell Cycle Regulation of the Epithelial-Mesenchymal Transition during Sea Urchin Morphogenesis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kristoffer Harris-Smith Harris-Smith*, *New Mexico State University*; Zebib Abraha, *New Mexico State University*; Silvia Sepulveda-Ramirez, *New Mexico State University* and Charles Shuster, *New Mexico State University*

Abstract: Cell motility is a central feature of animal development, and a critical factor contributing to pathogenesis. It has been proposed that cell motility is tied to the cell cycle in cancer cells, but there is little evidence for this during normal development. In *C. elegans*, anchor cell invasion occurs in G1, but it is unknown whether events such as Epithelial to Mesenchymal Transitions (EMT) are similarly regulated. In the sea urchin embryo, mesodermal cells called Primary Mesenchyme Cells (PMCs) undergo an EMT where they ingress from the epithelium and enter the blastocoel, and undergo a final division before they differentiate. We hypothesize that EMT is functionally linked to the cell cycle such that PMCs undergo ingression during G1. Beginning at 15.5 hours post-fertilization, *Lytechinus pictus* embryos were incubated in either DMSO (control) or inhibitors that synchronized embryos in G1 (Palbciclib), S (Aphidocolin), and G2 (Dinaciclib). Embryos were cultured for an additional 6 hours and scored for ingression. Results from three experiments revealed whereas 96% of controls underwent EMT, 63% of S phase-arrested embryos and only 20% of G2-arrested embryos underwent EMT. G1 arrest with Palbociclib resulted in toxicity and EMT could not be evaluated. While better methods to achieve G1 arrest need to be developed, the data suggest that PMC ingression is tied to G1 phase of the cell cycle. To date, this is one of the first examples of cell cycle regulation of EMT during development and further live cell analyses will determine if this is, indeed, the case.

FRI - 603 The Role of HIM-3 during Meiotic Division in *Caenorhabditis Elegans*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Valery Aguilera Ortiz*, *Monterey Peninsula College*; Anna Russo, *University of California, Santa Cruz* and Needhi Bhalla, *University of California, Santa Cruz*

Abstract: Meiosis is a specialized form of cell division that produces haploid gametes such as sperm and eggs. Errors in meiosis can lead to gametes that inherit an incorrect number of chromosomes (aneuploidy), which can result in infertility, miscarriages and genetic disorders such as Down Syndrome. The Bhalla lab is interested in how steps during meiosis such as pairing, synapsis and crossover recombination are coordinated with each other so that chromosomes segregate correctly. A protein complex called the synaptonemal complex (SC) assembles between homologous chromosomes to stabilize them before Meiosis I. HORMA-domain proteins are axial element proteins that are essential for homolog recognition and SC assembly. How these proteins regulate synapsis is an active area of investigation. *Caenorhabditis elegans (C.elegans)* is a great model for studying meiosis because their germlines are organized as a complete time course of prophase I of meiosis, where we can visualize nuclei entering and exiting each stage cytologically. In *C.elegans,* a structural component of the SC called HIM-3 is essential to promote pairing and synapsis. We hypothesize that specific regions of HIM-3 are critical for regulation of synapsis and interactions with other critical meiosis proteins such as PCH-2. To see which regions of HIM-3 are critical for these events, we are characterizing an allele of *him-3* with a deletion in its N-terminus (*him-3* ΔN7-18). We are testing whether deletion of this region affects synapsis and crossover recombination. This will allow us to better understand how these proteins contribute to regulation of meiotic chromosome segregation.

FRI - 604 Characterization of a Genetic Suppressor of a Histone H3 Mutations That Perturbs Transcription Elongation in Budding Yeast.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Linh Nguyen*, *Cabrillo College* and Grant Hartzog, *University of California, Santa Cruz*

Abstract: The basic unit of chromatin, the nucleosome is a protein/DNA complex consisting of 146 base pairs of DNA wrapped around a histone octamer. Nucleosomes are targets of regulation for many biological processes which function on DNA, such as gene transcription. We are interested in how histone H3, one of the four core histone proteins, regulates the structure and function of chromatin during transcription elongation. Our lab has previously identified histone H3 mutations which we hypothesize to disrupt chromatin structure, making chromatin more permissive to transcription elongation. Recently, we isolated genetic suppressor mutations of one of these H3 mutations. We hypothesized that this suppressor mutation restores normal chromatin structure in our H3 mutant. Whole genome sequencing of a yeast strain carrying one of these suppressors revealed mutations in two genes; *IPP1*, which encodes an inorganic phosphatase*,* and *PEP12*, which encodes a t-snare protein. However, genetic analysis shows that the suppressor falls in a single gene. To determine if either the *ipp1* or *pep12* mutation is responsible for suppression, we performed genetic linkage analysis, to determine if either *PEP12* or *IPP1* is linked to the H3 suppressor mutation. Preliminary data suggest that *PEP12* is linked to the suppressor. Our working model is that the genetic suppressor leads to a more restricted chromatin structure. Neither Ipp1 nor Pep12 has been previously implicated in chromatin function. Thus, once we have definitively identified the H3 suppressor, we will examine its effects on chromatin structure.

FRI - 605 The Roles of Tau and Myosin in Mechanical Neuronal Protection

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Sarah Sackey*, *University of California, Los Angeles*; Dail Chapman, *Stanford Universty* and Miriam Goodman, *Stanford Universty*

Abstract: Neurons rely on an internal structural support system, the cytoskeleton, made up of actin microfilaments, intermediate filaments and microtubules. Without these essential structural components: the actin-myosin network and microtubules and associated proteins, neurons lose stability, function and eventually degenerate. Dementia, Alzheimer's and Parkinson's diseases are caused by such neurodegeneration. These diseases are correlated with inappropriate expression and function of the microtubule-associated protein, tau. Similar to tau's function in stabilizing microtubules, actin filaments work closely with myosin to maintain neuronal integrity. Without functional myosin, organisms develop neurodevelopmental disorders and neurodegenerative disorders. Both microtubules and actin work together to support neurite structure and function. However, how their accessory proteins work together is relatively unknown. Here, we study the role of the tau and myosin in mechanical neuronal protection in *C. elegans*. I hypothesized that the disruption of the microtubule stabilizing tau (*plt-1*) and cell membrane stabilizing myosin (*unc-54*) cause defects in the neuron's morphology and function. I suggest that the two proteins act synergistically to protect the neuron from mechanical stress. To investigate this, I developed a *ptl-1* and *unc-54* double mutant *C. elegans* line, then, performed a buckling assay and a touch response assay under a fluorescent microscope to assess neuronal stability, morphology and health. From these assays, I expect to observe the worms displaying a loss of touch sensation and moreover neuronal degeneration. The investigation of *ptl-1* and *unc-54* together could provide insight as to how the stability of the neuronal cytoskeleton is maintained/ stabilized by these accessory cytoskeletal proteins.

FRI - 606 Exploring the Mechanism of Intronogenesis in *S. Cerevisiae*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Alinne Gonzalez Armenta*, *University of California, Santa Cruz* and Manuel Ares, *University of California, Santa Cruz*

Abstract: Introns interrupt almost every human gene, but their contributions to evolution are not fully understood. Evidence suggests the presence of introns allows additional avenues of gene evolution that may have supported the emergence of more complex organisms. While the mechanism for intron loss has been studied, the origin of introns, or intronogenesis, remains unclear. Comparison of related genomes has provided evidence of intron loss and gain, but only provides limited insight into the mechanism. Among several known mechanisms for the appearance of new introns is intron transposition, where a copy of an existing intron is moved to a new location. We are designing a reporter that tracks the movement of a modified version of RPL17b intron to measure how often new introns are transposed in the genome. The modified RPL17b intron contains a mutant nonsense suppressor tRNA gene, SUP4-o, whose correct expression will allow us to screen for intron gain events. The mutant tRNA gene is repaired during splicing and excision of the donor intron from the reporter pre-mRNA. Once reverse splicing and intron transposition have taken place, expression of the repaired Sup4-o gene in its new location will confer several new transposition-dependent phenotypes. We will use inverse-pcr to map transposition events in the genome. Capturing and measuring the frequency of intron-gain events will allow us to investigate the sequence-specific features that drive efficiency of intron gain, identify host genes that contribute to intron transposition, and identify errors in intron transposition that reveal the mechanism.

FRI - 607 Characterizing WNT1 Positive Cellular Projections and Determining If Other Wnts Localize to Cellular Projections

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Leisha Moroney*, *University of California, Santa Barbara*; Lisa M. Galli, *San Francisco State University* and Laura W. Burrus, *San Francisco State University*

Abstract: In multicellular organisms, cells use signals to interact with one another in order to regulate development and adult homeostasis. Wnts are a family of protein signals that regulate proliferation, migration, and differentiation of cells. Misregulation of these signals in embryos causes birth defects and in adults causes cancer. In the Wnt producing cell, Wnts are translated in the endoplasmic reticulum where they are palmitoylated by the enzyme, Porcupine (PORCN). Palmitoylated Wnts are then transported by Wntless (WLS), a cargo transporter, to the cell membrane. However, it is not well understood how Wnts are transported from Wnt producing cells to Wnt receiving cells. One model emerging from work in fruit flies is that Wnts are transported via actin-based filopodia. Our lab has successfully tagged WNT1 with GFP and retained 60% of the wildtype WNT1 activity. Using this tool, we were able to observe in live cells the redistribution of WNT1-GFP to the plasma membrane and cellular projections with the overexpression of WLS. We do not yet know if these cellular projections are filopodia nor do we know if WLS can cause the redistribution of other Wnt family members. We hypothesize that WNT1-GFP positive projections will contain actin, but not tubulin, and that WLS will be able to cause the redistribution of WNT3A and WNT7A. To test this hypothesis, we will distinguish whether the cellular projections are actin-based and therefore characterized as filopodia, or tubulin-based. In addition, we will assess the ability of WLS to direct the redistribution of WNT3A-GFP and WNT7A-GFP.

FRI - 609 Discovering Molecular Mechanisms That Link Mitotic Entry to Cell Growth

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

David Sanchez Godinez*, *University of California, Santa Cruz*; Francisco Mendez Diaz, *University of California, Santa Cruz* and Doug Kellogg, *University of California, Santa Cruz*

Abstract: Cell cycle progression is subservient to cell growth. It only occurs once sufficient growth has occurred. However, the mechanisms that are used to measure growth and relay growth-dependent signals to the cell cycle machinery are largely unknown. The Wee1 kinase is thought to be a key link between cell growth and the cell cycle. Wee1 phosphorylates and inhibits mitotic Cdk1, which is thought to prevent mitotic entry until sufficient growth has occurred. Loss of function of Wee1 causes cells to enter mitosis before sufficient growth occurs, leading to smaller daughter cells. We hypothesize that Wee1 is regulated by a signaling pathway that responds to cell growth. To test this hypothesis, we will use *in vitro* reconstitution to define the mechanisms that control Wee1 activity. We will express tagged Wee1 in *E. coli* and use affinity chromatography to obtain purified protein. We will then use purified candidate kinases that respond to growth to test whether they can directly inhibit Wee1 activity. We will also construct an affinity column containing Wee1 conjugated beads to find additional cofactors or key regulators of Wee1. Together, these experiments will test for a direct link between cellular growth and cell cycle progression. Cell growth is fundamental and, most likely, highly conserved throughout eukaryotes. This research is important because improper growth control is a key feature of cancer. If we discover key features of cell growth control, then we may be able to target cancer directly.

FRI - 610 Mixed Lineage Kinase-3 Opposes Stress Fiber Formation in Vascular Smooth Muscle Cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jonathan Aguirre*, *Tufts University School of Medicine* and Robert Blanton, *Tufts University School of Medicine*

Abstract: Mixed lineage kinase-3 (MLK3) is a serine/threonine kinase which functions as a mitogen-activated protein kinase kinase kinase (MAP3K) in activating multiple MAPK pathways. MLK3 regulates signaling in Vascular Smooth Muscle Cells (VSMC), but its role in modulating VSMC phenotype remains unknown. Our lab observed that MLK3 deletion causes hypertension in mice, possibly through increased vascular stiffness. Therefore, the aim of this study is to determine the function of MLK3 in regulating VSMC stress fiber development. We hypothesize that VSMCs from mice with MLK3 genetic deletion (MLK3$^{-/-}$), will develop increased stress fibers, indicating a mechanism of vascular stiffness. To test this, we will compare VSMC stress fiber formation from cultured VSMC from aortas of MLK3$^{-/-}$ and MLK3$^{+/+}$ mice. VSMCs from aortas of MLK3$^{-/-}$ and MLK3$^{+/+}$ were stained with Phalloidin-conjugated to a fluorescent probe to bind to actin, as well as with DAPI to stain nuclei, followed by visualization with fluorescent microscopy. VSMC area was measured (n=99 cells in WT, 83 cells in $^{-/-}$) and we discovered MLK3$^{-/-}$ VSMCs had reduced area (9820.0 pixels/cell in $^{-/-}$) compared to VSMCs from MLK3$^{+/+}$ mice (14579.6 in $^{+/+}$, p= 0.011). These findings suggest that MLK3 genetic deletion reduces VSMC size. Future studies will determine whether MLK3$^{-/-}$ cells also have an increased number of stress fibers. These findings support a role for MLK3 in reducing vascular stiffness and blood pressure through regulation of individual VSMC size and stress fiber content.

FRI - 611 Visualization of Beta-Galactosidase Activity in Candidatus *Saccharibacteria* from Oral Plaque with Fluorescence in Situ Hybridization

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jordan Maldonado*, *San Jose State University*; Matthew Cope, *California State Univerisity San Marcos*; Manasa Rapuru, *San Jose State University*; Farsheed Ghadiri, *San Jose State University* and Cleber Ouverney, *San Jose State University*

Abstract: Candidate Division TM7, otherwise known as Candidatus *Saccharibacteria*, is an uncultivable phylum of bacteria that is ubiquitous in many environments and the human oral cavity. The role these bacteria play in the human body is only weakly understood but previous studies have indicated that specific TM7 strains are potentially pathogenic. To date, no functional studies have attempted to characterize the role TM7 cells may play in the oral plaque microbiome. The objective of our research was to better understand the metabolic capabilities of TM7, particularly within the context of the human oral microflora, to establish a model for how they affect human health. For our methodology, we used fluorescence *in situ* hybridization (FISH) to identify TM7 bacteria in human oral plaque samples. By using fluorescently labeled probes and fluorescent lactose analogs, we captured the first images of oral TM7 metabolizing lactose through enzymatic hydrolysis *in situ*. As a positive control, we isolated a beta-galactosidase gene from a TM7 bacterium, cloned it into an expression vector, and then transformed this plasmid into a strain of *Escherichia coli*. Preliminary results using lactose analogs such as X-Gal and ONPG, yielded favorable results for the metabolization of lactose by the TM7 beta-galactosidase. We propose that TM7 bacteria are capable of utilizing lactose as an energy source through the production of a beta-galactosidase in situ. Going forward, we plan to determine optimal activity conditions for this enzyme to further our understanding of the needs of TM7 bacteria.

FRI - 612 Cell Landscapes: Relating Organelle Size, Localization, and Morphologies to Cell State

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Adrian Barrera-Velasquez*, *San Francisco State University* and Mark Chan, *San Francisco State University*

Abstract: Eukaryotic cells represent a higher degree of complexity in life, and they differ from bacteria and archaea by possessing specialized internal compartments known as organelles. These cells rely on the individual regulation of and coordinated interactions between their different organelles to carry out proper cellular functions. Given this relationship we expect to see certain “cell states” where the size, localization, or morphology of a cell’s organelles can inform us of the functions currently being carried out. We see evidence for this in our model organism *Saccharomyces cerevisiae*, otherwise known as budding yeast. The ER and mitochondria co-localize in order to carry out mitophagy, the controlled break down of the mitochondria. Organelle size and morphology are similarly associated with cell states where we see enlarged vacuoles following DNA replication or increased mitochondrial networks during respiration. The question naturally arises then, what other organelle size distributions, localizations, and morphologies do we commonly see and what cell states do they imply? To answer this, we have fluorescently tagged different organelle’s membrane proteins to visualize these metrics. We do this using fluorescence confocal microscopy to obtain 3D landscapes of the cell and image processing techniques. By observing a population of cells, we should see a variety of different landscapes with certain variations occurring more commonly than others. Characterizing these cell states can be a powerful tool in monitoring cell environments such as detecting heavy metal toxicity or even discovering distinct cancer cells’ organelle morphologies.

FRI - 613 Characterizing the AFF3 Promoter Region

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Lesslie Jocol-Perez*, *California State University Northridge* and Cindy Malone, *California State University, Northridge*

Abstract: AF4/ Fragile Mental Retardation 2 (FMR2) Family member 3 (AFF3) is a nuclear transcriptional activator that is tissue-restricted to lymphoid tissue and is associated with normal lymphoid development, but also with lymphoid tissue oncogenesis. Thus, AFF3 gene expression must be accurately controlled. The putative promoter region was identified using GenBank, PCR amplified from genomic DNA, and inserted into the pGL3 luciferase reporter vector. Sequential 5' deletions of the putative promoter region were transiently transfected and the putative promoter with the greatest transcriptional activity was found 267bp upstream of the transcription start site. Bioinformatics analysis using Alibaba 2.1, PROMO, and MATCH algorithms defined consensus transcription factor binding sites c-Ets-1, AP-1, and c-Myc. A multiple sequence alignment of nine species showed that only AP-1 and c-Ets-1 were evolutionary conserved. The AP-1 and c-Ets-1 conserved consensus transcription factor binding sites will be mutated and analyzed by transient transfection to determine functional activity. The hypothesis is that c-Myc controls the AFF3 promoter expression. Identifying which transcription factors influence AFF3 gene expression can provide insight on diseases caused by AFF3 dysregulation.

FRI - 614 A Screen for Cryptic Epigenetic Variation in Natural Populations of *Drosophila Melanogaster*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Joanna Portillo*, *California Lutheran University*; David Marcey, *California Lutheran University*; Lauren McAllister, *California Lutheran University*; Alyssa Abano, *California Lutheran University*; Madison Katz, *California Lutheran University*; Kaitlyn Hofmeister, *California Lutheran University*; Devin Romines, *California Lutheran University*; Makenna Wolfrom, *California Lutheran University*; Dagem Getahun, *California Lutheran University*; Mary Kaveney, *California Lutheran University* and Chloe Walian, *California Lutheran University*

Abstract: We are conducting a screen for novel sources of cryptic genetic variation (CGV) in populations of *Drosophila melanogaster.* CGV may be a component in the spectrum of natural variation. Our screen is based on a model for *extra eye* (*ee*), an incompletely penetrant, variably expressed, and conditionally dominant mutation. A component of the *ee* mutation co-maps with a P-transposable element inserted into the 5' exon of the *Cpr* gene such that P-antisense RNA will be embedded in *Cpr* transcripts, providing a possible source of P-element dsRNA in the presence of P-element sense transcripts. The model posits resulting RNAi-mediated suppression of genes near P-elements via epigenetic heterochromatization. One such target is *Su(var)2-10*, a repressor of activated STAT, implicated in embryonic eye field establishment. The proposed model for *ee* predicts that new mutant phenotypes may be uncovered in crosses between *ee* lines and flies from natural populations that harbor P-elements at various genomic locations. Such novel mutants are predicted to be caused by epigenetic silencing via RNAi-induced heterochromatization of genes near P-elements. We are conducting screens for such cryptic, epigenetic mutations by crossing wild-derived lines to *ee.* We report here the recovery of two new mutations that exhibit the properties expected of epigenetic suppression. We propose that variation may include cryptic, epigenetic sources linked to transposable elements, which are revealed under genetic contingencies. Screens of wild-derived strains for additional cases of cryptic phenotypes are ongoing, as are genetic and molecular characterizations of P-element insertions and mutations recovered to date.

FRI - 615 Exploring the Role of a Newly Discovered Vitelline Layer Gene on Eggshell Formation in *C. Elegans*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Alejandro Tovar*, *Pomona College* and Sara Olson, *Pomona College*

Abstract: Embryos from all animal species are surrounded by an egg coat that protects them after fertilization. In nematode worms, such as *C. elegans*, this coat is called an eggshell, and has proven to be one of the most impermeable membranes in the animal kingdom. Understanding how this protective barrier is built and what makes the matrix so impenetrable can lend insight into reproductive biology, and help identify potential drug targets to combat parasitic nematode infection. The *C. elegans* eggshell is made up of four layers: the outermost being the Vitelline layer followed by the Chitin layer, Chondroitin Proteoglycan (or CPG) layer, and Permeability Barrier layer. Our lab has identified a new protein that interacts with proteins on the Vitelline layer, but nothing is known about its function or localization. Using CRISPR/Cas-9 as a way to genetically modify both a deletion and a GFP tag of the gene, its function can be better understood. The goal of this study will be to create strains of worms that have either been modified to lack expression of this gene or express this gene with green fluorescence, therefore allowing us to study how this gene will affect the formation of the eggshell and if it plays a major role in generating its permeability.

FRI - 616 Reassembly of Active Dihydrofolate Reductase Fragments in *Plasmodium Falciparum* and Potential Applications in Protein Interaction Studies

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Anne Berhe*, *Pomona College* and Andrew Osborne, *University College London*

Abstract: *Plasmodium falciparum* is the most deadly malaria parasite of humans, and it is essential that techniques for studying its basic parasite biology are improved. In particular, methods for detecting novel protein interactions in the parasite are lacking. Protein complementation assays that use split enzymes to detect protein interactions have been widely used in many systems, but not in *Plasmodium*. By implementing an enzyme reassembly system in *P. falciparum*, we hope to develop a method for detecting protein-protein interactions. Dihydrofolate reductase (DHFR), has been widely used in such protein complementation assays. Typically, N- and C-terminal fragments of DHFR are expressed but do not reconstitute an active DHFR enzyme unless they are fused to interacting proteins that bring the two halves of the enzyme together. While the fragments do not have enzymatic activity alone, their oligomerization produces a fully functional DHFR enzyme. In order to test whether DHFR reassembly is possible in a parasite species, *P. falciparum* parasites were transfected with plasmid DNA containing mouse DHFR (mDHFR) fragments and a homodimerizing leucine zipper sequence. Parasites were subsequently cultured *in vivo* in human erythrocytes. Parasites expressing complementary mDHFR fragments demonstrated the dimerization of mDHFR through their resistance to the drugs WR and pyrimethamine. This is the first time that DHFR reassembly has been shown to operate in any parasite species, making this model a stepping stone for further study of protein interactions and other aspects of parasite biology.

FRI - 617 Histological Analyses of Depleted Uranium Implantations in Zebrafish

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Phillip Kalaniopio*, *Northern Arizona University*; Ronald Allen, *Northern Arizona University* and Matthew Salanga, *Northern Arizona University*

Abstract: Modern combat theaters pose an immense safety risk to service members and civilians in the form of depleted uranium (DU) exposure. DU-containing munitions are used by militaries around the world; therefore we aim to answer questions pertaining to DU chemical toxicity, the specific mechanisms of action, and potential environmental modifiers. Specifically, we want to know if DU that is internalized through shrapnel or wound contamination is carcinogenic. We will utilize a humanized zebrafish line to test these embedment possibilities using two different DU oxide compounds: UO_2 and U_3O_8. These fish express the human oncogene $BRAF^{V600E}$ under the control of a melanocyte promoter, and reliably develop ectopic nevi and melanoma. This background would represent a genetically compromised and sensitive individual while also modeling a relevant exposure route: shrapnel injury *in vivo*. This project will use different histological analyses to assess and quantify tissue damage and carcinogenicity.

FRI - 618 Impact of Blood Collection and Handling Procedures on Zinc Assessment

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Bonny Alvarenga*, *University of California, Berkeley* and David Killilea, *Children's Hospital Oakland Research Institute*

Abstract: An estimated 30% of the world population is zinc deficient, leading to increased infection, disease, and even death in children who lack adequate zinc intake. Zinc assessment is usually determined by blood analysis, but this can be compromised when suboptimal processing results in artifactually elevated zinc concentrations. To evaluate the impact of collection and handling procedures, we tested for several known problems in blood collection tubes and blood zinc analysis. First, we measured zinc levels in plasma from collection tubes with different anticoagulant types and mineral certification using inductively coupled plasma optical emission spectrometry (ICP-OES). Variance in the blood handling procedures over a 7-day period showed that suboptimal handling can have a significant impact on zinc content, with extended exposure resulting in up to a 4-fold increase in zinc concentration depending on types of anticoagulant and tube certification. Then, we measured the effects of hemolysis on the zinc levels in blood samples and created a visual hemolysis indicator to help researchers quickly assess the quality of blood samples for zinc analysis. Finally, we determined the sensitivity and accuracy of different methods for measuring hemoglobin, including the HemoCue 201+ instrument and Drabkins assay, to standardize the use of hemolysis thresholds. These study results will be provided to technical groups including the International Zinc Nutrition Consultative Group (IZiNCG) to provide guidance to zinc assessment study designs.

FRI - 619 Identification of Factors Which Play a Role in the Binding of Long Non-Coding RNA to Chromatin in Drosophila

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Javier Montelongo*, *California Lutheran University* and Maya Capelson, *University of Pennsylvania*

Abstract: Dosage compensation is an epigenetic mechanism which equalizes the gene expression of an uneven number of chromosomes. Many organisms have developed various mechanisms to correct this imbalance. In *Drosophila melanogaster*, there is an up-regulation of the single X-chromosome in the males to compensate for its monosomy. Up-regulation of this male X-chromosome is performed by the dosage compensation complex (DCC). The DCC contains long non-coding RNAs Rox1/2 which organize the chromatin of the X chromosome in Drosophila males so that transcription can occur at a rate two times higher to match that of females. But how this critical non-coding RNA binds to the chromatin remains unknown. My project focused on identifying which factors participate in targeting non-coding RNA to chromatin. The UAS/Gal4 RNAi activation system was used in Drosophila to knock down candidate genes that affect different steps in RNA processing. Following knockdown, RT-qPCR was conducted on male salivary glands to determine efficiency of knockdown. If a successful knockdown was determined, then FISH (fluorescence in situ hybridization) against the non-coding RNA roX1 was conducted in salivary gland cells. Knockdown of Hrb98DE showed no delocalization of roX1 by RNA FISH while knockdown of Rrp6 and Dis3 (exosome component) showed partial delocalization of roX1. Knockdown of Saf-B and SF1 (spliceosome components) showed presence of extra nuclear soluble roX1. Together, the results of this project will shed light on which factors are required to bring a noncoding RNA to chromatin and will lead to a better understanding of dosage compensation.

FRI - 620 A Novel Combination of Plasmid Mediated Antibiotic Resistant and Heavy Metal Resistant Genes in Environmental *Klebsiella Pneumoniae*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jack Shanahan*, *University of California, Irvine* and Luis Mota-Bravo, *University of California Irvine*

Abstract: Bacterial infections are resurging as a major public health threat as plasmid mediated antibiotic resistant genes (ARGs) spread in Gram-negative bacteria. Understanding the global patterns of dissemination among ARGs is crucial in addressing the threat antibiotic resistance poses to public health. Our hypothesis is that the environment could be a reservoir for the dissemination of ARGs. The objective of this study was to analyze the genetic context of a plasmid isolated from *Klebsiella pneumoniae*in Southern California's Cucamonga Creek for ARGs. Plasmid DNA was sequenced to reveal a 249,464 bp plasmid with eleven ARGs and sixteen heavy metal resistance genes (HMRGs). Disk diffusion test showed the resistance phenotype for six classes of commonly used antibiotics, beta-lactams, trimethoprim, aminoglycosides, sulfonamides, tetracyclines, and fluoroquinolones. Bioinformatic analysis revealed similar plasmids in Australian and Spanish clinics, but this is the first report of this plasmid which contains a unique set of ARGs in the presence HMRGs. The present work suggests that environmental *K. pneumoniae*in Southern California are a reservoir for ARGs found in hospitals across the planet. Furthermore, our results show that these ARGs are capable of existing in the same genetic environment as HMRGs, thereby suggesting a metal facilitated co-selection of antibiotic resistance. This combination of ARGs and HMRGs may render bacteria with the capacity to survive harsh environments contaminated with metals and spread ARGs more extensively, a problem that must be further studied in response to antibiotic resistant bacteria.

FRI - 621 Characterizing the Role of Long Non-Coding RNAs in Malaria Parasites Gene Expression and Survival

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Anthony Cort*, *University of California, Riverside*; Karine Le Roch, *University of California, Riverside*; Gayani Batugedara, *University of California, Riverside*; Tina Wang, *University of California, Riverside*; Desiree Williams, *University of California, Riverside* and Xueqing Lu, *University of California, Riverside*

Abstract: The human malaria parasite, *Plasmodium falciparum*, infects over 200 million people and claims 438,000 lives each year. The absence of an efficacious vaccine and resistance to all currently used antimalarial drugs emphasizes the need for new therapeutic strategies that can disrupt the parasite's complex lifecycle. These lifecycle stages are tightly regulated by changes in gene expression; however, the exact mechanisms regulating gene expression are unknown. Previous studies in our lab have suggested that one promising mechanism controlling gene expression is epigenetic regulation by nuclear long noncoding RNAs (lncRNAs). Epigenetic regulation involves chemical or structural "twists" that affect DNA accessibility and gene activity without altering the underlying genetic code itself. My project aims to investigate the role of lncRNAs in gene expression and parasite survival. Using fluorescence *in situ* hybridization (FISH) assays and chromatin isolation by RNA purification (ChIRP) sequencing techniques, I have validated the existence and localization of nuclear lncRNAs. I will now use novel genetic and molecular techniques such as the CRISPR-Cas 9 gene editing system to knockout candidate lncRNAs for functional characterization. Altogether, this work will bring insight into an entirely new class of regulatory elements that could be crucial for malaria survival. With a better understanding of gene expression regulators, new drug targets can be identified to create new, specific, and effective antimalarial therapies.

FRI - 622 Profiling Immune Signaling Networks Using Mass Cytometry to Predict an Inflammatory Bowel Disease Patient's Response to Anti-TNF Therapy

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Joseph M. Gaballa*, *Mayo Clinic*; Adebowale B. Bamidele, *Mayo Clinic*; Manuel B. Braga Neto, *Mayo Clinic*; Michelle M. Gonzalez, *Mayo Clinic*; Guilherme P. Ramos, *Mayo Clinic*; Mary R. Sagstetter, *Mayo Clinic*; Olga F. Sarmento, *Mayo Clinic* and William A. Faubion, *Mayo Clinic*

Abstract: Crohn's disease and ulcerative colitis are two types of inflammatory bowel diseases (IBD) characterized by chronic inflammation of the gastrointestinal tract. Biologic therapies targeting molecules associated with driving inflammation have led to a paradigm shift in the way that IBD is clinically managed. One class of biologic therapies, anti-TNF inhibitors, block activity of tumor necrosis factor alpha (TNF-α) and are often effective at inducing remission and controlling inflammation for extended periods of time. However, the heterogenous nature of IBD accounts for up to 40% of patients failing to respond to anti-TNF therapy. Given such high variability, developing individualized approaches to selecting the right therapy for a patient is critical for improving clinical outcomes. Sharing many similarities with flow cytometry, mass cytometry is a technique that can be used to profile immune signaling networks in high-dimension with single-cell resolution. In this study, we isolated peripheral blood mononuclear cells (PBMCs) from IBD patients that either responded to, or failed to respond to anti-TNF therapy, as well as healthy controls. We stimulated these cells under 10 different conditions, and performed mass cytometry on them using a panel of antibodies targeting surface markers, and phosphorylation sites involved in JAK/STAT, NF-κB, and MAPK signaling. Here we highlight preliminary data demonstrating the novelty of this approach for identifying functional variances in immune signaling networks, and explore how these findings will help unravel the molecular underpinnings associated with lack of response to anti-TNF therapy in IBD.

FRI - 623 Characterizing NHR-23 Activity in the *Caenorhabditis Elegans* Molting Cycle Using Fluorescence Microscopy

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Joseph Aguilera*, *University of California, Santa Cruz*; Londen Johnson, *University of California, Santa Cruz* and Jordan Ward, *University of California, Santa Cruz*

Abstract: Parasitic nematodes affect the health of over 1.5 billion people globally. We are exploring whether the conserved transcription factor Nuclear Hormone Receptor 23 (NHR-23) is a good target to inhibit the growth and reproduction of these parasitic nematodes. First, we are characterizing the role of NHR-23 in the non-parasitic model nematode *Caenorhabditis elegans* (*C. elegans*) molting cycle. Immediately upon hatching, *C. elegans* larvae enter the first of four larval stages (L1, L2, L3, & L4); they must successfully enter and exit each larval stage to become fully mature. If a nematode fails to shed their old cuticle, they will not be able to grow and reproduce; therefore, the molting cycle makes for an excellent drug target. NHR-23 was previously found to be essential in the *C. elegans* molting cycle, however expression of the protein remained unknown. Here, I determine when and where NHR-23 is expressed in the L1 stage. This was done by tagging the C-terminus of NHR-23 with a Green Fluorescence Protein (GFP) via CRISPR/Cas9. Then using a fluorescence microscope, I examined NHR-23 expression. NHR-23 was observed in the hypodermal and seam cells at unique time points in the L1 stage; both cell types are known to drive the secretion and formation of the nematode's cuticle. The results give us great insight to when we should use the Auxin-inducible degradation (AID) system to conditionally deplete NHR-23, ultimately determining when NHR-23 may be essential for the molting cycle to proceed.

FRI - 624 Development of Rheumatoid Arthritis: Joint-Specific Hoxd Gene Expression in Synovial Fibroblasts

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Samuel Hernandez*, *Knox College*; Kerstin Klein, *University Hospital of Zurich*; Monika Krosel, *University Hospital of Zurich*; Kira Nathan, *University Hospital of Zurich*; Oliver Distler, *University Hospital of Zurich*; Mojca Frank-Bertoncelj, *University Hospital of Zurich* and Caroline Ospelt, *University Hospital of Zurich*

Abstract: Rheumatoid arthritis (RA) is a chronic autoimmune disease that induces inflammation of joint synovial tissue leading to synovial joint destruction and disability. Rheumatoid arthritis synovial fibroblasts (RASFs) have a prominent role in RA's destructive inflammatory process. Previous observations indicate that RASFs demonstrate stable altered phenotypes, based on epigenetic changes; however, these phenotypes are poorly understood. To that end, RNA sequencing analysis of human RASFs from hand, shoulder, and knee joints demonstrated a particular gene locus to be differentially expressed at distal joint locations: the HOXD locus, involved in embryonic limb positional development. We hypothesized that HOXD gene expression in RASFs may be involved in the development of joint specific RA patterns.

To gauge the effect of HOXD expression on RASF cell survival, Gapmer gene-silencing of HOXD10, HOXD11, and HOXD13 was conducted. Using qRT-PCR, we measured the amount of HOXD expression from various disease states (osteoarthritis, RA, and healthy) throughout commonly affected joints. RNA sequencing discerned functional differences and similarities between HOXD10, HOXD11, and HOXD13.

We demonstrate prolonged silencing of HOXD gene expression (HOXD10 and HOXD13) increases apoptosis in RASFs, HOXD expression is more prominent in distal locations (hands and ankles) than more proximal locations (hip and shoulders), and HOXD genes (HOXD10, HOXD11, and HOXD13) have functional pathway differences.

These findings suggest that HOXD gene expression may influence RASF cell survival, HOXD expression is joint-specific, and HOXD genes while related have distinct functional roles. Ongoing experiments include localization of HOXD expression in synovial tissue and in vivo silencing of HOXD expression.

FRI - 625 The Yeast Kinase Ksp1 Regulates Cellular Stress Response

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Angela Hsu*, *University of Michigan*; Nebibe Mutlu, *University of Michigan* and Anuj Kumar, *University of Michigan*

Abstract: Pseudohyphal growth is a cellular stress response in yeast. Under low glucose or nitrogen conditions, yeast cells undergo a change in growth pattern from unicellular vegetative growth to filamentous growth in which yeasts form elongated, connected chains of cells. The transition is essential for virulence in pathogenic yeast such as *C. albicans* and is also relevant to the ERK/MAPK pathway. The Kumar lab discovered that the *KSP1* gene encodes a kinase that is required for pseudohyphal growth, which is likely due to Ksp1's association with the Target of Rapamycin Complex (TORC1). A loss-of-function *ksp1* mutation decreases the extent of pseudohyphal growth in yeast. Ksp1 kinase activity is also found to regulate the localization of TORC1, and Ksp1 colocalizes with TORC1 when yeast is under stress. This could suggest that Ksp1 is important for cell stress responses since TORC1 is known to regulate translation under stress. Furthermore, a putative binding site for the cap binding translation initiation factor eIF4E, whose homolog in yeast is Cdc33, is found in Ksp1, so we hypothesized that there is an interaction between Cdc33 and Ksp1. Yeast two-hybrid and co-immunoprecipitation are used to identify if there is a protein-protein interaction between Cdc33 and Ksp1, which would provide more insight into Ksp1's role in cell stress response.

FRI - 626 Multidrug Resistant *Escherichia coli* ST1193 Collected from an Aquatic Environment

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

JoAnne Villagrana*, *University of California, Irvine*; Andrey Tatarenkov, *University of California, Irvine* and Luis Mota-Bravo, *University of California Irvine*

Abstract: Antibiotic resistance poses a threat for the public health. The novel fluoroquinolone-resistant *Escherichia coli* clone ST1193 is emerging in the United States and is mainly associated with urinary tract infections. We hypothesize that resistant ST1193 *Escherichia coli* isolates are present in the environment. The objective of the study is to identify the resistance phenotype and genotype of an environmental *E. coli* ST1193. Isolate SW4904 was collected from Capitol Lake, Baton Rouge, Louisiana and identified as *E. coli* via MALDI-TOF mass spectrometry. We established a resistance profile. Plasmid and total genomic DNA were extracted and sequenced. The sequence reads were assembled and analyzed. Plasmid and chromosomal characterizations were conducted using PATRIC, Goseqit, CGE, and the NCBI databases. Transformation was conducted to

identify plasmid-borne resistances. Using multilocus sequence typing, it was confirmed that the isolate belongs to the ST1193 sequence type. It showed full resistance to aminoglycosides, beta-lactams, quinolones, sulfonamides, tetracyclines, and trimethoprim antibiotics. It contains 3 plasmids of 95 kb, 4 kb, and 2 kb respectively. Transformation results confirmed that the largest plasmid harbored *bla*$_{TEM\text{-}1B}$, *strA*, *strB*, *sul2*, *tetB*, and *dfrA17* resistance genes associated with the resistance phenotype observed. Mobile genetic elements flank the multidrug resistant region containing those genes. When compared with databases, the resistance region appeared to be unique. Clinical *Escherichia coli* ST1193 are known to hold similar phenotypic resistance to SW4904. Our results indicate the environment might represent a reservoir of multi-drug resistant *Escherichia coli* ST1193 that could cause infections difficult to treat in clinical settings.

FRI - 627 EndophilinA2 Phosphorylation Regulates Endocytosis of Nutrient Transporters

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Cuauhtemoc Ramirez*, *University of California, Irvine*; Brendan Finicle, *University of California, Irvine* and Aimee Edinger, *University of California, Irvine*

Abstract: Sphingolipids, a group of evolutionarily conserved molecules, selectively starve cancer cells to death by limiting access to both extracellular and intracellular nutrients. The endogenous tumor suppressive sphingolipid ceramide limits access to extracellular nutrients by internalizing nutrient transporters from the cell surface. Activation of the serine/threonine protein phosphatase 2A (PP2A) is necessary for this endocytic event. To identify proteins that are dephosphorylated in response to ceramide, possibly by PP2A, a quantitative kinetic phosphoproteomics screen was performed. EndophilinA2 (EndoA2), a protein known to be involved in endocytosis, was identified in the screen to be rapidly dephosphorylated in response to ceramide at Ser288. As EndoA2 plays a critical role in endocytosis, its dephosphorylation could be responsible for the internalization of surface nutrient transporter proteins. To gain insight into the potential regulatory role of phosphorylation of EndoA2 at this site, two EndoA2 missense mutations were generated via site-directed mutagenesis at Ser288: 1) a serine to aspartic acid (S288D), to mimic a phosphorylated site that cannot be dephosphorylated, and 2) a serine to alanine (S288A), to mimic a dephosphorylated site which cannot be phosphorylated. These plasmids will be transfected into mammalian cells to determine whether dephosphorylation of EndoA2 is necessary and/or sufficient to cause nutrient transporter loss and cell death in cells exposed to synthetic and natural sphingolipids. These findings would further define pathways by which nutrient access is regulated in mammalian cells.

FRI - 628 Characterization of SHP-1 Signaling to Sepsis-Induced Changes in Macrophages Function and Overall Survival

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Myles Bartholomew*, *Xavier University of Louisiana*; Chun-Shiang Chung, *Brown University*; Yaping Chen, *Brown University* and Alfred Ayala, *Brown, Alpert Medical School*

Abstract: Sepsis is the leading cause of death in critically ill patients. Our lab previously demonstrated that heightened expression of PD-1 and PD-L1 were observed in septic background control mice and were associated with a dysfunctional adaptive and altered innate immune response. The PD-1 receptor has two conserved signaling sequences of amino acids located within the cytoplasmic tail, referred to as an intracellular tyrosine inhibitory motif (ITIM) and intracellular tyrosine switch motif (ITSM). Their phosphorylation allows other enzymes such as Src homology region 2 domain-containing phosphatase 1 (SHP-1) to reduce activation of the Akt/PI3K pathway. Akt inhibits the expression of proteins that promote apoptotic processes. By antagonizing the recruitment or function of SHPs during the process of antigenic T-cell activation, the Akt/PI3K pathway can perpetuate proliferation and bolster the immune response. Considering this information, we hypothesize that in response to the increased expression of PD-1 caused by sepsis, SHP-1 is recruited and activated. In turn, this upregulation should hinder the immune cell's ability to respond to the pathogenic challenge. To examine this hypothesis, we provide data on the phosphorylated(p)SHP-1/total(t)SHP-1 ratio observing significant increases in (p)SHP-1 for J774 mouse macrophage cell lines over time, as well as in peritoneal macrophages. Additionally, the effects of tyrosine phosphatase inhibitor 1 (TPI-1) and the cytokine profile during these septic models is observed. It is hoped that this study will elucidate not only if SHP-1 is activated in excess by sepsis, but if it might be a novel target for increasing resistance to experimental septic mortality.

FRI - 630 Dissecting Determinants of Protein Stability upon Translation Readthrough

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Heddy Menendez*, *University of California, Santa Cruz* and Joshua Arribere, *University of California Santa Cruz*

Abstract: Errors occur during the replication and decoding of the genome. If not efficiently dealt with, products of those errors accumulate and have deleterious outcomes for cells. To combat the consequences of mutation and error, cells possess quality control mechanisms to survey and remove aberrant gene expression products. We are studying one particular quality control pathway which identifies and removes proteins that result from readthrough of a stop codon. We have found that the amino acid sequence encoded by the 3' UnTranslated Region (3' UTR) downstream of the stop codon is responsible for protein loss. We are investigating determinants of this process by tethering 3'UTR-encoded peptides to the C-terminus of GFP in the model organism *Caenorhabditis elegans*. In analyzing sequence determinants of protein loss upon readthrough by the ribosome for one gene (*unc-54*), we identified a short segment that is critical for repression and GFP loss: the 5 amino acid hydrophobic sequence "LFLLL" located within a 30 amino acid sequence encoded by the *unc-54* 3' UTR. Ongoing work focuses on generating mutations in this sequence to determine the effect on protein expression through analyzing various levels of hydrophobicity. Our results tackle the questions: Is hydrophobicity alone sufficient for the observed effect? Is repression all-or-nothing, or are varying degrees possible? By determining the threshold for the effect that hydrophobicity in the 3' UTR has on GFP expression, we get one step closer to understanding how the genome is affected by the changes in gene expression and function caused by DNA sequence.

FRI - 631 The Role of MYO7A in Usher 1B Syndrome

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Sonia Bustos*, *University of California, Los Angeles*; Joyce Zhang, *University of California, Los Angeles*; William Blake Gilmore, *University of California, Los Angeles* and David Williams, *University of California, Los Angeles*

Abstract: Usher syndrome is an autosomal recessive disease characterized by congenital deafness and progressive retinal degeneration. Usher Syndrome type 1B is characterized by loss-of-function mutations in the *MYO7A* gene which encodes an unconventional myosin protein expressed in the retinal pigment epithelium. Early-stage clinical trials are using gene therapy to deliver a healthy MYO7A gene to USH1B patients, thereby providing a curative treatment. The therapy consists of a lentivirus containing cDNA from one of the two major MYO7A isoforms, isoform 2 (IF2). A recent study revealed two USH1B patients contain a disruption in a splice acceptor of IF1, therefore, these patients should only express isoform 2. Interestingly, both patients demonstrate severe USH1B symptoms. This suggests gene therapy using IF2 may not be sufficient to overcome USH1B symptoms. It is necessary to determine whether the other major isoform, IF1, is required for disease resistance. The focus of this study is to determine how the presence or absence of each isoform relates to retinal pigment epithelium cell health and function. We will generate iPSC lines from USH1B patient samples and determine MYO7A isoform expression by qPCR. Furthermore, we will assess the capacity of each MYO7A isoform to rescue USH1B phenotypes in MYO7A knockout iPSC-RPE cells. This work will provide valuable insight into the viability of USH1B gene

replacement therapies, as well as improve our understanding of retinal cell biology and Usher Syndrome disease pathology.

FRI - 701 The Influence of Location, Sex, and Habitat on Winter Deer Activity

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Courtney Kurashima*, *Chaminade University of Honolulu*; Elizabeth Flaherty, *Purdue University*; Zackary Delisle, *Purdue University* and Robert Swihart, *Purdue University*

Abstract: The white-tailed deer (*Odocoileus virginianus*) is a wide-ranging ruminant with unique economic, ecological, and societal value in North America. Estimates of population density are used when managing white-tailed deer populations, and knowledge of daily activity patterns is needed when using camera trap data. The aim of this project was to examine how sex, habitat, and region affect the activity patterns of white-tailed deer within the state of Indiana. We predicted no relationship between activity patterns and these factors due to the adaptability of white-tailed deer. We analyzed time stamps of images from 72 unbaited camera traps deployed in different habitat types across 3 different regions of Indiana. We recorded 3,342 unique instances of deer activity from 5 February − 11 March 2019. Using a Wald test, we examined the effect of sex, habitat type, and region on the activity patterns of deer. We found that habitat and region affected activity patterns, while sex had no effect. Specifically, Permanent Cover habitats contained bimodal activity peaks at 0700 hr and 1800 hr while Row Crop habitats contained a unimodal broad activity peak at 1800 hr. In regional management units (RMU), both RMU 3 and 4 illustrated abrupt uneven bimodal peaks at 0800 hr and 1800 hr whereas RMU 9 illustrated broad bimodal peaks at 0800 hr and 1800 hr. Understanding activity patterns can improve detection with cameras yielding more reliable population estimates and also contributes to a more complete natural history of this keystone species.

FRI - 702 The Role of Ephrins in Regulating Lens Regeneration in Newts

Discipline: Life Sciences
Subdiscipline: Biology (general)

Alyssa Miller*, *Miami University* and Katia Del Rio-Tsonis, *Miami University*

Abstract: **Purpose**: Newt lens regeneration is a fascinating biological process. Following removal of the lens, cells from the dorsal iris undergo transdifferentiation and reprogram into a new fully functioning lens. Interestingly, cells from the ventral iris are unable to regenerate a lens. In order to understand this process, our lab investigates the molecular mechanisms that govern the differences between the regeneration-competent dorsal iris and its morphologically indistinguishable counterpart, the ventral iris. Based on transcriptomic and proteomic analysis, our hypothesis is that an Ephrin and Ephrin receptor (Eph) signaling network restricts lens regeneration to the dorsal iris.

Methods: Red spotted newts were treated post-lentectomy, with FC chimera proteins to inhibit Ephrin receptors and ligands. Thirty days post-lentectomy, histological and immunohistochemical analysis were performed. Select conditions were repeated *ex vivo* and analyzed as described above.

Results: Ventral lens regeneration was induced, *in vivo*, with EphA4 and EphA5 inhibition. In the majority of cases, both a dorsal and ventral lens were present. EphB2, EphrinB2, and EphrinA5 inhibition did not induce a ventral lens. Similar results were observed *in vitro*using separated dorsal and ventral iris segments.

Conclusion: This was the first time that inhibition of a specific target unlocked the regenerative potential of the ventral iris in vivo. By inducing regeneration in a tissue that was previously thought to be incapable of doing so, we can continue to piece together the puzzle of regeneration in higher vertebrates which could hold great clinical and therapeutic significance.

FRI - 703 First Record of a Transferable Class 1 Integron in an Environmental *Enterobacter Kobei* bacterial Isolate

Discipline: Life Sciences
Subdiscipline: Biology (general)

Christian Checkcinco*, *University of California Irvine* and Luis Mota-Bravo, *University of California Irvine*

Abstract: Throughout the United States, over 2 million people are infected by antibiotic resistant bacteria every year. Bacteria that cause these illnesses have antibiotic resistant genes (ARG's) often carried by mobile genetic elements (MGE's), which include integrons carried by plasmids. In this study the objective was to analyze ARGs and their spread by studying plasmids in bacteria from natural environments. We hypothesized that MGE's in these plasmids play a key role in the spread of ARG's in the environment. Bacteria samples were collected from a pond in Chantilly, Virginia filtered, and plated on selective agar. One selected isolate (SW3326) was identified as *Enterobacter kobei* with a mass spectrometry method MALDI-TOF. This isolate was then tested against 36 clinically relevant antibiotics, sequenced, and compared to the NCBI nucleotide database. The isolate was resistant to 6 different antibiotics covering 3 different classes. The genes encoding this resistance were found in a class 1 integron with *dfrA21* and *sul1* genes that confer resistance to sulfonamide and trimethoprim classes of antibiotics. These were found through sequencing to be on one of the three plasmids this isolate contained which was 112kbp. Through a comparative analysis using the NCBI database, this antibiotic resistant region was found to be transferable as this ARG region was found across different plasmid incompatibility types which cannot be inherited together. In conclusion, this sample was found to contain ARG's which were spread through mobile elements in the bacteria by plasmids through a new integron ARG carrying region in this species.

FRI - 704 How a Mesh Trap Compares to a Standard Trap at Assessing Asian Citrus Psyllid Populations and Avoiding the Capture of *Tamarixia Radiata*, Its Biological Control Organism

Discipline: Life Sciences
Subdiscipline: Biology (general)

Gisel Garza*, *The University of Texas Rio Grande Valley*; Genoveva Carriles, *The University of Texas Rio Grande Valley*; Richard Casares, *Texas State University*; Abelardo Rodriguez, *The University of Texas Rio Grande Valley*; Gabriela Sanchez, *Texas Citrus Pest and Disease Management Corporation*; Mamoudou Setamou, *Texas A&M University-Kingsville Citrus Center*; Jon Dale, *Texas Citrus Pest and Disease Management Corporation* and Teresa Feria Arroyo, *The University of Texas Rio Grande Valley*

Abstract: The Asian citrus psyllid (ACP), *Diaphorina citri* Kuwayama is the vector of *Candidatus* Liberibacter *asiaticus* a bacterium that causes citrus greening disease (CGD). This disease makes citrus fruit unfit for sale and ultimately causes the death of the tree. CGD has no current cure and mitigation is primarily done by control of vector populations. Assessing ACP populations is an important step when preventing the spread and establishment of CGD. Currently standard ACP traps are used to assess ACP populations, but they often capture beneficial organisms that serve as biological controls of the ACP. Traps with mesh have been shown to successfully capture ACP, however there have been no assessments that compare the effectiveness of mesh traps against standard traps in avoiding the capture of *Tamarixia radiata*, an important biological control agent of ACP. To compare these two traps at avoiding *T. radiata* and assessing ACP populations, data was collected from April 2018 through November 2018 from 17 independent citrus groves where both types of traps were placed in four separate corners (A, B, C, and D) at similar conditions. Random sampling was performed and traps representing the 17 citrus groves and their respective corners were selected to count the number of *T. radiata* and ACP. There was no significant difference between the mesh and standard trap method at assessing ACP populations. However, mesh traps were more successful in avoiding *T. radiata*. Qualitative observations show a decrease in the number of beneficial organisms captured in the mesh traps (e.g., Coccinellidae).

FRI - 706 Molecular Taxonomy of Hawaiian Mesophotic *Gracilaria* (Rhodophyta)

Discipline: Life Sciences
Subdiscipline: Biology (general)

Charles Hambley*, *University of Guam* and Alison Sherwood, *University of Hawai'i at Manoa*

Abstract: Red algal (Rhodophyta) biodiversity has been well-studied in shallow Hawaiian reef communities, down to 30 m depth. Recent technological breakthroughs in deep sea exploration have allowed us to gather and characterize samples from mesophotic coral reef communities. One genus of red algae, *Gracilaria*, has an integrative role in Hawaiian culture, is a traditional food crop, and is also an export product. Previous biodiversity studies have revealed several undescribed species of *Gracilaria* in the Hawaiian Islands, and based on the rate of discovery of new species in the Hawaiian mesophotic flora we hypothesize that undescribed species of *Gracilaria* are also present in our collections. At least 20 samples preliminarily identified as belonging to the genus *Gracilaria* were examined in this study. Molecular-assisted alpha taxonomy was performed using three genetic markers: the 23S rRNA universal plastid amplicon (UPA) and Rubisco large subunit gene (*rbcL*) for plastid markers, and the mitochondrial cytochrome oxidase subunit 1 (CO1), to elucidate species-level diversity of this genus for Hawaiian samples of algae, in comparison to sequences available for global collections of this genus. The depths of Hawaiian mesophotic samples ranged from 40-122 m. Thus far, DNA sequence comparisons indicate that one new species of *Gracilaria* is present in the Hawaiian mesophotic flora. Further research will be undertaken on the morphological characters of these *Gracilaria* specimens to allow final taxonomic conclusions to be drawn.

FRI - 708 Effects of Photopollution on Mammalian Glucocorticoid Production

Discipline: Life Sciences
Subdiscipline: Biology (general)

Karla solis*, *Northeastern Illinois University*; Gabriela Naveda, *Northeastern Illinois University*; Rachel Santymire, *Davee Center for Epidemiology and Endocrinology; Lincoln Park Zoo* and Aaron Schirmer, *Northeastern Illinois University*

Abstract: Many aspects of an organism's behavior and physiology are modulated by circadian clocks with periods of approximately 24 hours. These endogenous molecular oscillators are present in all mammalian cells and are synchronized with the external environment. Exposure to artificial nighttime light, known as photopollution, can disrupt the normal function of our circadian clocks which can lead to health problems such as difficulty sleeping, depression, and obesity. Cortisol, one of the main glucocorticoids, is produced with a circadian pattern. This hormone is important in regulating stress response, homeostasis, and proper health. We hypothesize that increasing levels of nighttime light will alter cortisol production. To test this hypothesis, we will use a Adrenocorticotropic hormone (ACTH) challenge to examine the effects of photopollution on cortisol production in a mammalian model system (*Mus musculus)*. We will perform the ACTH challenge on animals under increasing amounts of nighttime light (0 , 6, and 30 lux) and will compare levels of fecal cortisol metabolites. Each fecal collection will be taken multiple times per day for 3 days before and after the ACTH injection. Preliminary data suggests that nighttime light increases the levels of fecal cortisol metabolites. Chicago is considered one of the most photopolluted cities in the world. Photopollution disrupts nocturnal ecosystems and it has adverse health effects that are not well understood. This research will improve our understanding of the relationship between photopollution and stress and the impact of photopollution on the health of urban mammals, including humans.

FRI - 709 Examination of TIE1 Functions in Flow-Mediated Lymphatic Valve Development in Vitro

Discipline: Life Sciences
Subdiscipline: Biology (general)

Jesus Perez*, *University of Puerto Rico-Aguadilla Campus* and H. Scott Baldwin, *Vanderbilt University*

Abstract: The lymphatic system is a network of vessels with important roles in fluid homeostasis, immune surveillance and lipid absorption. Lymphatic capillaries collect fluid, proteins, lipids and cellular waste (lymph), transport it to collecting vessels which ultimately return it to venous circulation. Lymphatic valves (LVs) within collecting vessels prevent backflow of lymph. Consequently, LV abnormalities are associated with lymphedema, inflammation, atherosclerosis, and hypertension; pathologies detrimental to cardiovascular health. LV development relies on coordinated signaling from turbulent lymph flow near branch points and regional expression of critical transcription factors. The molecular mediators that sense mechanical signals from lymph and relay them intracellularly remain undefined. TIE1, an endothelial receptor with no known ligand, has roles in flow-mediated processes such as atherosclerotic plaque formation. During mouse LV development, TIE1 is upregulated in valve forming regions. Embryonic lymphatic-specific deletion of TIE1 inhibits valve formation, demonstrating a crucial role in LV development. We hypothesize that TIE1 transduces biomechanical signals to orchestrate LV formation through regulation of key molecular and cellular processes. To determine TIE1's functions in regulating flow-mediated LV morphogenesis, an in vitro system will be used with human lymphatic endothelial cells, with and without TIE1, exposed to oscillatory flow which mimics the in vivo flow involved in LV formation. Analyses of gene expression through quantitative real-time PCR will provide novel insight into TIE1-specific roles necessary for proper LV formation and function. Understanding TIE1's functions may contribute to development of diagnostic tools and treatments to improve lymphatic function in patients with inherited or acquired lymphatic defects.

FRI - 711 Cortical Granule Motility in Response to Hormone Stimulation during Sea Star Meiosis

Discipline: Life Sciences
Subdiscipline: Biology (general)

Isabella Terrazas*, *New Mexico State University*; Clara Ross, *New Mexico State University*; Debadrita Pal, *New Mexico State University* and Charles Shuster, *New Mexico State University*

Abstract: Fertilization and proper development requires that a single sperm binds and enters the female oocytes. Upon sperm-binding, the oocyte or egg responds with the exocytosis of specialized vesicles called cortical granules (CGs), and the release of CG granule contents, prevents further sperm binding. Actin and the Rho GTPases that control the actomyosin cytoskeleton are known to have a fundamental part in oocyte maturation, but how these G proteins are regulated and how their actions control CG recruitment are less well understood. Work in the lab has established that in the sea star oocyte, there is a Rho-dependent burst of actin polymerization following hormone stimulation, and we hypothesize that this activation of Rho and actin plays a role in promoting translocation of CGs to the cell surface. To track CG movements following hormone stimulation, fluorescent protein tagged versions of sea star Rab 27 and Rab 3 were generated, and using these probes we tracked CG motility during oocyte maturation using 4D confocal microscopy. Image analysis has demonstrated a net movement of CG's toward the cell surface as well as two modes of motility; long distance, rapid movement deep in the cytoplasm and shorter movements closer to the membrane. The velocities and processivity of the deep cytoplasmic motility is suggestive of Myosin V-mediated transport, and current efforts are focused on quantifying vesicle motility in control oocytes prior to- and following hormone stimulation, as well as motility under conditions where Rho activity is blocked.

FRI - 712 The Role of SIP1/Zab2 Morpholino in the Central and Peripheral Nervous System Development

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Sasha Machulsky*, *California State University, Northridge* and Crystal D. Rogers, *California State University*

Abstract: Cadherin proteins are transmembrane, calcium-dependent cell-cell adhesion molecules that have been shown to regulate early cell fate specification, cell migration, and cell differentiation in vivo. Cadherins are important in developmental biology studies because they play a crucial role in how cells and tissues undergo the epithelial to mesenchymal transition (EMT), they actively induce and inhibit migration in different tissues, and they control cell aggregation necessary for proper derivative differentiation during development of living organisms. Expression of Neural cadherin (Ncad) is an important factor in controlling the development of the neural tube, which becomes the brain and spinal cord, and neural crest cells, which become craniofacial bone, cartilage and the peripheral nervous system. Altering the expression of Ncad during embryonic development may influence the development of these tissues. In humans, abnormal development of the neural tube and neural crest cells can develop into various neurological and structural defects such as Waardenburg-Shah syndrome, frontonasal dysplasia, and DiGeorge syndrome. We are interested in understanding the role of a transcription factor, SIP1/Zab2 Morpholino, in the developmental progression of neural crest stem cells to cranial neurons through the use of molecular analysis (Immunohistochemistry) and performing gain and loss of function experiments in late stage chicken (*Gallus gallus*) embryos. In addition, the results of our project has brought attention to axon guidance disruption. In future experiment we will analyze the effect of Sip1 on axon guidance to the peripheral nervous system.

FRI - 714 Developmental Outcomes of Embryonic Exposure to OTC Medication in Axolotl and Chicken Embryos: Low-Dose Effects and Phenotypic Responses

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Nikolas Morrison-Welch*, *California State University* and Crystal D. Rogers, *California State University*

Abstract:

Over the counter (OTC) medicine, drugs, must undergo a semi-rigorous process proving that they are safe for adult consumption, and for use without the supervision of a medical practitioner. Such studies have rarely provided information regarding the safety of these drugs on the most vulnerable and delicate states of life, the fetal and embryonic periods. In this study, we have analyzed the effects of Class B OTC drugs, which are understudied in animal models, on the embryonic development of two vertebrate species, the chicken (*Gallus gallus*) and the axolotl (*Ambystoma mexicanum*). Beginning with NSAIDs such as aspirin, ibuprofen, and naproxen; experimentation is being done to test variables such as embryonic viability after treatment, stage-dependent mortality rates, developmental delays, and phenotypic abnormalities. Additionally, we will test the expression of proteins that mark specific tissues using immunohistochemistry. Resulting evidence may shed light on the effect of exposure to putative teratogenic OTC drugs during embryogenesis including congenital disabilities such as cleft palate, malformed limbs, microcephaly, and heart and lung deformities. Many such teratogenic defects are preventable. Using comparative anatomical, molecular, and biochemical analyses genotypical and phenotypical conclusions can be used to compare and contrast results between the control and differing treatment groups.

FRI - 715 ROBO1 Signaling Governs Alveolar Cell Fate in the Mammary Gland By Regulating NOTCH Activity

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Jocelyn Cervantes*, *Department of Molecular, Cell, and Developmental Biology, University of California*; Oscar Cazares, *University of California* and Lindsay Hinck, *University of California*

Abstract: The mammary gland, or breast, is composed of two epithelial compartments: an outer basal myoepithelial cell layer, encircling an inner layer of luminal epithelial cells, within an adipocyte-rich stroma. During pregnancy, alveolar progenitor cells within the luminal compartment undergo differentiation to generate millions of milk-producing cells required for lactation. Studies show breastfeeding as an important nutritional factor providing infants immune protection against diseases; however, the mechanisms regulating milk production are ill-defined. Recently, the Hinck lab identified the Roundabout Guidance Receptor 1 (ROBO1) to be essential for milk production. *Robo1 –/–* animals show significantly fewer alveolar structures, and reduced milk gene expression at day 17.5 of pregnancy. Additionally, RNA-sequencing of FACS purified luminal progenitor cells, show elevated Notch activity in the *Robo1 –/–* compared to the wild-type littermate. Previous studies have shown that activated NOTCH results in dramatically decreased alveolar structures, suggesting that inactivation of NOTCH is critical for alveolar differentiation. To investigate the role of ROBO1 during pregnancy, and provide a potential model for milk production, a *Robo1-iCreERT2-P2A-EGFP* lineage tracing animal has been developed. Taking advantage of the eGFP, I performed immunohistochemistry to localize the expression of *Robo1* at different mammary gland development stages. Preliminary data shows that *Robo1* is expressed in the luminal compartment in virgin animals and upregulated in the basal compartment during pregnancy. We hypothesize that *Robo1* is expressed in the basal compartment to attenuate Notch activity in neighboring luminal alveolar progenitor cells thus allowing for differentiation. Currently, biochemical experiments are being performed to validate this model.

FRI - 716 Investigating the Role of *Pak1* in EMT during Sea Urchin Embryonic Development

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Tzu-Chieh Michael Wen*, *Duke University*; Raymond Allen, *Duke University*; Esther Miranda, *Duke University* and David McClay, *Duke University*

Abstract: An epithelial-mesenchymal transition (EMT) is the process where polarized epithelial cells develop the cell surface properties of mesenchymal cells, become motile, breach the basement membrane and enter the blastocoel. The EMT is important in understanding embryogenesis, tissue regeneration, and cancer metastasis. In sea urchin embryos both the skeletal cells and many non-skeletogenic mesoderm (NSM) cells go through an EMT and the process can be studied directly *in vivo*. We used results from a transcriptome analysis that show effector genes expressed in various cell types during late blastula and gastrula stages of *Lytechinus* variegatus to uncover *Pak1* as a potential gene involved in EMT. This study attempts to understand the role *Pak1* plays in the gene regulatory network (GRN) in the context of EMT. We have successfully cloned *Pak1*, synthesized an RNA probe, and performed *in situ* hybridization experiments to see where the gene is expressed throughout development. We then knocked down *Pak1* using an inhibitory drug to determine what role the gene plays during EMT. We show that *Pak1*, a kinase involved in cell motility and morphology, is expressed in both the skeletal cells and a subpopulation of NSM before and after they go through an EMT and that it may be involved in cell deadhesion.

FRI - 718 Evaluating the Aggregation Propensity of Tdp-43 Using *Caenorhabditis Elegans*

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Yaseen Ali*, *Northeastern Illinois University*; Yuriy Khlopas, *Northeastern Illinois University* and Cindy Voisine, *Northeastern Illinois University*

Abstract: Amyotrophic Lateral Sclerosis (ALS) is an age-related neurodegenerative disease that leads to the loss of motor neuron function. Previous research has linked mutations in the gene encoding the TAR DNA-binding protein (TDP-43) to familial forms of ALS. TDP-43 is an essential protein involved in RNA processing and is found in cytosolic aggregates in affected neurons. Our research intends to understand the link between TDP-43 aggregate propensity and neurotoxicity in ALS patients using the nematode *Caenorhabditis elegans.* For our studies, we are taking advantage of *C. elegans* short life cycle and transparency. We generated *C. elegans* transgenic lines expressing either wild type or mutated TDP-43 fused to a yellow fluorescent protein (YFP). The change in aggregation patterns will be compared between these strains. To monitor these changes, age synchronized animals are grown in liquid culture and protein lysates are prepared for young and aged animals. Centrifugation followed by western analysis will be used to evaluate aggregate formation. I hypothesize that mutated TDP-43 will be more aggregated than wild type, consistent with previous reports. Furthermore, TDP-43 aggregation will increase in both strains as animals age. Our goal is to understand how mutations in TDP-43 are linked to neurodegeneration in ALS.

FRI - 719 Postnatal Growth Restriction Causes Sex-Divergent Changes in Rat Lung Elastin and Mechanics

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Benjamin Ringham*, *University of Utah*; Nicolette Jessen, *University of Utah*; Haimei Wang, *University of Utah* and Lisa Joss-Moore, *University of Utah*

Abstract: Postnatal growth restriction (PGR) increases bronchopulmonary dysplasia (BPD) in preterm infants, with outcomes worse in males. BPD is characterized by impaired lung elastic fiber deposition and lung mechanics. A critical component governing elastic fiber deposition and lung mechanics is the fatty acid docosahexaenoic acid (DHA), which is also deficient in BPD. We previously showed, in a rat model, PGR decreases DHA in male, but not female, rats.

We hypothesize that PGR causes sex-divergent changes in rat lung elastic fiber deposition and mechanics, and that DHA normalizes the changes.

PGR was induced using variation in litter size, with newborn rat pups randomized to PGR (16 pups/litter) with regular diet or a diet supplemented with DHA (0.01% or 0.1%), or Control (8 pups/litter) with regular diet. At day 21, we measured lung elastic fiber deposition using Hart stain, and lung mechanics using a Flexivent. PGR and diet effects were assessed using ANOVA.

Results are %control±SD (*=p<0.05). PGR rat pups on all diets weighed less than control from day 5 onwards. Regular diet PGR increased elastic fiber density in male rats (143±41%*), but not in female rats (115±52%). The effects of DHA on PGR elastic fiber deposition, and the effects of PGR and DHA on lung mechanics are still being evaluated.

In the rat lung, PGR causes sex-divergent changes in elastic fiber deposition. We speculate that reduced DHA availability drives increased elastic fiber density in male rats, and that supplemental DHA may be a valuable therapeutic means of restoring DHA in BPD.

FRI - 720 Pelagic Cormorant Nesting Success and Oceanic Conditions in Northern California

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jade Morning Sky Little*, *University of California Davis*; Daniel Barton, *Humboldt State University*; Shannon Brinkman, *Bureau of Land Management Arcata Field Office* and Claire Nasr, *Humboldt State University*

Abstract: Nesting success is an important component of the growth of coastal seabird populations. Nesting success can be defined as the proportion of nesting or laying pairs that raise young to the age of fledging (i.e., the age when a fully-feathered offspring voluntarily leaves the nest for the first time). This study focused on the nesting success of one coastal seabird species, Pelagic Cormorant (*Phalacrocorax pelagicus*). In the marine ecosystem, coastal bird species roles can be observed by not only aiming focus to their behavior and physiology but, also their interactions with the environment (i.e. the ocean). Upwelling productivity in the California Current system brings abundant food to the ocean's surface and increases food web abundance. The objective of this study was to examine and analyze the relationship between oceanic conditions and the nesting success of Pelagic Cormorants. Nesting site observations were analyzed and compared to changes in oceanic conditions in the area across a 5-year interval from 2014-2018, a time period which includes an el Niño event and extreme warm water in the northeast Pacific Ocean (the "blob"). Oceanic data (i.e. upwelling index) was examined and analyzed from the Multivariate Ocean Climate Indicator (MOCI) and National Oceanic and Atmospheric Administration. Based on the results, nesting success rates were high in years with high productivity and low in years with low productivity, as measured by MOCI and Upwelling Index. This study provides information on how local-scale oceanic variations influence coastal bird species populations and provides important context for conservation efforts.

FRI - 721 Effect of Prolonged Drought on Wildflowers Communities on the Kaibab Plateau

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Briana Prado*, *University of California, Santa Cruz* and Clare Aslan, *Northern Arizona University*

Abstract: The historic drought of 2012-2017 in the South-West drastically reduced the amount of annual precipitation by over 40%, and snow cover in the watershed by 67% in the Kaibab Plateau, on the north rim of the Grand Canyon. Previous studies have correlated drought with a reduction in flowering. Our research investigates the relationship between precipitation, native flower phenology, and pollinator interactions, specifically at elevations of 7,565 ft - 8,214 ft. We conducted pollinator and vegetation surveys during late July and early August 2016 and 2018 by laying out 50 *m* by 6 *m* wide transects in a random bearing and surveying for 30 minutes at a time. We quantified the number pollinators visiting the flowers of roughly 25 native species of angiosperms. We used U.S Drought Monitor data to correlate abundance of flowers with precipitation and pollinators for 2016 and 2018 on the Plateau. Our results showed a 54.4% decrease in the number of native flower species in our transects during 2018, compared with 2016. We also found a 54.7% decrease in the total number of flowers in the transects. A reduction of native flowers in high-stress environments has negative impacts on the native populations, due to a reduction in fecundity, and has negative effects on the availability of food for pollinators, which rely heavily upon the flowers for food. These community shifts give us a glimpse into the possible future for the Kaibab Plateau in the face of climate change.

FRI - 722 Negative Effects of Heatwaves on Bumble Bee Immunity and Parasite Resistance

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Kerrigan Tobin, *Illinois State University*; Abraham Martinez*, *Illinois State University* and Ben Sadd, *Illinois State University*

Abstract: Ongoing climate change, including more frequent temperature extremes such as heatwaves, has direct consequences for organisms by imposing thermal stress. Changes in thermal environments can also influence health by altering interactions with other species, including parasites and pathogens. These effects may have consequences for the population viability of species of conservation concern. Indeed, climate change has been predicted to have negative consequences for many threatened pollinators. Using the bumble bee *Bombus impatiens,* a key pollinator, we test the hypothesis that thermal stress from heatwaves will be detrimental to immunity and parasite resistance. Adult bees were exposed to either control or heatwave thermal regimes, modeled on real temperature data from central Illinois. Total phenoloxidase, an enzyme involved in the melanization response of insect immunity, and induced humoral antibacterial activity were measured, in addition to total protein. Parasite resistance against the trypanosome *Crithidia bombi* was also assessed, with experimental infections taking place either before or after heatwave treatments. There was no significant effect of heatwave treatment on phenoloxidase activity or total protein. However, antibacterial activity was reduced in heatwave exposed bees. Infection intensities did not differ between heatwave treatments when bees were exposed to the parasite prior to the heatwave, but, in line with the reduction in antibacterial immunity, bees were more susceptible to infection following heatwave exposure. These results suggest that manifestations of ongoing climate change in the form of heatwaves will have a detrimental influence on the ability of bumble bees to fight infection, and consequently on their population health.

FRI - 723 The Seedling Skirmish: Native Vs. Non-Native Plant Competition Under Climate Change Induced Drought in Hawaii

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Amanda Wong*, *University of Hawai'i at Mānoa* and Kasey Barton, *University of Hawai'i at Mānoa*

Abstract: Native plant decline is, at least in part, attributed to the spread of non-native plants, especially in island plant communities that appear to be particularly vulnerable to invasive species. However, the role of competition in native plant displacement remains unclear given the lack of experiments designed to test competition explicitly. We experimentally investigated whether invasive plants outcompete native plants as a potential mechanism underlying native species declines in

Hawaiian forests, and additionally tested whether drought stress alters the competitive outcome. Competition was tested in a controlled greenhouse experiment using two ecologically important plant species in the Myrtaceae family: *Metrosideros polymorpha* and *Psidium cattleyanum*. Seedlings were grown alone or together in pots, and half of all pots were exposed to a simulated drought treatment. Plant performance was measured as survival and growth of seedlings, and ecophysiological traits were measured for insights into the mechanisms underlying competition and drought effects. Preliminary results indicate that *P. cattleyanum* is a stronger performer than *M. polymorpha*. These results will shed light on whether seedling competition may drive the displacement of *M. polymorpha* by the invasive *P. cattleyanum* and shed light on whether drought may exacerbate this interaction. Considering the foundational role of *M. polymorpha* in Hawaiian forests, this research may be of particular interest to conservation and restoration practitioners working to preserve the native forests of Hawai'i in the face of climate change.

FRI - 724 **Effects of Urbanization on Extra-Pair Paternity in the Song Sparrow**

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Valerie Brewer*, *New Mexico State University*; Samuel Lane, *Virginia Polytechnic Institute and State University*; Kendra Sewall, *Virginia Polytechnic Institute and State University* and Karen Mabry, *New Mexico State University*

Abstract: Urbanization can affect the behavior of free-living animals. The hypothesis is that low-density urbanization affects extra-pair mating in urban and rural populations of song sparrows (*Melospiza melodia*) in Montgomery County, VA. We genotyped 70 song sparrow nestlings from 27 nests, along with their social parents and all other captured adults at 15 microsatellite loci. We assigned genetic paternity using the program CERVUS, successfully assigning 38 of 70 nestlings (54%) to a father. Only one nestling was assigned to a male that was not the social father, confirming extra-pair paternity. However, 22 additional nestlings were tested against a genotyped social father, but not assigned to a genetic father, leaving the possibility of extra-pair siring by an unsampled male. The lack of successful assignment of nestlings to sampled social fathers suggests that up to 34% of nestlings may be the result of extra-pair mating, in line with other studies of extra-pair paternity in song sparrows. Preliminary results suggest that there are higher rates of extra-pair offspring and nests in rural areas, as compared to urban areas. However, due to a limited sample size of rural nests (N=3), we cannot yet draw definitive conclusions about the effects of urbanization on extra-pair mating. Future plans include increased sampling of rural nests, and the use of single nucleotide polymorphisms (SNPs) to increase power to detect extra-pair mating.

FRI - 725 **The Evolution of Feeding Preferences in Herbivorous Insects**

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Judith Ijeoma Okoro*, *University of California, Berkeley*; Julianne Pelaez, *University of California, Berkeley* and Noah Whiteman, *University of California, Berkeley*

Abstract: Chemosensory receptors are responsible for binding chemicals from the environment and triggering neuronal responses to elicit appropriate behaviors, such as feeding and egg-laying. Gustatory receptors (Grs), are found to be expressed in the mouth of insects. The herbivorous drosophilid fly, *Scaptomyza flava*, can be used as a model to understand the role of Grs in the evolution of feeding preferences. *S. flava* has lost several Grs that are expressed in the bitter gustatory neurons of *Drosophila melanogaster*. We used a capillary feeder choice test to compare the feeding preferences of *S. flava* and *D. melanogaster* to characterize how feeding preferences have changed in herbivorous insects. The flies were given two choices: sucrose and a combination of sucrose and a bitter compound. The bitter compounds tested were those commonly used in Drosophila experiments and those most common in mustard plants, specifically glucosinolates, their main chemical defense. For *D. melanogaster*, the results confirm their known aversion to lobeline (t(25)= -4.02, p=0.001) and previously untested aversion to the glucosinolate sinigrin (t(14)= -2.93, p=0.011). For *S. flava*, there was no difference in their consumption of sucrose alone versus with lobeline (t(8)= -1.74, p=0.119), nor versus sinigrin (t(10)= -1.30, p=0.223), indicating broad changes to bitter reception in *S. flava*. Our next steps will involve performing more behavioral experiments looking at the role of specific Grs using RNAi knockdown techniques in *D. melanogaster*. Identifying the roles of these receptors will enable us to understand the evolution of feeding preferences and the genetic basis underlying these changes.

FRI - 726 **Island Spotted Skunk (*Spilogale gracilis amphiala)* Population Monitoring Project on Santa Cruz Island**

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

ricardo estrada*, *Oxnard College*; Jesús E. Maldonado, *Smithsonian Institution*; Anthony Gomez, *Ventura Community College*; Angel Ramirez, *California Polytechnic State University, San Luis Obispo*; Isabel rivera, *CSUCI Channel Islands*; Scott Logan, *University of Santa Barbara*; Evelyn bobadilla, *Santa Barbara community college* and Mario Castellanos, *UCSB EOP's Smithsonian Scholars*

Abstract: Population dynamics seeks to answer species interactions and abundance given resource availability and stress factors. As part of a comprehensive and ongoing research project, the UCSB-Smithsonian Scholars program, a student led research program seeks to better understand the distribution and population density of the endemic Island spotted skunk (*Spilogale gracilis amphiala*), whose population numbers is uncertain. Currently, four camera sets have identified the presence of individual spotted skunks in 12-months of sampling and through ongoing image analysis, the deployment of additional camera sets in concentrated habitat types, and through the use of capture-recapture analysis, we anticipate improving current population density estimates. Island spotted skunk populations began declining as the Island fox (*Urocyon littoralis santacruzae)* populations began to increase after the removal of the Golden eagle (*Aquila chrysateos*) (Roemer et al. 2002). We deployed 22 Reconyx camera traps in 11 key habitat locations on Santa Cruz island, California. Geographic Information System software (GIS) was used to determine these locations using parameters such as vegetation/habitat types, buffer distance to roads, and proximity to other cameras. Each site consists of an experimental two-camera system that takes advantage of the skunks unique black and white spot patterns to allow researchers to identify individuals, therefore assessing population density within each camera point. Moving forward, the project aims to incorporate machine learning to streamline our data analysis and upload to the eMammal database. The information obtained will provide natural resources managers a better understanding of the population dynamics of this elusive mustelid using low-cost non-invasive techniques.

FRI - 727 **Something in the Water: Environmental DNA Profiling of Tide Pool Biodiversity**

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Shannon Chou*, *California State University, Fullerton*; Jennifer L. Burnaford, *California State University, Fullerton* and Ryan P. Walter, *California State University, Fullerton*

Abstract: The harsh environment of the rocky intertidal zone makes it one of the most diverse and unique ecosystems on Earth; its inhabitants rely on a fragile balance of environmental factors which are easily disturbed. As pollution levels and human disturbance steadily increase, reliable monitoring is crucial for conservation efforts of intertidal species, particularly by providing a baseline measurement of the species present in the environment. Recently, the analysis of environmental DNA (eDNA), or genetic material left behind by an organism in the form of tissue, excrement, or bodily fluid, has been instrumental to the conservation of other aquatic ecosystems. As no exclusive analysis of intertidal rocky tide pool habitats has been performed to date, we examined the capacity for eDNA extraction and analysis in the rocky tide pools of Southern California as a novel method for biodiversity monitoring. We extracted eDNA from water samples taken from isolated tide pools at two different rocky intertidal sites across a three-day period. Using the portable

MinION nanopore sequencer (Oxford Nanopore Technologies) we performed polymerase chain reaction amplification and real-time DNA barcoding of our eDNA samples. Our results suggest that nanopore sequencing is a viable method for the barcoding of intertidal organisms, despite complicating environmental factors such as the translocation of eDNA in the tide. Possible changes in current conservation methods to implement nanopore sequencing may ultimately improve the speed of species identification and reduce the need for multiple individuals to enter the field, thereby helping to limit human disturbance in the intertidal zone.

FRI - 729 Phylogenetic and Functional Diversity Effects on Resistance to Invasive Species

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Kyla Knauf*, *University of San Diego*; Adrienne Ernst, *Northwestern University* and Andrea Kramer, *Northwestern University*

Abstract: In Illinois, less than one-tenth of one percent of its tallgrass prairie still remains. This major loss has made restoration efficiency all the more important. One of the largest threats to restoration efforts is invasive species. While studies traditionally count species (species richness) to characterize a native community and its subsequent resistance to invasive species, this does not consider the specific advantages/disadvantages of species traits. My project aims to assess lesser-studied functional diversity (FD) and phylogenetic diversity (PD) of native species and how these different diversities affect resistance to invasive species. FD measures the variety of traits present, whilst PD measures the evolutionary history represented, which each approximate the niche space occupied by the native community. My hypothesis is that as FD and PD increase, invasion resistance will also increase because maximizing the niche space occupied decreases space for invasive species. To test this, we experimentally restored prairie plots with three levels of PD and two levels of FD. Three different invasive species were planted in each plot at the beginning of the summer, and their basal rosette diameter and survivorship will be measured near the end of the summer as metrics of invasive species success. The expected result is that due to decreased niche space in the plots, the invasive species will have a smaller basal rosette diameter and higher mortality in higher diversity plots. These results will advance restoration efforts by providing native species compositions that have a stronger natural defense.

FRI - 730 Redefining *Hermissenda* Ranges and Relationships from Tsunami-Driven Rafted Specimens and Citizen Science Data

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Katherine Montana*, *University of California, Berkeley* and Rebecca Johnson, *California Academy of Sciences*

Abstract: In the aftermath of the 2011 East Japanese earthquake and tsunami, anthropogenic debris from the east coast of Japan floated across the Pacific Ocean to the west coast of North America. One such vessel from Iwate Prefecture arrived on the coast of Oregon, and the fouling community included specimens identified as the nudibranch *Hermissenda crassicornis,* which was thought to be found from Japan to Baja California but has since been split into three species, *H. crassicornis* (Alaska to Bodega Bay)*, H. opalescens* (Bodega Bay to Baja)*,* and *H. emurai* (Japan). Previous work suggested that all of the motile invertebrates found on the tsunami debris were either Japanese in origin or pelagic. Our study sought to determine whether the nudibranch specimens collected from the Iwate vessel were, according to the new classification system, only *H. emurai* or whether the Eastern Pacific *Hermissenda* were present as well. Preliminary results from DNA sequencing and morphological analysis suggest that specimens of *H. crassicornis* were found on the vessel. This finding indicates either that these specimens settled after arrival to the west coast of North America or that *H. crassicornis* is found in Japan, suggesting *Hermissenda* ranges need to be redefined. Occurrence data shared on the iNaturalist platform were also used to assess current ranges. Haplotype networks built from COI data from all *Hermissenda* species elucidate the relationships between them. This study is a testament to the power of combining volunteer naturalist data with lab-collected data to understand evolutionary relationships, species ranges, and biogeography.

FRI - 731 A Less Invasive Method for Genotyping Pipefishes for Conservation and Population Genetics

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Julia B. Teeple*, *California State University, Fullerton*; Taylor Naquin, *California State University, Fullerton*; Jennifer N. Ibarra, *California State University, Fullerton*; Mayra Silva, *California State University, Fullerton*; Kevin S. Whittemore A.A., *California State University, Fullerton*; Abigail Cho, *California State University, Fullerton*; Jennifer L. Burnaford, *California State University, Fullerton*; William J. Hoese, *California State University, Fullerton* and Ryan P. Walter, *California State University, Fullerton*

Abstract: Population genetic data can provide insightful clues to for conservation purposes, but requires the recovery of DNA from individuals. For fishes, partial fin-clipping is one of the standard methods for tissue sampling of DNA recovery, but fin-clipping is not ideal for smaller and less vagile fishes like pipefishes (Syngnathidae). Skin-swabbing provides a less invasive method to collect DNA for genetic analysis, but direct comparisons between standard methods and swabbing are few in the literature. In this study, we explicitly test whether skin swabbing is a suitable surrogate for fin clipping for DNA extraction and amplification in southern California pipefish. A total of 37 pipefishes of the genus *Sygnathus* were sampled using SCUBA or seine from two coastal locations in greater Los Angeles region. Each individual was partially fin-clipped (caudal fin) and skin-swabbed. DNA was successfully recovered from each individual for both sampling methods, and used to PCR amplify two microsatellite loci designed for use in eastern Pacific Syngnathids. PCR amplification success rates were similar for both loci and comparable for both methods (83% swabbing vs. 87% fin clipping). A principal coordinate analysis demonstrates that both methods produced comparable results among both methods. Future studies may wish to further explore this potentially less invasive method of DNA recovery for conservation genetic purposes.

FRI - 732 Effect of Restoration Substratum Composition on Oyster Recruitment and Resultant Habitat Complexity in San Diego Bay, California

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Salvador Gutierrez Gutierrez*, *California State University Fullerton*; Danielle Zacherl, *California State University, Fullerton*; Jesus Torres, *California State University, Fullerton*; Bryce Perog, *California State University, Fullerton* and Rick Torres, *Cal State University of Fullerton*

Abstract: Marine restoration projects that increase habitat complexity can promote increased species richness in degraded coastal wetlands. Oysters are foundation species that increase rugosity (surface irregularities) and thus create more complex habitats, but they have experienced global declines and are thus targeted for restoration via augmenting mudflats with hard substrata of various compositions. Two oyster species are common in southern California, the native Olympia oyster, *Ostrea lurida*, and the non-native Pacific oyster, *Crassostrea gigas.* We investigated which restoration substratum might best encourage settlement and recruitment of *O. lurida*, and which would most increase surface complexity. We tested three materials: terra cotta (clay), concrete, and baycrete (concrete mixed with crushed shell and other locally-sourced natural materials), and suspended replicate tiles (n=7) of each material at 0 m MLLW at two locations within San Diego Bay from May through September 2018. We measured and calculated average post-deployment rugosity to find which material generated the most habitat complexity and then correlated rugosity with the ratio of native to total oyster recruitment to better explain how more complex habitat was created. We expected baycrete tiles dominated by *O. lurida* versus dominated by *C. gigas* to have the highest rugosity due to differences in growth form. Qualitative observations and preliminary rugosity measures indicate that terra cotta tiles returned lowest rugosity and achieved lowest recruitment of both species; additional data collection is ongoing. Restoration practitioners can use our findings to deploy more eco-friendly marine infrastructure that creates more habitat complexity within impacted wetlands.

FRI - 733 Plants in Space: Does Lignification and Microgravity Interact to Impact Photosynthesis?

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Bianca Serda*, *The University of New Mexico*; Margaret Turpin, *The University of New Mexico, Biology*; Norman Lewis, *Washington State University,Institute of Biological Chemistry* and David Hanson, *The University of New Mexico*

Abstract: Plants with the C_3photosynthetic pathway rely on diffusion of $CO_2$from the atmosphere to the chloroplast to capture carbon for growth and development. Leaf anatomy, including cell wall thickness, impacts resistance to CO_2diffusion and this can be detected using stable isotopes. The heavier stable isotope of CO_2($^{13}CO_2$) diffuses more slowly than the light one ($^{12}CO_2$), and the enzyme Rubisco uses $^{12}CO_2$faster than $^{13}CO_2$. The net result of these anatomical and enzymatic effects is that C_3plants capture more ^{12}C when the resistance to diffusion is low, e.g. when cell walls are thin. Lignin is the part of cell walls that gives them rigidity and increases strength for withstanding gravity. Therefore, we selected a C_3species, *Arabidopsis thaliana*, with modifications to lignin content and photosynthesis, for growth on the International Space Station and Kennedy Space Center, to examine the combined effects of lignification and microgravity on CO_2diffusion. We hypothesize that the plants grown in space will have thinner cell walls, which will decrease resistance to CO_2diffusion and decrease the ratio of $^{13}C/^{12}C$ in plant tissues, and increase rates of photosynthesis measured using variable chlorophyll fluorescence. Our preliminary data from plants grown on Earth demonstrates that our method for visualizing plant anatomy and lignin content works with frozen tissues, like those we will receive from the ISS and we do not see differences in $^{13}C/^{12}C$. Measurements of photosynthesis in space and on Earth show a trend of higher rates in space but no impact of lignification.

FRI - 734 Comparing Apples to Apples: Enhancing Reference Genomes for Cross-Cultivar Functional Genomics in Tree Fruit

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Brittany Cook*, *California State University, Fullerton* and Joshua P. Der, *California State University, Fullerton*

Abstract: Apples are one of the most valuable tree fruit crops in the United States, and modern advances in controlled-atmosphere storage has made apples commercially available year-round. However, a number of economically important cultivars are susceptible to a number of storage disorders impacting post-harvest tree fruit quality. Understanding the physiology of these disorders has become an important component of apple breeding programs. While the apple genome was sequenced in 2010, the reference genome comes from a double haploid version of the Golden Delicious cultivar, but substantial genetic diversity among apple cultivars has represented a barrier to using genomic approaches in other economically relevant apple cultivars. We are using an RNA-seq and whole genome re-sequencing approach to characterize genetic diversity within apples and to improve the utility of the reference genome for cross-cultivar functional genomics. We have obtained and analyzed transcriptome data from 62 samples of Honeycrisp (HC) and Granny Smith (GS) representing both healthy and diseased apples undergoing several storage treatments to identify genes related to post-harvest fruit quality. With a subset of transcriptome samples from GS, we evaluated the mapping rate of RNA-seq reads to the Golden Delicious reference. We found that only 70% of our apple transcriptome data confidently mapped to the reference genome, highlighting the need for an improved reference. We are further analyzing *de novo* transcript models and have re-sequenced the GS genome using both Illumina and PacBio whole genome shotgun data.

FRI - 735 The Genetic Variation Underlying the Salt Stress Response in *Oryza Glaberrima*

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Jada Carter*, *California State University, Monterey Bay* and Michael D. Purrugganan, *New York University*

Abstract: The now orphaned African rice, *Oryza glaberrima,* was a staple in sub-Saharan Africa until the debut of fast-growing, high-yielding Asian rice (*O. sativa*). However, as climate change rapidly alters the agricultural landscape, rising sea levels present a growing threat to coastal paddies. Here, we aimed to assess *glaberrima's* salinity tolerance as well as examine the genetic component of its stress response. A rice panel of 171 *O. glaberrima* varieties was grown in a diurnal, tropical, hydroponic system with a control group and salinity treatment group. By monitoring chlorophyll content we have quantified the collapse of the endosymbiotic relationship between the plant and its chloroplasts. Results show that within the salt treatment group there were several varieties displaying a yellow leaf phenotype consistent with a decrease in the amount of chloroplasts per unit area. The subsequent decrease is photosynthetic product thereby decreases the overall energy produced by the plant. By collecting data on number of leaves present on each plant over the course of the next five weeks we will show that with less energy available fewer new leaves are created, giving us insight into the repercussions of salt stress at later developmental stages. Further, we generated a genome-wide polymorphism data set for our rice panel to perform a Genome-wide Association Study (GWAS), searching for the genetic variations associated with salinity tolerance. Our results will aid in the reintroduction of African rice to the market and highlight the genetic variation underlying abiotic stress tolerance for breeders and plant scientists.

FRI - 736 Examining the Effects of Density on Blow Fly Larval Development

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Yvonne Sandoval*, *John Jay College-City University of New York* and Jennifer Rosati, *John Jay College - City University of New York*

Abstract: Forensic entomology involves the use of insects in legal investigations, primarily homicide investigations by using blow fly developmental rates to provide information helpful for post-mortem interval (PMI) estimations. Blow fly species, such as *Lucillia sericata (*Meigen*)* and *Calliphora vicina* (Robineau-Desvoidy) are forensically important species because they are among the first insects to colonize or lay eggs on human remains, often within minutes after death. Currently, forensic entomologists may use larval size as an indicator for age, however, this measure may be influenced by many different factors, such as competition. This study will determine the effects of resource competition (density) on blow fly larvae. For each species, larvae were exposed to varying levels of density to simulate resource limitation. Varying levels of density included three treatments with 30 grams of fresh pork liver; each treatment had different number of larvae: 50 (control), 100 (medium density) and 300 (high density). Density effects were quantified by measuring larval mortality, time to adult emergence, and adult blow fly size. The results from this work will further the understanding on the role of density-dependent effects on larval development and species size, ultimately improving upon current predictive models based off size for use in forensic investigations.

FRI - 737 GLUT1 and Its Role in Gonadotrope Function

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Vashti Knight*, *University of California, San Diego*; Dequina Nicholas, *University of California, San Diego*; Tomohiro Terasaka, *University of California, San Diego* and Mark Lawson, *University of California, San Diego*

Abstract: Reproduction is an energy intensive process. The gonadotrope cells of the anterior pituitary respond to GnRH and secrete the gonadotropins LH and FSH which are necessary for ovulation and spermatogenesis. Our laboratory has demonstrated that glucose is an important energy source for gonadotrope cells. Glucose uptake into the cell is regulated by glucose transporters and we have shown that GLUT1 is the primary transporter. GLUT1 expression in gonadotropes significantly increases in response to GnRH. Because GnRH increases GLUT1, we hypothesized that GLUT1 mediates GnRH-

induced glycolysis which supports gonadotropin production. We tested this by generating two LβT2 (mouse gonadotrope) cell lines by transduction with a lentivirus vector: GLUT1 knockdown was achieved using a vector containing GLUT1-targeted shRNA and upregulation of GLUT1 was achieved using a CMV promoter-driven cDNA for overexpression. We used qPCR and Western blots to verify the knockdown and overexpression of GLUT1 and to ensure the cells could respond to GnRH. We also performed qPCR to evaluate whether knockdown of GLUT1 is compensated for by other GLUT transporters. Measuring lactate (a proxy for anaerobic glycolysis) produced by shGLUT1 cells in response to GnRH showed that GnRH cannot induce glycolysis in gonadotrope cells without GLUT1. We also showed that GnRH pulse-induced secretion of LH from the shGLUT1 cell line is reduced compared to control. Without GLUT1, the main transporter needed for glucose uptake, gonadotrope cells cannot engage anaerobic glycolysis in response to GnRH and secrete less LH than control cells. Therefore, GLUT1 is necessary for maximal LH secretion from gonadotropes.

FRI - 738 Litter Lords of Madagascar: A Taxonomic Review of the Madagascar Endemic Ground Beetle Genus *Brachypelus*

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Kendra DelToro*, *Oregon State University*; R. Antonio Gomez, *Oregon State University*; Petr Bulirsch, *Unaffiliated* and David H. Kavanaugh, *California Academy of Sciences*

Abstract: Invertebrates make up 95% of life on Earth, yet 85-99% of these species are hypothesized to be unknown to science. This deficit in taxonomic knowledge hinders conservation efforts worldwide, particularly in regions with unique faunas and rapidly-changing landscapes such as the island of Madagascar. We are conducting a taxonomic review of the Madagascar endemic genus *Brachypelus*. Members of *Brachypelus* are flightless leaf litter-dwelling beetles in the family Carabidae, a diverse radiation of terrestrial insects. *Brachypelus* species are poorly known, and the genus currently includes 15 described species. Through increased leaf litter sampling efforts in the last decade, additional specimens are available for study. We are using traditional morphological methods to study internal and external characters to guide species delimitation in *Brachypelus*. Our preliminary data suggest that there are at least 10 new species in the genus. We are documenting these species using high quality macrophotography to capture variation in microscopulture, external structures, and genitalia. We will also create a dichotomous key to all species of the genus as well as a map of their geographic distributions. The label data suggest that *Brachypelus* species have small ranges or a limited dispersal capacity, suggesting that further sampling efforts in Madagascar are likely to yield additional new species. Because of the numerous threats to biodiversity due to habitat destruction in Madagascar, it is critical to describe new species from the island in order to improve our understanding of Madagascar's biodiversity and our ability to conserve it.

FRI - 739 DNA Damage Repair Pathway of OTUD6 and ASCC3 Proteins in Drosophila Melanogaster

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

A nika Padala*, *University of California, Merced*; Fred Wolf, *University of California, Merced* and Sammy Villa, *University of California, Merced*

Abstract: OTUD6 is a deubiquintinase (DUB) of the Ovarian tumor (OTU) family. As a DUB protein, OTUD6 cleaves Ubiquitin from substrate. This protein enhances DNA damage repair, however its specific role, molecular mechanism and specific DNA damage repair pathway are unknown. To identify the DNA damage repair pathway, OTUD6 fruit fly mutants (catalytically inactive and null) were exposed to Methyl Methanesulfonate (MMS), a DNA alkylating agent. During the exposure, the mutant flies died expeditiously compared to the control fruit flies. This MMS sensitivity of the mutants implies that the OTUD6 protein is part of the DNA alkylation repair pathway. To identify the significance of OTUD6 in the pathway, we tested ASCC3 mutant flies. ASCC3 is a DNA ligase in the ASCC protein complex. ASCC3 responds to DNA damage, however the specific DNA repair pathway is unknown. The ASCC3 and OTUD6 proteins interact in humans, however the nature and mechanism of interactions are unknown. To test this, ASCC3 mutants were exposed to MMS, similar to the OTUD6 mutants. Enhanced death was observed in the ASCC3 catalytically inactive mutants compared to the control flies, which means ASCC3 responds to DNA alkylation damage. The MMS sensitivity of both mutants could mean both proteins interact in the same pathway. With this information, the specific mechanism of OTUD6 and the interaction between OTUD6 and ASCC3 can be found.

FRI - 800 Building Lattices: Catalan Recursion on the External Order of Unit Interval Positroids

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Jan Tracy Camacho*, *University of California, Davis* and Anastasia Chavez, *University of California, Davis*

Abstract: The Catalan numbers form a sequence that counts over 200 combinatorial objects. A remarkable property of the Catalan numbers, which extends to these objects, is its recursive definition; that is, we can determine the n^{th} object from previous ones. Matroids are combinatorial objects that generalize the notion of linear independence and have connections with other fields of mathematics. A family of matroids, called unit interval positroids (UIP), are Catalan objects induced by the antiadjacency matrices of unit interval orders. Associated to each UIP is the set of externally ordered bases, which due to Las Vergnas, produces a lattice after adjoining a bottom element. We study these lattices and the implied Catalan-induced recursion on them. Explicitly, we describe an algorithm for constructing the lattices of rank n UIPs from the lattices of lower ranks. Using their inherent combinatorial structure, we also aim to find a simple formula to enumerate the bases for a given UIP.

FRI - 801 The Modified Szpiro Conjecture and Elliptic Curves with Specified Isogeny

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Gabriel Flores*, *Wheaton College, Illinois*; Owen Ekblad, *University of Michigan, Dearborn*; Abigail Loe, *Carleton College* and Alex Barrios, *Carleton College*

Abstract: Given three positive, relative prime integers a,b,c such that $a+b=c$, it is rare to have the product of the primes dividing them to be smaller than each of the three. In 1985, David Masser and Joseph Osterl\'{e} made this precise through their celebrated \textquotedbllef$ABC$ Conjecture.\textquotedblright In 1988, Oesterl\'{e} showed that the ABC conjecture is equivalent to the modified Szpiro conjecture which states that for each $\epsilon>0$ there are finitely many rational elliptic curves $N_{E}^{6+\epsilon}<\max\left\{ \left\vert c_{4}^{3}\right\vert ,c_{6}^{2}\right\} $ where N_{E} is the conductor of E and c_{4} and c_{6} are the invariants associated to a minimal model of E. Recently, Barrios showed that for a rational elliptic curve E, there is an explicit lower bound which depends only on the torsion subgroup of E. Our project seeks to create databases of rational elliptic curves in order to study the relationship between the modified Szpiro conjecture and elliptic curves with specified isogeny degree. This work is part of PRiME (Pomona Research in Mathematics Experience, NSF-1560394).

FRI - 802 Methods of Counting Ties, Ascents, and Descents of Naples Parking Functions

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Alex Christensen*, *University of Arizona*; Andres Ramos, *University of Puerto Rico, Rio Piedras*; Zakiya Jones, *Pomona College*; Pamela Harris, *Williams College*; Mayleen Cortez, *California State University Channel Islands*; Robert Rennie, *University of Illinois*; Morgan Hobson, *Spelman College*; Gordon Rojas Kirby, *University of California, Santa Barbara*; Marissa Loving, *University of Illinois, Urbana-Champaign* and Summar Ellis, *Spelman College*

Abstract: Parking functions, first introduced in 1966 by Konheim and Weiss, are tuples of numbers (from 1 to n) with each entry representing the parking preference of the car at that index. A variation of these parking functions was introduced by Baumagardner in which the car is able to move back one spot if their preferred spot is filled. If the spot directly behind their preferred spot is also occupied, they continue forward to search the remaining spots in line (just as in the basic parking functions) until they find a place to park. This collection of generalized parking functions is referred to as Naples Parking Functions. Although much is known about counting parking functions using certain statistics such as ties, ascents, and descents, little research has been done regarding numerical patterns and conditions that these Naples Parking Functions contain. We explore methods for counting ties, ascents, and descents in this variation.

FRI - 803 K-Parking Functions: Naples and Beyond

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Alex Christensen, *University of Arizona*; Mayleen Cortez, *California State University Channel Islands*; Summar Ellis, *Spelman College*; Pamela Harris, *Williams College*; Morgan Hobson, *Spelman College*; Zakiya Jones*, *Pomona College*; Gordon Kirby, *University of California, Santa Barbara*; Marissa Loving, *University of Illinois, Urbana-Champaign*; Andres Ramos, *University of Puerto Rico, Rio Piedras* and Robert Rennie, *University at Illinois at Urbana-Champaign*

Abstract: Consider *n* cars and *n* parking spots on a one-way street. Let $\alpha = (a1, a2, a3, . . . , an)$ where $1 \le ai \le n$ for all i and with ai denoting the ith car's preferred parking spot. Let $\beta = (b1,b2,\ldots,bn)$ be the increasing rearrangement of α such that $b1 \le b2 \le b3 \le \cdots \le bn$. We say that α is a parking function if and only if $bi \le I$ for all i. There is a closed form for the number of parking functions which is denoted by $|PFn| = (n + 1)$^$(n-1)$. We consider a special set of parking functions called Naples parking functions in which a car first drives to its preferred parking spot, and if it is taken then it can back up *k* spots prior to driving forward to seek a parking spot. If the car takes 0 spots back, this can be counted by the regular parking function and if the car is allowed to take *n* spots back then all of the parking preferences will be parking functions and we can count this with *n*^*n*. We focus on the cases when the car can back up *k*=1,2,...,*n*−2 spaces. We discuss an approach to finding bounds on $|NPFn,k|$.

FRI - 805 Evaluating the Impact of Vocational Training and Housing Assistance Programs on the Dynamics of Homelessness in Los Angeles, California

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Jackson Carpenter*, *Arizona State University*; Jennifer Sanchez, *Yachay Tech University*; Mohammed Alharbi, *University of Texas at Arlington*; Vincent Jones, *University of Pennsylvania*; Omar Aragon, *Francisco Gavidia University* and Anuj Mubayi, *Arizona State University*

Abstract: Homelessness is a major socio-economic issue in the United States with more than 500,000 individuals homeless on any given night in 2018 (HUD). The second highest number of homeless (approximately 84,000 individuals, 15% of the national average) was reported from Los Angeles County (LAHSA). Studies have suggested several factors associated with lifetime homelessness including regional socioeconomic disadvantage, isolation from social network communities, mental health issues, and addiction problems, among many others. However, it has been challenging to clearly identify individuals who are at-risk for homelessness and interventions that may reduce the homeless population consistently over time. In the present research, we focus on the dynamics of homelessness for the vulnerable impoverished community based on the socio-economic levels of their living environments and influences of their various social networks. The main objective of the study is to compare the effects of two intervention strategies (vocational training and housing assistance programs) on the spread and control of homelessness using a compartmental mathematical model and data from Los Angeles county. The model stratified the population at risk for homelessness into vulnerable, disaffiliated, and homeless classes (defined in our research). The model analysis suggests conditions under which each intervention can be effective in the long term as long as there are positive influences exerted by an individual's social networks. The results of our analysis show that while providing housing for homeless individuals does help alleviate the problem, interventions such as job training opportunities for disaffiliated individuals before entering homelessness are more effective.

FRI - 806 Data Fitting and Behavioral Analysis of the Zika Virus

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Mahzaib Quraishi*, *California State University, Fullerton*; Anael Verdugo, *California State University, Fullerton*; Christine Deeb, *California State University, Fullerton* and Victoria Meza, *California State University, Fullerton*

Abstract: This work deals with the analysis of the recent Zika virus epidemic by comparing real biological data with a mathematical model in the field of disease dynamics. The model comes from a set of ordinary differential equations motivated from the Replicator-Mutator model and it aims to explain the long-term dynamic behavior of the Zika virus epidemic in Puerto Rico. Parameters are calculated using data from the Center of Disease Control and Prevention (CDC) over a 15-month period in Puerto Rico. Once parameters are chosen, then linear stability analysis on the model shows the existence of one stable fixed point, which yields accurate predictions for the long-term behavior of the infected population. Future work can be extended by means of validating our current model to fit data in other US territories (states, cities, or towns). This will in turn help fine-tune our parameters and thus a more robust model that accurately predicts the Zika virus epidemic behavior in various locations in the US.

FRI - 807 Forecasting Dissolved Oxygen in Loko ʻia (Hawaiian Fishponds) Using ARIMA Model

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Xavier Garrido*, *University of Hawaii West Oahu* and Esther Widiasih, *University of Hawaii West Oahu*

Abstract: Dissolved oxygen is one of the most important aspects of aquaculture, as it is essential to fish growth and health. Oxygen levels below 5ppm cause stress on fish, and below 3ppm could be lethal. The Loko 'ia (Hawaiian fishpond) is one form of aquaculture, practiced for centuries on the island chain. In the past, elevated water temperature in combination with other factors such as weakening trade winds, have resulted in a rapid decrease of dissolved oxygen, causing large fish kills in some loko 'ia around O'ahu. The amount of dissolved oxygen in the system is a function of many factors, including solar irradiance, windspeed, and temperature.

Recently, dissolved oxygen and temperature sensors are placed in some loko i'a and the time series data is publicly available through smartcoastlines.org, including Mokauea fishpond on Oʻahu. We hypothesize that using data from these sensors, one can predict a fish kill event at Mokauea loko ʻia. Autoregressive integrated moving average (ARIMA) is a statistical technique to analyze and forecast time series data. We apply ARIMA with input variables temperature from smartcoastlines.org as well as wind speed from NOAA. Preliminary results show that an increase in temperature and a decrease in wind speed could predict a lowered level of dissolved oxygen. For this model to be useful to loko ʻia practitioners, a lead time of one week or less would be most desirable.

FRI - 808 The Role of Variation in Mate Choice and Wolbachia Infection on *Aedes Aegypti* Population Dynamics

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Brian Chau*, *University of Central Florida*; Zhen Wang, *Shanghai University*; Ulises Jaime-Yepez, *University of California, Davis*; Bernardo Ameneyro, *University of Colima*; Maximiliano Chavez, *National Autonomous University of Mexico* and Anuj Mubayi, *Arizona State University*

Abstract: Wolbachia, an endosymbiont bacteria, is common in various invertebrates and known for host reproductive manipulation strategies as well as for slowing the replication of certain viruses. When infected by Wolbachia, Aedes aegypti mosquitoes become resistant to transmitting some mosquito-borne diseases (MBD) such as dengue, diseases prevalent in tropical and subtropical regions.

Releasing a large number of Wolbachia infected mosquitoes in the environment is assumed to be a more effective strategy than other various methods to control the spread of MBD. However, evaluation of such Wolbachia-based interventions over a long term temporal scale is limited in the literature. Moreover, the Wolbachia's host manipulation strategy, cytoplasmic incompatibility (CI), benefits the Wolbachia in the form of decreasing the number of non-infected mosquitoes. Additionally, Changes in mating preference could impact the benefit from CI, as it requires that infected males mate with uninfected females.

We developed and analyzed models that capture the life cycle and mating preference of mosquitoes with and without Wolbachia. Our research primarily focuses on the effects of non-random mating on the population dynamics of mosquitoes. The analysis of models suggest that Wolbachia persists in the mosquito population as long as a sufficiently large Wolbachia infected mosquito population (critical population size) is released. This critical population size is a function of mating-related factors and stage progression rates.

We hope that the results of this modeling study will help in identifying significant change to the dynamics which could better inform us about the effectiveness and sustainability of this method to combat MBD.

FRI - 809 Epidemiological Models for Chlamydia Trachomatis in Puerto Rico

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Genesis Rivera-Bachier*, *University of Puerto Rico at Cayey* and Maytee Cruz-Aponte, *University of Puerto Rico at Cayey*

Abstract: Sexual transmission infections (STIs) as Chlamydia trachomatis (CT) has increased in the Puerto Rican population and is the STI with the biggest prevalence in Puerto Rico. In this research work, we developed a dynamical system of differential equations based on an SIR type mathematical model. We use a SEIAT, to analyze the behavior of the chlamydia transmission in the heterosexual female and male population between 15 – 35 years old. Doing a mathematical analysis, we determined if, in effect, chlamydia is an epidemic and the methods to decrease its prevalence. The experimental parameters from the developed model directly interfere in the behavior of the CT infection. Based on the numerical simulations we determined that the parameters we must manipulate for decreasing the infection are the probability of infection from an infected person to a completely susceptible population, the individuals that interrupts the treatment, individuals that have sexual intercourse during the treatment, days in recovery, changes in sexual partners and the treatment rate of symptomatic individuals.

FRI - 810 On a Generalization of Lucas Numbers

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Skylyn Irby*, *The University of Mississippi* and Sandra Spiroff, *The University of Mississippi*

Abstract: We consider a generalization of Lucas numbers. Recall that Lucas numbers are the sequence of integers defined by the recurrence relation: $L_n = L_{n-1} + L_{n-2}$ with the initial conditions $L_0=2$ and $L_1=1$. That is, the classical Lucas number sequence is 2,1,3,4,7,11,18,.... The goal of this research is to study properties of certain generalizations of the Lucas sequence. In particular, we consider the following definition: $s_n = as_{n-1} + s_{n-2}$ if n is even $bs_{n-1} + s_{n-2}$ if n is odd, for n=2,3,4,..., where a and b are any nonzero real numbers, with the initial conditions $s_0 = 2$ and $s_1 = 1$; and $l_n = (-1)^n l_{n-1} + l_{n-2}$ for n=2,3,4,... with the initial conditions $l_0 = 2$ and $l_1 = 1$.... More precisely, we will determine the generating function and a Binet-like formula for $s^{\infty}_{n=0}$, and discuss its periodic behavior, as well as that of $l^{\infty}_{n=0}$.

FRI - 811 A Look into Hamming Codes through Set Theory and Graph Theory

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Luis Perez*, *California Lutheran University* and John Villalpando, *California Lutheran University*

Abstract: Error-correcting codes (ECC) are used every day for data transmission which many people are not aware of. ECC, found in information theory, use methods to handle possible errors that may arise from electronic noise to a scratch of a CD in a way where they are detected and corrected. ECC can be used in applications from performing magic tricks to detecting and repairing mutations in DNA sequencing. In addition, error-correcting codes, including Hamming Codes, can be viewed through set theory which gives another perspective on how this type of ECC works. The methodology of this project is comprised of an extensive look into reading, understanding and applying literature. This includes an in-depth look into different ways Hamming Codes are explained through mathematics, current applications in a hat trick and card trick, and general information about error-correcting codes. This research examines why it is the case that Hamming Codes can be explained through set theory. We also prove the properties of Hamming Codes through graph theory. Finally, we investigate further applications of the Hamming Code in a team competition and magic tricks through a set theoretic approach and find reasonings as to how these applications are guaranteed to work given properties of the Hamming Code. Moreover, current applications of the Hamming Code are expanded to show its true significance as a one-bit ECC.

FRI - 812 Application of Principle Component Analysis (PCA) Based Methodology in Characterization of Single Molecule Dynamics

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Howard Weatherspoon*, *Albany State University* and Ara Apkarian, *University of California-Irvine*

Abstract: The application of Surface Enhanced Raman Spectroscopy (SERS) in the detection and identification of single molecule behavior is the ultimate goal of analytic sensitivity. The SERS spectrum of a molecule is highly sensitive to various environmental factors such as molecular orientation and antenna junction structure. These factors can be further manipulated with the use of lasers thereby inducing a greater variety of signals being produced, which in turn leads to more complex spectra. Principle Component Analysis (PCA) is a method which transforms several correlated variables into a smaller number of uncorrelated variables, called principal components. Our principle aim is to demonstrate the potential use of PCA in resolving complex SER spectra of single molecules and devise a protocol for their automated processing and assignment. We hypothesized that the bimodal fluctuation experienced by the BPE molecule can be visualized through the application of PCA in SERS spectra characterization. To test our hypothesis, a time series of bipyridyl ethylene (BPE) spectra (excitation: 633nm) was recorded at the nanojunction of gold nanosphere dimers. The time series of spectra was decomposed into its principle components and were placed through a lowpass filter to reduce hash, then the covariance matrix, eigenvectors, Eigenvalues were calculated to produce a 3-D scatter plot, an average spectra plot, and a connectivity plot in Mathematica. Preliminary results demonstrated that BPE experienced a bimodal fluctuation during the SERS application. Future research involves assignment of the observed fluctuations to specific structures through automated machine learning algorithms for pattern recognition.

FRI - 813 Lattice Patterns for the Support of Kostant's Weight Multiplicity Formula on Sl4(C)

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Lucy Martinez*, *Stockton University*; David Melendez, *University of Central Florida*; Daniel Tinoco, *San Francisco State University*; Robert Rennie, *University at Illinois at Urbana-Champaign* and Pamela Harris, *Williams College*

Abstract: Kostant's weight multiplicity formula is an alternating sum over the symmetry group of a Lie algebra's root system, known as the Weyl group. This formula is used to compute the multiplicity of a weight in an irreducible highest weight representation of a Lie algebra. In this poster we focus our attention to describing the Weyl alternation sets, which consist of subsets of the Weyl group elements that contribute nontrivially to Kostant's weight multiplicity. From this, we present geometric constructions for these sets.

FRI - 814 Community Detection and Nonlinear Dimension Reduction Techniques in Data Science

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Maati McKinney*, *Spelman College*; Michael Lacey, *Georgia Institute of Technology*; Hrishikesh Bodas, *Carnegie Mellon University* and Annika Cleveland, *New Mexico State University*

Abstract: We studied two techniques in community detection and nonlinear dimension reduction. These techniques operate on the presumption that high dimensional data lies on some lower dimensional manifold, and that by approximating Laplacians and random walk diffusions, we can utilize the manifold structure and map the data to a lower dimension.

Community detection is common and effective, used in fields such as social network analysis and optical handwriting recognition. The specific community detection technique we examined was spectral clustering as described by von Luxburg, which uses the eigenvalues of the Laplacian to cluster data based on similarity. We encoded the algorithm given and implemented it to cluster both a 3-Gaussian and double-moon data set.

Linear dimension reduction is a well-studied and efficient method of analyzing high dimensional data, but it does not work as well when the data set is lying on a nonlinear manifold. Nonlinear dimension reduction is more challenging, but proves to be much more successful for complex data sets. We explored diffusion mapping as proposed by Coifman and coauthors. Diffusion mapping uses local geometry to approximate the global data structure in a lower dimension, while preserving essential qualities. For this technique, we implemented code to perform diffusion mapping on a Swiss roll. In doing so, we investigated the tradeoff between model accuracy and data set size. We observed that when data neighbors are too few, the embedding produced is impoverished; contrarily, when we vastly increase the number of neighbors, the embedding is much richer and well-mapped.

FRI - 815 Exact and Numerical Solution of Stochastic Burgers Equations with Variable Coefficients

Discipline: Mathematics
Subdiscipline: Statistics

Jose Palacio*, *The University of Texas, Rio Grande Valley*; Tamer Oraby, *The University of Texas Rio Grande Valley*; Stephanie Flores, *The University of Texas Rio Grande Valley*; Elijah Hight, *The University of Texas, Rio Grande Valley*; Erwin Suazo, *The University of Texas, Rio Grande Valley*; Jasang Yoon, *The University of Texas Rio Grande Valley* and Everardo Olivares-Vargas, *The University of Texas Rio Grande Valley*

Abstract: Title: Numerical Solution of Stochastic Burgers Equation with Variable Coefficients

Deterministic and stochastic Burgers equations are used to model turbulence of fluid motion and dynamics of interfaces. Stochastic Burgers equation (SBE), in particular, is the center of many research efforts. Numerical solutions of SBEs with space-time white noise has been previously studied via the path integral formulation and ensemble average. It was also studied using finite difference and Galerkin approximations. The goal of this investigation is to introduce a numerical scheme, as well as an exact solution in some cases, for stochastic Burgers equation (SBE) with variable coefficients. We introduce a new numerical algorithm of two types of SBEs with variable coefficients and a uniform-space white noise using a coupled deterministic Burgers equation with first order or second order stochastic differential equations (SDE). We showed using Itô calculus that some exact solutions of stochastic Burgers equations with variable coefficients could be found using deterministic Burgers equations. The numerical algorithm solves a deterministic Burgers equations over stochastic meshes that happens to be solutions of stochastic differential equations. We conjecture that a similar approach could be used to simulate other stochastic partial differential equations with space-uniform white noises and in some cases with time-space white noises.

FRI - 816 Evaluating the Impact of Timing of Antiretroviral Therapy Initiation on Outcomes in Human Immunodeficiency Virus-Infected Adults

Discipline: Mathematics
Subdiscipline: Statistics

Scott Cleven*, *University of Iowa*; Margaux Douvier, *Winona State University*; Katiely Munoz, *Kean University* and Hyunkeun Cho, *University of Iowa*

Abstract: The purpose of this study is to provide further statistical analysis towards the relationship between treatment times and incidence of tuberculosis (TB) within the people of Haiti with HIV. The World Health Organization has conducted tests on the timing of antiretroviral therapy (ART) on this population. The subjects were sectioned into two samples, immediate/early treatment and delayed treatment. In a previous study, the analyzers looked only at the relationship between early/delayed treatment and incident TB and found that delayed treatment increased the odds of a subject contracting TB (Collins et al. 2014). The goal of this study is to focus on the health of the subjects and further analyze the delayed treatment group that previous studies did not analyze themselves. The target population of this study is the people of Haiti with HIV that received delayed ART treatment and didn't have tuberculosis before entering the study. We split the subjects of the delayed treatment group that describe our target population into two subgroups by the time in years before they received ART with the median value being the cutoff for being in the shorter or longer years to ART subgroups. Using logistic regression, we found significant evidence that healthier subjects had longer time to ART. However, despite these subjects being healthier at baseline, their odds of receiving TB was much higher than the odds of the shorter time to ART subgroup. Thus, we concluded that treatment time is more significantly influential on incidence of TB than health of the individual.

FRI - 817 Exploring Infinity and the Bounds on Logic !

Discipline: Mathematics
Subdiscipline: Other Mathematics

Cristian Ocampo*, *Bakersfield College, Bakersfield* and Jonathan Brown, *Bakersfield College*

Abstract: The Continuum Hypothesis has been a conspicuous gap in modern mathematical logic since it was first presented in 1878. We will be walking through Cantor's work on cardinalities of standard number systems, learning the structure of a proof and looking at some examples proofs I've authored. Then we will venture into the fact that the Continuum Hypothesis is independent from the standard ZFC (Zermelo–Fraenkel set theory) model and with the help of Gödel’s incompleteness theorems and Russel’s paradox we hope to attain a better understanding of the issue.

This line of research was inspired by the work of Malliaris and Shelahm on the infinite sets of p and t. We plan to unravel some of the technical aspects of their paper, which holds promise for new approaches to the Continuum Hypothesis. We present some examples of Applied Non-Standard Analysis to show the real-world relevance of such abstract concepts. Finally, we will explore the critical decision in current mathematics of accepting one of two new contradicting axiom schemes (Forcing axiom and Ultimate-L) and their implications.

FRI - 818 The Use of Nylon 6,6 Artificial Muscle Actuators in Biomimetic Applications for Use in Prosthetic Devices

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Colleen Evans*, *Los Angeles City College* and Jayesh Bhakta, *Los Angeles City College*

Abstract: The research in artificial muscles have produced viable, low cost and efficient means in creating actuators for a variety of possible applications from energy efficient windows to children’s toys. Research has been conducted into the use of nylon actuators for applications in soft robotics and medical devices such as prosthetic limbs. The objective of the research here is to investigate the viability of using nylon artificial muscles to provide the force and static tensile strength required for daily use in an artificial hand for use by an amputee. In using open source 3-D printed files for the exoskeleton of the hand, artificial muscle actuators are added to the design to articulate the prosthetic by means of electrical power. By using actuators that are activated by the application of heat along the fibre bundles the space needed for moving the joints of the hand become more compact and efficient without sacrificing strength to move the component. By following the biomimicry of the human arm, it becomes

possible to articulate the hand in a more natural manner. Preliminary tests of the exoskeleton hand show a static strength strong enough to lift >60lb of weight with no creep. Testing of the individual fibres indicate that they can lift loads over 100 times as much as human muscle of the same length and weight. By using a biomimicry approach, the goal of this project is to create a viable and low cost means of creating a durable hand prosthetic for daily use.

FRI - 819 Bioengineered Topographical Construct for Muscle Regeneration

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Jeffrey Nguyen*, *California State University, Long Beach*; Kimberly Padron, *California State University, Long Beach*; August Elder, *California State University, Long Beach*; Bryan Vu, *California State University, Long Beach* and Perla Ayala, *California State University, Long Beach*

Abstract: Volumetric muscle loss (VML) resulting from major acute injuries such as car accidents and surgical procedures can lead to both loss of tissue function and fibrosis. Although skeletal muscle demonstrates an innate capacity to regenerate minor damages, major injuries tend to be impossible to repair. For this project, we created a basis for the integration of engineered biomaterials with specified physical capabilities to support myoblast growth *ex vivo* and both vascularization and skeletal tissue formation *in vivo*. Collagen type 1 was extracted from porcine dermal tissue, purified using an acid solubilization method, and then casted upon a poly-dimethyl siloxane (PDMS) mold with micro channels. The mold was designed using SolidWorks and created using a *Projet 6000* 3D printer. To determine cell proliferation and differentiation, C2C12 myoblasts were cultured on the collagen films for 1-3 weeks and analyzed using fluorescent and immunostaining. Myoblasts cultured on molded collagen scaffolds showed enhanced proliferation, desired physical orientation properties, and formation of multi-nucleated fibers. Muscle cells within the micro channeled molds demonstrated formation of multi-nucleated fibers as the cultivation period was increased from 7 to 21 days. Specifically, using a combination of F-actin, nuclei, and immunostaining, a culture of 21 days demonstrated observable formation of myofibrils and orientation of myoblasts in the same direction. Future work will include use of hybrid hydrogels to enhance both structural integrity and biochemical properties of the construct. These designed collagen bioengineered constructs continue to demonstrate significant potential for applications in muscle tissue engineering.

FRI - 820 Magnetically Assisted Disaggregation of Amyloid-β Plaques

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Valeria Juarez*, *University of Texas at San Antonio*; Samantha Eaton, *University of Texas at San Antonio* and Gabriela Romero Uribe, *University of Texas at San Antonio*

Abstract: Alzheimer's disease (AD) is characterized by the aggregation of amyloid-β (Aβ) protein. This plaque build up impairs the brain's neural network and causes neuronal injury and death. Although AD pathogenesis is not fully understood, it is hypothesized that disaggregating Aβ plaques could improve cognitive function and impair the disease state progression. Recently, the natural formation of magnetic Iron Oxide Nanoparticles (MNPs) within the Aβ plaque cores in AD patients has been found. Magnetic hyperthermia has been used for the past two decades for the local heat dissipation of MNPs under alternating magnetic fields (AMF). We propose to design a magnetically assisted approach for the treatment of AD by engineering MNPs to target Aβ plaques and break them down in a controlled manner. The local heat generated by MNPs upon AMF exposure will be utilized first, to disrupt Aβ plaques, and second for the controlled release of neural growth factors. To do this, we have synthesized and characterized MNPs using dynamic light scattering and electron microscopy. We have also differentiated a neuroblastoma cell line (SH-SY5Y) into neurons to develop an *in vitro* AD model containing Aβ. We will optimize magnetic hyperthermia using MNPs and AMFs to design an appropriate therapeutic system for protein disaggregation and drug release. From this study, we will be able to develop alternative therapeutic approaches for AD. Future directions for this research includes applying our findings to Aβ plaque samples obtained from AD patient cadavers. This project is funded in part by NIGMS MARC U*STAR GM007717.

FRI - 821 Development of Vascularized Muscle Tissue in Bioengineered Collagen Scaffold

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Madison Kane*, *California State University, Long Beach*; Daniel Mata, *California State University, Long Beach*; Thuy Nguyen, *California State University, Long Beach*; Keenan Anderson-Fears, *California State University, Long Beach*; Jeffrey Nguyen, *California State University, Long Beach*; Bryan Vu, *California State University, Long Beach* and Perla Ayala, *California State University, Long Beach*

Abstract: Patients who sustain traumatic muscle loss or injury often have limited treatment or rehabilitation options. To overcome this challenge, an engineered vascularized muscle tissue developed in vitro could be used as a potential artificial transplant option. The purpose of this study was to investigate the growth of myotubules and capillary structures when seeded on a bioengineered collagen scaffold with embedded micro-channels. Type I collagen derived from porcine skin, via an acid solubilization process, was used to create the collagen scaffold on molds containing parallel micro-channels to influence the growth of aligned myofibers. Myoblasts (C2C12 mouse cell line) and human umbilical vein endothelial cells (HUVECs) were co-cultured on the scaffold for 10 days with different culture conditions to study the development of endothelial tubules and lumen concurrently with the growth of myofibers. Imaging and immunostaining techniques were performed to observe cell viability, myotubule development, and angiogenesis. Preliminary results indicate that the engineered collagen scaffold supported the growth and proliferation of both cell lines. Fluorescent imaging showed that the parallel micro-channels helped to direct the proliferation of myoblasts into forming multi-nucleated myofibers having similar orientations. Endothelial cells showed signs of proliferation, however observation of effective angiogenesis is inconclusive. Current work is focused on integrating HUVECs into a collagen hydrogel prior to addition to the scaffold, and introducing human mesenchymal stem cells to the co-culture to support angiogenesis. Results from this work will help create a biomaterial suitable as functional muscle tissue for stimulated muscle regeneration.

FRI - 822 Hyperspectral Imaging to Quantify Oxygen Delivery in Microcirculation

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Alfredo Lucas, *University of California, San Diego*; Carlos Munoz, *University of California, San Diego*; Amanda Breton*, *University of California, San Diego* and Pedro Cabrales, *University of California, San Diego*

Abstract: The use of the microcirculation to study the effect of therapeutics, blood transfusions and circulatory system related pathologies has been widespread. The measurements which provide the most information about appropriate function of the microcirculation are measurements of oxygen tension (pO_2) and hemoglobin (Hb) oxygen (O_2) saturation (SO_2) in arterioles and venules. Although techniques such as phosphorescence quenching microscopy (PQM) allow for measuring pO_2 and is commonly used and validated, it only provides single point measurements, thus only providing a snapshot of the process. In this study, we propose a hyperspectral imaging pipeline that allows for fast and accurate measurements of the HbO_2 saturation distribution along the entire microcirculation of the window chamber from a single image, taking less than 10 seconds to acquire. Using a benchtop hyperspectral imaging system, Golden Syrian hamsters instrumented with a dorsal skinfold model were subjected to either hypoxia at 8% oxygen or anemia through human albumin exchange. Images of the window chamber was acquired in less than 5 seconds, with post processing taking approximately 4 minutes per picture. The proposed approach successfully distinguished arterioles and venules based on their expected saturation profiles and determined saturation within 10% of the values measured through PQM during both hypoxia and anemia. Semi-quantitative

analysis of microcirculatory SO_2, provides a reproducible and transparent tool in experimental and clinical research to monitor and evaluate the changes in O_2 delivery to tissues in the microcirculation during physiological and pathological conditions.

FRI - 823 Amniotic Fluid-Derived Cardiomyocyte Model to Investigate Stretch-Response Signaling Pathways Involved in Hypoplastic Left Heart Syndrome

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Alyssa Salazar*, *Department of Bioengineering, University of Colorado, Anschutz Medical Campus*; Mallory Lennon, *Department of Bioengineering, University of Colorado, Anschutz Medical Campus* and Jeffrey Jacot, *Department of Bioengineering, University of Colorado, Anschutz Medical Campus*

Abstract: Hypoplastic left heart syndrome (HLHS) is a congenital heart defect that causes the left ventricle, mitral valve, aortic valve and ascending portion of the aorta to be underdeveloped. This reduces the heart's ability to pump oxygen-rich blood through the body. Genetic mutations have been found to be associated with HLHS in some cases. However, for the majority, the cause of this congenital defect is unknown. Apart from genetic mutations, cardiomyocyte (CM) deficiencies, such as proliferation rate and cell structure, have been observed in HLHS. Given that CM must respond to biomechanical stretch for proper heart development, we hypothesize that disruption of mechanical signaling pathways in CM are responsible for the defects observed in HLHS. We used an amniotic-fluid derived model of HLHS to investigate how the structure and function of HLHS-CM are altered in response to cyclic stretch. Healthy control and HLHS-CM were stretched for 24 and 48 hours at 10% stretch at 1 Hz frequency. The software, ImageJ, will be used to compare the total cell area and cell shape (circular versus elongated) of cardiomyocytes from HLHS patients and control patients. In addition to cell area, proliferation rates and sarcomere organization within the cell will be analyzed. We predict that the proliferation rate, cell area, and sarcomere organization will be abnormally reduced in HLHS patients as compared to healthy controls. Investigating the mechanosensitive pathways involved in HLHS will provide insight into how this defect develops and will lead to new therapies for the treatment of HLHS.

FRI - 826 A Compative Study of a 3D Bioprinted Gelatin-Alginate Based Bioink for Three Different Tissue Scaffold Structures

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Erick Dominguez*, *University of Texas at El Paso*; Binata joddar, *University of Texas at El Paso* and Matthew alonzo, *University of Texas at El Paso*

Abstract: This layer-by-layer method that allows for cell-laden hydrogels can be combined to allow complex, composite tissue and organ structures. A limiting factor of current bioprinting technology is the limited range of available bioinks with the desirable characteristics to print and allow for cell growth/adhesion while maintaining structural fidelity/printing shape fidelity. Gelatin-alginate as model hydrogels were mixed at various concentrations to obtain hydrogel formulations with the goal of optimizing an ideal bioink with the needed biomechanical properties and was used to test its printing capabilities on a Cellink bioprinter (Cellink, Sweden) followed by scaling up on an advanced BioAssembly Bot (Advanced Life Sciences, USA). Pluronic F-127 and 4% alginate were used as positive and negative control bioinks for the printing process. Gelatin–alginate composite hydrogels with a single optimized printable material/formulation of 7% alginate and 4 % gelatin exhibited an excellent balance between structural integrity/extrusion uniformity. This optimized bioink formulation was used to fabricate three different tissue scaffold structures, bone, cartilage and cardiac in a comparative study to test against the properties of each structure. All scaffolds were analyzed for swelling/degradation properties, and their porous structures examined via scanning electron microscopy (SEM). Biocompatibility was evaluated with in-vitro cell culture and live/dead assays respectively. This study developed a framework for evaluating printability and investigated the effect of bioink composition and constitution on various printing outcomes including extrudability, extrusion uniformity, and structural integrity. Methodology introduced in this study could also be used to evaluate the printability of other bioinks in the future.

FRI - 827 Food Dye Behavior and Stability during Storage

Discipline: Engineering
Subdiscipline: Chemical Engineering

Luis Orellana*, *University of California, Riverside* and Christopher Bardeen, *University of California, Riverside*

Abstract: Color additives are a prominent staple of both aqueous and alcoholic beverages due to their aesthetic value. Regulatory agencies such as the US Food & Drug Administration (FDA) continue to develop stricter regulations in response to more frequent and recent health studies. Current industry regulatory guidelines for manufacture and use of such additives emphasize short-term or on-site analysis. However, long-term storage and light exposure are potential environments for these beverages, which can cause photochemical changes within the dyes.

The objective of this project is to compare the practical absorption spectrometry in different midterm-term storage environments of the FDA-approved color additives Allura Red AC, Sunset Yellow FCF and tartrazine in dilute aqueous or ethanol solutions. The storage environments are common to both household and industry settings such as constant room temperature light exposure or light-absent scenarios. The solutions were all created to adhere to Beer-Lambert's law with absorbance in respect to molar concentration.The Cary-60 Ultraviolet/Visible Light Spectrometer quantifies absorbance. From there, the absorbance spectra are also quantified with diffused laser irradiation exposure. Prior to laser exposure, the absorbance stability across all three dyes is consistent in respect to time (Δ+1%). However, introduction of laser exposure increases absorbance (Δ+11.63%) across all dye solution scenarios. Although direct laser exposure and beverage storages typically are not of complication, ultraviolet and light exposure are common with sunlight. These results offer a template for storage and handling guidelines for beverages that contain color additives for the safety and wellbeing of consumers.

FRI - 828 Investigating Vapor Phase Emission during Accelerated Aging of Pt Diesel Oxidation Catalysts

Discipline: Engineering
Subdiscipline: Chemical Engineering

Mariah Curley*, *The University of New Mexico*; Deepak Kunwar, *The University of New Mexico* and Abhaya Datye, *The University of New Mexico*

Abstract: Platinum, an expensive and rare element, is used in approximately ninety percent of automotive exhaust systems. One application of Pt is in diesel oxidation catalysts (DOC) which are used in catalytic converters to oxidize the unburnt hydrocarbons and carbon monoxide to lessen CO_2 released to the environment. DOC catalysts are subjected to accelerated aging according to the USDRIVE Low Temperature Aftertreatment Test protocols (800 °C in air) to simulate changes in catalyst structure that might occur over 120,000 miles of driving. At this high temperature, Pt reacts with oxygen to form PtO_2 which is volatile and can be transported within and outside the reactor. The rate of Pt emission from catalyst layers is not fully understood and is being studied in this project using model catalysts. Depositing the catalyst powder on thin silicon wafers and placing in a tube furnace with flowing air produces a measurable sample, which can be measured through Scanning Electron Microscopy - Energy Dispersive Spectroscopy (SEM-EDS). We hypothesized that the Pt loss would depend on the flow rate of air through the tube if the air surrounding the Pt was saturated in PtO_2 vapor. However, our observations suggest that the flow rate of air has no effect on Pt loss. Using this information, we have constructed a mechanistic model for the emission of Pt from catalyst thin films. This information will be useful for the design of catalysts that are better able to withstand accelerated aging protocols and contribute to the goals of clean energy.

FRI - 829 Damage Analysis of Manufactured Homes Impacted By Hurricane Irma

Discipline: Engineering
Subdiscipline: Civil Engineering

Karen Vazquez*, *University of Kansas* and Elaina Sutley, *University of Kansas*

Abstract: The goal of this research is to advance the current state of knowledge in analyzing damage to manufactured homes in Florida using new findings from 2017 Hurricane Irma. To meet this goal, we combined post-Irma National Science Foundation-funded RAPID reconnaissance imagery with Florida public records, Google Maps imagery, and wind speed predictions for the storm. These data were collectively used to characterize multi-hazard (wind, flood, and debris impact) damage to manufactured homes into four sequential physical damage states: (1) minor, (2) moderate, (3) severe, and (4) complete, where occupancy is no longer safe after reaching damage state 3.

Results from the damage classification were assessed against other factors including wind speed, location of homes (inland versus island), and the build year of the home following important cutoffs associated with manufacturing regulation changes. Results identified homes in the isle region experienced greater variation in damage states than inland areas. The results also confirmed a well-documented finding that homes built prior to 1976 experienced greater damage at wind speeds exceeding 100 miles per hour, while homes built after 1976 experienced reduced, while still distributed, damage at the same wind speeds. Findings from this work can be used to promote retrofit programs to provide essential safety to residents living in older homes and use to promote increased design standards for new homes.

FRI - 830 Performance of Ultra-High Performance Concrete Shells for Use in Concrete Beams and Columns.

Discipline: Engineering
Subdiscipline: Civil Engineering

Bolivar Perez*, *University of Central Florida* and Kevin Mackie, *University of Central Florida*

Abstract: Due to the current deterioration and aging of concrete infrastructure throughout the world, new materials and construction methods are essential to ensure efficient repairs of existing structures, and extended longevity and durability for newly constructed structures. Ultra-high performance concrete, UHPC, has gained popularity in the construction industry for use in both new construction and repair work due to its high strength, low porosity, and high durability. Currently, one of the main limitations of using UHPC is that its compatibility with normal strength concrete, NSC, is not fully understood. In this project, the interfacial bond between UHPC and NSC was studied, to help solve this issue. To do this, UHPC shells were designed as an overlay material to NSC cylinders and beams. This was done to mirror potential field applications for new construction and repair work of concrete beams and columns. The beams were tested using a third-point flexural loading test, and the cylinders were tested using a compression test. The results of the compression loading portion of the study indicated that use of a UHPC shell substantially increased the total stress and loading capability of NSC. Only a select number of specimens showed interfacial detachment between the NSC and UPHC.

FRI - 831 Mechanical Waves in Tissues Under Geometric Confinement

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Monika Tadrous*, *California State University, Fullerton*; Wylie Ahmed, *Cal State Univ- Fullerton* and Vanni Petrolli, *Univ-Grenoble Alpes*

Abstract: Organisms develop from a single cell through a complex developmental cascade that entails multiple factors such as hormones, proteins, and mechanical forces. Previous studies portrayed the importance of mechanical forces in the cell specifically during morphogenesis, as these forces are trigger molecular pathways to organize gene expression. In this study, we work with Madin-Darby Canine Kidney (MDCK) cell line as they are an epithelial cells with migratory properties. Fro example, in case of wound healing, MDCK cells sense their environment, and migrate towards the cut and fill the space. MDCK cells are studied by seeding them on a micropattern that was created via photolithography technique. Time-lapse video microscopy of confined MDCK cells reveal oscillating cell motion and suggest cells experience a mechanical wave which is an alternating mechanical compression and elongation over time along the micropattern. We hypothesize that cells use the mechanical wave to determine their position and sense their environment. By understanding the dynamics of cell migration, a better understanding of biological processes such as tumor metastasis, wound healing, will be better understood. Thus, We aim to characterize this mechanical wave using Particle Image Velocimetry and space-time correlation functions.

FRI - 832 Application of Geographic Information System (GIS) Data in an Augmented-Reality Sandbox to Illustrate and Map the Maunalua Bay Watershed

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Jaynine Parico*, *Kapiolani Community College* and Aaron Hanai, *Kapiolani Community College*

Abstract: Over the last few years, the Maunalua Bay region has been severely affected by continuous floodwaters, resulting in the destruction of community infrastructure and pollution of local fishponds. The goal of this project is to simulate these rainfall flow paths and locate watershed basins. The focus will be on the Maunalua Bay, a specific area of the Ahupua'a (land division) Kona, O'ahu. This information may be used to help understand the local geography of our Ahupua'a and to provide possible solutions for flood zones.

The Augmented Reality (AR) Sandbox will be used to provide live color-coded feedback projection of topographical and hydrological features onto a sand basin. The apparatus is equipped with a Kinect 3D camera, a dedicated Linux computer (open-source freeware specifically made for AR sandbox), a sandbox, and a projector. Mapping information of the Maunalua Bay was stored in a Geographic Information System (GIS) file and then converted into an STL filetype to create 3D polygonal models. The *(166 x 178 x 55 mm)* 3D PLA model of Maunalua Bay was printed using that STL file. This would allow the AR sandbox to show more accurate topographic and contour projections onto the 3D model in place of sand.

Further research will be conducted to test the accuracy of the sandbox software. The next project iteration plans to implement a drain and fill mode where we can simulate water being added or removed to/from the watershed.

FRI - 833 Studying the Feasibility of Owning/Operating a Battery Electric Vehicle with Workplace-Only Charging

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Francisco Mayorga*, *University of California, Irvine*; Faryar Jabbari, *University of California, Irvine* and Edgar Ramoz Munoz, *University of California, Irvine*

Abstract: There is a vast market of drivers who are not interested in purchasing battery electric vehicles (BEVs) due to the lack of charging infrastructure. This concern is heightened for apartment dwellers who cannot install an electric vehicle charger at home. A potential solution for this concern is for BEV manufacturers or government agencies to subsidize the installation of electric vehicle charging stations at various workplaces. Doing so, could potentially open an untapped market of BEV customers that can meet their charging needs at work. In this work, the feasibility of owning and operating a BEV without access to a home charger will be studied. Driving patterns from the National Household Travel Survey will be used to simulate the driving patterns of potential BEV owners. Various BEV models will be studied under several scenarios. Limitations from Level 1 and Level 2 charging stations, common charging station power rates, and BEV charging rates will be taken into consideration. Driving patterns will be used to generate the charging/discharging patterns of the simulated BEVs for several weeks. The simulated charging patterns will be analyzed to determine the percentage of drivers that can operate a BEV with workplace-only charging, while minimizing/eliminating the need to visit fast-charging stations. The goal is to determine the scenarios in which both apartment dwellers and BEV manufacturers will benefit from the installation of workplace charging stations.

FRI - 834 Modeling Opinion Dynamics Using the Affine Boomerang Model

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Emily Lopez*, *University of California, Santa Barbara*; Elizabeth Huang, *University of California, Santa Barbara*; Pedro Cisneros-Velarde, *University of California, Santa Barbara* and Francesco Bullo, *University of California, Santa Barbara*

Abstract: Social network analysis is the study of interpersonal behaviors between members of a group by representing the group members as nodes and using edges to characterize the relationship between members. This representation of a social network allows us to model the group interactions mathematically and apply graph theoretical tools to analyze the overall behavior. Applying social network analysis to model how opinions evolve in a group has gained traction in recent years. The aim of this study is to analyze a recently proposed opinion dynamics model, which is structured under the assumption that if two people have a positive relationship, then their opinions will come closer to agreement, and if they have a negative relationship, their opinions will diverge. We will study the model by simulating it for randomly generated network structures and observing how the structure of positive and negative relationships drives the opinions of the members of the network. In the case where the network has two opposing factions, we should observe that within each faction, members will agree, but the opinions of the factions will polarize. Furthermore, in the case where there are more than two factions, the opinions of some of the factions will oscillate. Understanding how social network structures impact the ability for a group to come to agreement gives us further insight about human interaction, which can be applied toward information dissemination, political science, and economics.

FRI - 835 On-Surface Synthesis and Dry Transfer of Atomically Precise Graphene Nanoribbons for High Performance Field-Effect Transistors

Discipline: Engineering
Subdiscipline: Electrical Engineering

Safi Mohammed*, *University of California, Berkeley*; Zafer Mutlu, *University of California, Berkeley*; Juan Pablo Llinas, *University of California, Berkeley*; Ilyas Piskun, *University of California, Berkeley*; Hsin-Zon Tsai, *University of California, Berkeley*; Rastko Nastic, *University of California, Berkeley*; Edgar Ibarra, *University of California, Berkeley*; Felix Fischer, *University of California, Berkeley*; Michael Crommie, *University of California, Berkeley* and Jeffrey Bokor, *University of California, Berkeley*

Abstract: On-surface synthesized atomically precise graphene nanoribbons (GNRs) possess unique structural and electrical properties that make them critical for the development of high-performance field-effect transistors (FETs). Currently, the fabrication of GNR-based transistors is conducted by synthesizing GNRs on metallic substrates (Au (111), etc.) and transferring them onto non-metallic substrates (SiO_2, etc.) through a wet-transfer method. However, this process involves the use of solvents and strong acids which often results in the degradation of intrinsic GNR properties. Herein, we present a dry-transfer method which involves picking up on-surface synthesized 7-atom wide armchair-edge GNRs (7-aGNRs) from a gold substrate using a polymer film and stamping them onto a SiO_2 substrate for FET device fabrication. Using Raman spectroscopy, atomic force microscopy, and scanning tunneling microscopy, we identify and characterize the GNRs before and after the transfer process to ensure high structural and electrical homogeneity. The dry-transferred GNRs are expected to exhibit excellent electron transport characteristics and are therefore potentially ideal for use as the channel material in post-silicon Complementary Metal–Oxide–Semiconductor (CMOS) transistors, enabling the ultimate scaling of high performance digital electronics.

FRI - 836 Designing 3D-Printed Models of Geographic Locations to Use with the AR Sandbox

Discipline: Engineering
Subdiscipline: Engineering (general)

Alden Andrei Fernandez*, *Kapiolani Community College* and Aaron Hanai, *Kapiolani Community College*

Abstract: Augmented reality (AR) is an interactive real-world experience where a system enhances the user’s perceptual experiences. Its application is dependent on the user's environment, and therefore limited by what the system physically experiences. The AR Sandbox, developed by the University of California - Davis, was designed to illustrate topography, geology, and hydrology. A projector and a Kinect camera are mounted above a sandbox to measure distance and detect movement. The devices are connected to a computer that creates an elevation color map and water simulation projection onto the sand.

The purpose of this project is to design 3D-printed models for the AR sandbox to demonstrate real-world effects on Hawai'i's Maunalua watershed. The sand’s manipulability makes it vulnerable to alterations, making it unreliable to represent specific locations, unlike 3D-printed PLA models, which are sturdier and can accurately represent a location consistently. A digital model using Geographical Information System (GIS) data of the watershed within a square region without the ocean floor was created. A 7.0x6.5x2.2 in. non-scaled prototype of the Maunalua watershed was test-printed to use with the AR sandbox.

In order to print a scaled model for a 40x30x6 in. sandbox, the digital model was partitioned so it can be printed into separate units. The equipment will be calibrated to compensate for the height limit of 3D prints. A successfully-printed model should consistently generate an accurate color map. In the future, bathymetry data will be used to map the ocean floor to expand the model.

FRI - 837 Revscripter: A Dynamic Web-Based Tool for Building Phylogenetic Analysis Pipelines

Discipline: Engineering
Subdiscipline: Other Engineering

Lorenzo Chavarria Vargas*, *Iowa State University*; Walker Pett, *Iowa State University* and Tracy Heath, *Iowa State University*

Abstract: In biology, phylogenetic trees are important for understanding the evolutionary processes responsible for generating the Earth’s biodiversity. Bayesian statistical methods enable biologists to infer phylogenetic trees under complex, hierarchical models. RevBayes (*revbayes.com*) is a program for Bayesian phylogenetics that provides a flexible framework for modular model design, enabling applications to a wide range of biological questions. The core interface of RevBayes is an interpreted programming language that may be challenging for scientists with no programming experience. Thus, a graphical user interface is necessary to introduce new users to this research tool. RevScripter is a web-based tool that generates analysis scripts for RevBayes. RevScripter is implemented using the programing language JavaScript, markup language HTML, and style sheet language CSS. The user is presented with options for building a model and analysis. Each time an option is chosen, RevScriptor reacts to ensure that the model is built correctly. When the user is done choosing all the options, they then generate a script. Like RevBayes, the design of RevScripter is modular and builds the model components based on a set of core functions and code snippets that are combined from each option to generate a complete script. The user can then deploy the script in RevBayes, which will execute the phylogenetic analysis. User interfaces like RevScripter enable researchers to easily use complex programs like RevBayes and make hierarchical modeling and interpreted programming languages more accessible to a wide range of scientists.

FRI - 838 Synthesis of Silver Nanostructures for Gas Sensing Using SERS

Discipline: Materials Research
Subdiscipline: Materials Research

Kenneth Martinez Algarin*, *University of Puerto Rico at Cayey*; Adrian Camacho, *University of Puerto Rico at Cayey* and Wilfredo Otano, *University of Puerto Rico at Cayey*

Abstract: Surface Enhanced Raman Spectroscopy (SERS) is an ultra-sensitive detection method that can detect at nanomolar concentrations. It utilizes an analyte with a metallic substrate to amplify the standard Raman signal. Noble metals such as gold, silver and copper have been shown to work effectively as substrates in this technique. The effectiveness of these metal substrates has been related to the morphology at the nanoscale. Typically, the metal substrates are synthesized using expensive and complicated procedures. This project seeks to synthesize silver nanoparticles as substrates for SERS using physical vapor deposition (PVD), a cheaper and less complicated procedure that uses plasma to produce thin films from a wide array of materials. Sputtering plasma conditions can be modified to affect the morphology of the synthesized silver thin films and change the SERS amplification. PVD can also be combined with other techniques to alter the morphology of the silver structures used to produce the enhancement of the Raman signal. A proprietary technique, developed to produce different nanostructures, was used for the deposition of the silver and preliminary results show that controlling substrate temperature and plasma-processing parameters allows forming of nano-island arrays that significantly amplifies the Raman response. The project aims to optimize parameters in PVD to produce reliable silver substrates that can act as sensors for the detection of specific molecules using SERS.

FRI - 839 **Combining High Sensitivity and Dynamic Range: Wearable Thin-Film Composite Strain Sensors of Graphene, Ultrathin Palladium, and PEDOT:PSS**

Discipline: Materials Research
Subdiscipline: Materials Research

Anne Cardenas*, *University of California, San Diego* and Darren Lipomi, *University of California, San Diego*

Abstract: The future of health has consistently been migrating from hospitals to the comforts of home. One of the current obstacles in achieving this is finding a way to safely monitor patients outside of the clinic. A combination of sensitivity, dynamic range, and robustness is essential to the development of wearable mechanical sensors capable of this kind of tracking. These kinds of devices could be useful in monitoring obstructive sleep apnea, a sleep disorder in which the airways become blocked repeatedly during sleep. By creating a small and unobtrusive device that combines the conductivity of graphene, the high plasticity of PEDOT:PSS as a stretchable conductive binder, and the piezoelectric properties of an ultrathin film of palladium, a strain sensor with a wide range of sensitivity can be obtained. The device described in this work was capable of detecting conductivity from as low as 0.001% engineering strain and continued working up to a range of 86%. To optimize the robustness of the device, it was sandwiched between a soft layer of PDMS at the skin interface and a harder layer of PDMS at the air interface. When attached to the torso under the breast bone region of a human subject, the device was capable of detecting heartbeat (low strain) and breathing (large strain) simultaneously.

FRI - 840 **Tunable Organic Polymer/Inorganic Silicon *P-N* Diode Using an Ionic Liquid Gel Gate Dielectric**

Discipline: Materials Research
Subdiscipline: Materials Research

Luis Rijos*, *University of Puerto Rico at Humacao* and Nicholas Pinto, *University of Puerto Rico at Humacao*

Abstract: A *p-n* junction diode was fabricated using *p*-doped poly(3,4-ethylenedioxthiophene)-poly(styrene sulfonic acid) and an *n*-type Si substrate. The diode turn on voltage was ~0.4V. By integrating an ionic liquid gel (IL) as the gate insulator, the current on/off ratio could be tuned over three orders of magnitude *via* a voltage applied to the IL. In addition, the diode could be turned on in the first or the third quadrant of the current-voltage plot by changing the polarity of the gate voltage. The high specific capacitance of the IL permitted diode operation at low voltages (±2V) saving on power consumption. This is the first report on a tunable diode using an IL. By connecting the diode in a resistor loaded circuit, a low frequency (10 Hz) signal could be rectified with a maximum efficiency of 20%. The ability to rectify ac signals and control the output amplitude makes this diode useful in feedback chargers designed to reduce power delivery when charging nears completion. This work was funded by NSF under grants DMR-RUI-1800262 and DMR-PREM-1523463.

FRI - 841 **Molecular Dynamics Simulations of Para-Aminobenzamidine Functionalized Cellulose Nanocrystals**

Discipline: Materials Research
Subdiscipline: Materials Research

Jordan A Caraballo-Vega*, *University of Puerto Rico at Humacao*; Jose Sotero-Esteva, *University of Puerto Rico at Humacao* and Ezio Fasoli, *University of Puerto Rico at Humacao*

Abstract: Membrane based chromatographic processes have been discussed as promising alternatives for protein purification due to their easily accessible surface area and renewability. The goal of this study is to computationally identify an optimized combination of spacer arms length and density for cellulose nanocrystals affinity membranes by means of a molecular dynamics simulation. This project includes the implementation of a cellulose polymer and crystal editor, the optimization of force fields for this model, and a set of simulations where the densities and lengths of affinity ligands were varied in presence of proteins. These affinity ligands were developed by combining carbon based spacer arms of different lengths (5-atoms, 7-atoms, and 14-atoms) and para-aminobenzamidine; while force fields and partial charges were adapted to CHARMM and computed by GAMESS respectively. Systems were minimized in vacuum at NV conditions, solvated, and simulated at NTP conditions during 20 ns at 1.0 fs under periodic boundary conditions. Empirical observations showed that as the ligand density increases, the number of them that lean over the nanocrystal surface decreases. While on the other hand, as the number of affinity ligands decreases, they tend to lean very close to the surface. Notably, we have observed three main cases present in simulations based on their concentrations: straight, leaning, and twisting folds. Frequency charts and unsupervised machine learning algorithms were used to classify the folding structure of these affinity ligands. Future work includes the development of a mathematical model to describe the interaction between spacer arms and the nanocrystal surface.

FRI - 842 **Developing Sustainable Synthetic Routes to Lithium-Ion Battery Electrodes**

Discipline: Materials Research
Subdiscipline: Materials Research

Allyson Ee*, *University of California, Santa Barbara* and Raphaële Clément, *University of California, Santa Barbara*

Abstract: NMC-type cathodes ($Li_{1+x}Ni_{1-x-y-z}Mn_yCo_zO_2$) have replaced lithium cobalt oxide ($LiCoO_2$) in several commercial battery applications due to the higher energy density and lower cost of their reduced cobalt (Co) content. Yet, the synthesis of these materials is commonly achieved via a solid-state route, generally involving two high-temperature (~1000°C) calcination steps of about 15 hours each. Microwave (MW) synthesis obviates the need for this high energy and inefficient convective heating route by selectively, uniformly, and rapidly heating the sample. Compared to the conventional solid-state calcination, MW synthesis is reliable, cheap, and energy/time-efficient. As such, this project aims to develop a MW synthesis protocol for NMC-type cathodes, and to investigate differences in the structure and battery performance between electrodes synthesized via MW and conventional routes. Phase purity and composition of the samples will be assessed with X-ray diffraction (XRD) and inductively coupled plasma atomic emission spectroscopy (ICP-AES), respectively. The microstructure and morphology of the electrode particles will be examined using scanning electron microscopy (SEM). Moreover, solid-state nuclear magnetic resonance (ss-NMR) and electron paramagnetic resonance (EPR) experiments will be conducted to identify the effect of MW vs. convective heating on the local structure of the cathodes. Ex-situ and operando ss-NMR and EPR experiments can probe changes in the local structure of these cathodes as a function of state of charge; such changes can be directly related to the specific energy density, voltage and capacity fade, and efficiency. These identified structure-property relationships and synthesis development will conceivably lead to cheaper and more energy-efficient lithium-ion batteries.

FRI - 843 **Understanding the Formation of Garnet Phases upon Reaction of Molten Silicates with Thermal Barrier Oxides**

Discipline: Materials Research
Subdiscipline: Materials Research

Rodrigo Rodriguez*, *University of California, Santa Barbara*; Collin Holgate, *University of California, Santa Barbara* and Carlos Levi, *University of California, Santa Barbara*

Abstract: Thermal barrier coatings (TBCs) are thermally insulating ceramic layers added to the surfaces of actively cooled superalloy gas turbine components that enable them to operate more efficiently at high temperatures. Durability of TBCs depends on their tolerance to thermal cycling, which results from a porous microstructure that induces a low in-plane elastic modulus.

However, siliceous debris ingested with the intake air deposit on the coating surfaces, melt at peak temperatures in the engine cycle and penetrate the porosity, stiffening the coating and degrading their strain tolerance. The infiltration can be arrested by selecting a TBC composition that reacts rapidly with the penetrating melt, forming solid phases that fill the near-surface porosity precluding further flow into the coating. Current strategies are based on rare-earth zirconates which form a desirable oxi-apatite phase upon reaction. In some systems, however, the latter competes with a garnet phase which incorporates a larger spectrum of melt constituents than apatite, but tends to form more slowly and is arguably less effective in arresting melt penetration. This investigation explores the stability of the garnet phase in reactions between yttrium-aluminum/iron garnets in systems consisting of Ca, Mg, Fe, Al silicate melts. Reactants were produced by precipitation from precursor solutions, pyrolyzed into powder, pressed and heat treated in the range 1200-1400°C. The equilibrated microstructures were analyzed utilizing scanning electron microscopy, energy dispersive X-ray spectroscopy, and X-ray diffraction to determine phases and composition. The results are incorporated into a larger effort aimed at developing a thermodynamic database for these important systems.

FRI - 844 Type I Interferon and Chemokine Levels in Plasma of Children and Adults Exposed to Intense Seasonal *Plasmodium Falciparum* Malaria Transmission in Mali

Discipline: Other
Subdiscipline: Humanities

Triniti Turner*, *Northern Virginia Community College*; Peter Crompton, *National Institues of Allergies and Infectious Disease* and Anton Goetz, *National Institues of Allergies and Infectious Disease*

Abstract: Malaria is a detrimental disease, globally affecting over 200 million lives a year. The body’s immune system fails to establish long term protection against the malaria parasite, Plasmodium, causing repeated infections. Currently, there remains no vaccine effective in inducing sterile immunity. It has been observed that in parts of Africa, adults experience no symptoms when infected during transmission season, while children show aggressive and sometimes fatal symptoms. Recent data obtained using malaria mouse models showed increased levels of type I interferons associated with decreased inflammation by promoting production of IL-10. In this study we examined differences in interferon alpha (IFN-alpha) and inflammatory chemokine (CCL2, CCL5, CXCL-9 and 10) levels in the plasma of Plasmodium falciparum infected Malians. Using an ELISA, IFN-alpha levels during infection did not change significantly amongst asymptomatic adults and symptomatic children in Mali. CXCL-9 and CXCL-10 levels, proteins associated with cellular migration, have also been observed to be increased during P. falciparum-infections and contribute to inflammation in cerebral malaria in mice. A bead-based immune-assay showed that CXCL-9 levels increased significantly in infected adults and children, whereas CXCL-10 levels significantly increased in children and remained unchanged during asymptomatic infection in adults. This study bares pivotal information in understanding the body’s immune response to Plasmodium-induced inflammation and aiding in the development of an anti-inflammatory drug or effective vaccine against malaria.

FRI - 845 How Parents Who Have a Fetus/Neonate Diagnosed with a Life-Threatening Congenital Heart Defect Make Treatment Decisions: The Importance of Quality of Life

Discipline: Other
Subdiscipline: Other Professional Fields

Sierra Penn*, *Haskell Indian Nations University* and Angela Fagerlin, *University of Utah*

Abstract: Parents with a fetus/neonate diagnosed with a life-threatening congenital heart defect are confronted with making the time-sensitive decision of choosing between terminating the pregnancy, comfort care, or surgery. The purpose of this qualitative study was to understand how parents made this challenging treatment decision. Ten focus groups were conducted in Salt Lake City, Chicago, Durham and Washington, DC with 5 groups composed of parents who pursued surgery and 5 groups of parents who chose comfort care or termination. Transcripts were coded using content analysis to identify key themes. How parents approached the treatment decision and what mattered most to them in the decision-making process varied. One of the most prominent themes was about quality of life for the family and their fetus/neonate. More specifically, parents discussed financial circumstances (e.g, health insurance, income) and the impact of the decision on marriage and their other children. Additionally, parents varied considerably in what quality of life of their fetus/neonate meant to them, key quotes included: “showing the baby what love was,” “taking it day by day because it could change tomorrow,” “having their child experience the typical life of a child,” “spreading the same amount of love to every child,” or “knowing that there baby did not suffer.” Finally, parents often expressed that they wished they have more information and resources when making the decision. Future research needs to develop and test methods for improving parent knowledge and decision making.

FRI - 846 Spatiotemporal Characterization of Population Movement in North Kivu, Democratic Republic of Congo

Discipline: Other
Subdiscipline: Other Professional Fields

Divya Batchu*, *The Ohio State University* and Samuel Malloy, *The Ohio State University*

Abstract: The ongoing Ebola outbreak in North Kivu, Democratic Republic of the Congo (DRC) began in August 2018 and includes over 1023 confirmed cases and 679 deaths as of April 02, 2019, according to the DRC Ministry of Health. High mobility, driven largely by conflict, precipitates the risk of continued spillover into neighboring regions. As of January 2019, the proportion of known contact cases dropped from 63% to 10% because violent conflict has hampered efforts both to establish population patterns and to conduct contact tracing. Remotely acquired data, such as aerial observations and satellite imagery, offer the ability to assess population change independent of observations in the field.This investigation explores the validity of the normalized difference build-up index (NDBI) as a characterization of near real-time population in the context of the current outbreak in DRC. To do this, we analyzed high spatial resolution imagery using the NDBI on five informal settlement sites within the DRC that have experienced significant change during the last 12 months. These sites were selected because the International Organization on Migration collects accurate, up to date population counts at those sites. We then scaled the existing LandScan population model (Oak Ridge National Laboratory) using a simple linear scaling function. We find that the NDBI significantly improves population assessments in highly structured settlements, but requires improvement to be utilized in highly informal contexts. In future work, machine learning techniques may prove useful in characterizing less structured rapid migration.

FRI - 848 Changing the Formula Benefits the Mites: Grain Mite Response to Dog Food Formulations

Discipline: Other
Subdiscipline: Other Professional Fields

Brandon Henriquez*, *Oklahoma State University* and Wyatt Hoback, *Oklahoma State University*

Abstract: Grain mites, *Acarus siro,* are pests which can affect different types of stored grains and can also spread mold spores which can affect human health. Some dog foods consist of pieces with different textures and shapes and Smucker’s is testing new proprietary formulas of Kibbles and Bits to determine susceptibility to mite infestation. In the experiment, three formulas and 5 or 6 shapes of dog food were tested in benchtop trials. 35 ml vials had 3-5 pieces of individual shapes standardized by mass and then infested with approximately 25 mites. The mite infested vials along with controls were placed in tubs with mineral oil coating the bottom to prevent the spread of any escaped mites. The vials were placed in a growth chamber at 28℃ and were kept in 70-85% relative humidity. After four weeks, the vials were removed from the chamber, and mites were counted. The control formula had very few mites on any piece shape. The first test formula had very high mite numbers (thousands per vial and high visible damage in the form of dust). The third test formula had high amounts of mold growth resulting in few mites, but unusable product. The results of these tests show that the

existing formula is best at preventing mite population growth and that the new formulations must be altered or the product will lead to customer complaints.

FRI - 900 Analytical Determination of Methylone and Metabolites in Rat Brain By LC-MS/MS

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Raider Rodriguez*, *John Jay College of Criminal Justice* and Marta Concheiro-Guisan, *John Jay College of Criminal Justice*

Abstract: Methylone, a synthetic cathinone that induces physiological responses similar to 3,4-methylenedioxy-methamphetamine (MDMA) and methamphetamine, is a new, but highly prevalent psychoactive substance (NPS) commonly promoted through products known as "bath salts". Although several fatalities have been reported as a result of methylone abuse, Unfortunately the pharmacological behavior of methylone has not been thoroughly studied. Our long-term goal is to elucidate the pharmacokinetic and pharmacodynamic characteristics of methylone, and its main metabolites: 4-hydroxy-3-methoxymethcathinone (HHMC), 3,4-dihydroxymethcathinone (HMMC), and 3,4-methylenedioxycathinone (MDC). Towards this goal, we successfully developed an analytical method for methylone determination in rat brain based on liquid chromatography-tandem mass spectrometry (LC-MS/MS). The validation parameters of the analytical method, including linearity, bias, imprecision, matrix effect, dilution integrity, and process & extraction efficiency, were optimized and deemed sensitive, specific, and reproducible. As a proof of concept, we processed rat brain samples that had been previously treated with different dosages of methylone, and using the analytical method, quantified the concentration of methylone and its metabolites. Thus, we have successfully established LC-MS/MS as a viable analytical tool to analyze methylone-treated rat brains, and determine the pharmacokinetics and pharmacodynamic profiles of methylone. In addition, the development of this new analytical method represents a significant innovation for quantitative analysis in the areas of forensic and clinical toxicology.

FRI - 901 Sorting Cancer Cells Based on Metabolism Using Droplet Microfluidics

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Adriana Gutierrez Ramirez*, *Santa Clara University*; Claudia Zielke, *Santa Clara University* and Paul Abbyad, *Santa Clara University*

Abstract: The goal of the research is to develop a microfluidic device for the label-free sorting of cancer cells based on their metabolism. Cancer cells release high levels of lactate compared to normal cells via the Warburg effect. This leads to a difference in extracellular pH which we can use to sort cells. We produce microdroplets in oil containing cells in order to analyze them individually. We use unique surfactant conditions where the surface tension is very sensitive to pH. Droplets containing single cancer cells have a lower pH after incubation and can be selected by droplet surface tension. This selection is done by flowing confined droplets over a microfabricated rail oriented diagonally with respect to the flow. As a demonstration, we treat cells with either a pharmaceutical or hypoxia that influence metabolism. Using droplet pH the microfluidic device is used to sort cells into two populations, treated and not treated. Advantages of this microfluidic device is that it is label-free and passive; requiring no cell markers or active components. This device holds promise for applications in cancer cell research for isolating cells that can be more dangerous.

FRI - 902 Reproducing and Optimizing a Microbial Fuel Cell's Feed to Produce Higher Voltage

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Nallely Dominguez*, *Los Angeles City College*; Linda Godinez, *Los Angeles City College* and Terry Boan, *Los Angeles City College*

Abstract: A microbial fuel cell (MFC) is a bio-electric system that utilizes bacteria found in waste as a catalyst to produce electricity. The existing MFC models generate poor electron transfer with an average current of 0.350 V. The electron transfer can be optimized by modulating the bacteria's conditions to produce higher currents that can be harnessed as usable energy. An efficient optimized MFC can serve as a sustainable source of green energy as well as a means to process waste water. To reproduce this system, a two-chamber cell was built from basic materials including: tupperware containers for the two chambers, aluminum mesh and copper wire for the electrodes, duckbill valves to feed the system, PVC pipe affixed with a Nafion semipermeable membrane to connect the chambers, and finally epoxy to hold everything together with a water tight seal. The testing of cow manure, with a fixed feed composition, resulted in a reading of less than 0.100 V. Manipulating the contents in the feed introduced into the system increases the voltage reading by mixing the cow manure with different additives such as carbohydrates, sugars, and proteins in varying percentages. A high percentage of sugar additives produced a voltage increase from 0.100 to 0.303 V. The optimization of this MFC system has successfully produced a higher electron transfer and higher current reading than its original counterpart. Changing the right parameters on MFCs will make them the energy source of the future.

FRI - 903 In-Silico Dual Specificity Protein Phosphatase Differentiation Via Molecular Dynamic Simulations

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Daniel Aguirre*, *New Mexico State University* and Marat Talipov, *New Mexico State University*

Abstract: Dual Specificity Protein Phosphatases (DUSPs) constitute a class of phosphatases responsible for dephosphorylating certain kinases with both phospho-serine/threonine and phospho-tyrosine residues. DUSPs are a heterogeneous group of proteins that target substrates such as JNKs, MAPKs and more. One such protein, DUSP5, is a protein responsible for the dephosphorylation, and inactivation of Extracellular Signal-Regulated Kinases 1&2 (ERK1&2) in the nucleus, which are also known as MAPK3 and MAPK1 respectively. ERK1&2 are essential to the MAP kinase signal transduction pathway which affect cellular proliferation, differentiation, survival, adhesion and much more. Recent studies suggest that DUSPs with ERK1&2 as substrates, play differing roles in development of cancer, obesity and autoimmunity. DUSP5 has been shown to be over-expressed in mice with autoimmune symptoms. Despite these differing catalytic activities, DUSPs contain comparable catalytic motifs, which makes selective targeting particularly arduous. Our hypothesis is, DUSPs can be differentiated through modelling of the catalytic pocket, especially from DUSP5, which can be used as a baseline for therapeutic design. To test this hypothesis we utilized Molecular Dynamic (MD) simulations with AMBER force fields, to simulate a handful of DUSPs. Preliminary results suggest differences between DUSPs in the catalytic pocket as well as distal sites. In DUSP5 specifically, existence of a disulfide bridge and a secondary active site make DUSP5 unique, and potentially targetable. Overall the use of MD simulations shows a promising future in differentiating similar proteins for future therapeutic development.

FRI - 905 Mercury Levels in Rice and Oatmeal Infant Cereal

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Lisette Torres*, *California State University of Channel Island* and Simone Aloisio, *California State University of Channel Islands*

Abstract: Mercury, is a toxic heavy metal, leading to health problems such as fatigue, behavioral changes, damage to the central nervous system and cardiovascular system, hearing loss, and death. These factors are found in numerous populations however, it is believed that infants may be more prone to health risks, if exposed, due to their weak immune system. Since exposure to mercury can be from many sources including food consumption, our environment and more. The goal of this study is to measure the mercury levels of infant cereal, one of the first solid foods an infant is given. A study conducted in Spain has shown that rice infant cereals have a higher dose of mercury than any other type, but another cereal that has a really high concentration is the organic rice cereal. Moreover, this has led us to analyze mercury contamination, in many infant cereals such as rice from manufacturers in the United States. To perform the assay, mercury was analyzed using atomic absorption spectroscopy with thermal decomposition followed by amalgamation method. The oatmeal cereal had an average 0.269 ± (0.089) ppb mercury concentration, while the rice-based cereal has an average of 1.677 ± (0.141) ppb. The study that was conducted in Spain also compared non-organic and organic infant rice cereal and found that the organic rice cereal contained higher mercury levels. Our next goal is to see if organic infant cereal in the U.S. would also have a higher concentration and if it would impact infants.

FRI - 906 Synthesis of a Ligand for Use in Enantioselective Catalysis

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Valeria Reyes*, *University of San Diego* and Christopher Daley, *University of San Diego*

Abstract: Many chemical reactions yield enantiomer products, which are compounds that have the same type and number of bonds but are non-superimposable mirror images of each other, similar to one’s right and left hands. The enantiomers’ different spatial arrangements make them react differently with other enantiomer compounds. For example, enzymes in our bodies are chiral (single enantiomers), so they interact with each of the enantiomer forms of another chiral molecule differently. If a drug is administered as a racemic mixture (a 50:50 mixture of its enantiomer forms), each enantiomer can be metabolized differently; one producing the desired effect while the other may produce severe undesired side effects. Enantioselective catalysis is one method for controlling which enantiomer is produced. Our focus is on preparing organic molecules (ligands) that can be used with a metal to form catalysts; the catalysts will be used for numerous reactions to determine its effectiveness in driving the reaction to form only one enantiomer form. Currently, our ligand is prepared in a 2-step process; an *in-situ* cadmium-bound ligand complex formation followed by isolating the ligand from the complex using a thiol-based substitution reaction. While this methodology is successful, cadmium and thiols are harmful for the environment; therefore, our goal is to reduce the method's toxicity. We have successfully developed an alternative to the first step by preparing a less toxic zinc-ligand complex. The work on our attempts to isolate the ligand, through a substitution reaction with strong zinc-binding amine compounds, will be presented along with preliminary catalysis investigations.

FRI - 907 Cytotoxicity and Crystal Structure of Arsenoplatin-1-Iodide Complex

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Annie Fritz*, *Northeastern Illinois University*; Zohra Sattar Waxali, *Department of Chemistry and Chemistry of Life Processes Institute, Northwestern University*; Wenan Qiang, *Center for Developmental Therapeutics at the Chemistry of Life Processes Institute, Northwestern University*; Matthew Martin, *Northeastern Illinois University*; Denana Miodragovic, *Northeastern Illinois University* and Thomas O’Halloran, *Department of Chemistry and Chemistry of Life Processes Institute, Northwestern University*

Abstract: Arsenoplatins (AP) are a new class of anticancer compounds containing dual pharmacophore moieties from two inorganic, FDA approved anti-cancer drugs, cisplatin, $[Pt(NH_3)_2Cl_2]$ and arsenic trioxide, As_2O_3. Each of these two drugs induces apoptotic cell death but through different mechanisms: cisplatin targets nuclear DNA, whereas As_2O_3 targets zinc-finger proteins. Arsenoplatin compounds contain an arsenous acid moiety in which As(III) forms an unusual five coordinate geometry and it is bound to a square planar Pt(II) center. Results of the NCI-60 (NCI: National Cancer Institute) human tumor cell line screen have shown that the first arsenoplatin compound synthesized $[Pt(m\text{-}NHC(CH_3)O)_2ClAs(OH)_2]$, (AP-1), is more potent than As_2O_3 or cisplatin in the majority of cell lines tested. Furthermore, studies indicating increased anticancer activity of a cisplatin-iodide analog inspired us to synthesize an AP-1-iodide complex $[Pt(m\text{-}NHC(CH_3)O)_2IAs(OH)_2]$, (AP-5). Structural characterization of AP-5 has been determined by X-ray crystallography, elemental analysis, and NMR. In this study, the anticancer efficacy of AP-5 is tested *in vitro* against the triple negative breast MDA-MB-231 cancer cell line, an aggressive cancer currently lacking an effective method of treatment. The results of *in vitro* cytotoxicity assays have shown that AP-5 is even more cytotoxic than AP-1 or cisplatin, with IC_{50} values of AP-5, AP-1, and cisplatin of 5.7 (± 1.0) μM, 9.5 (± 0.1) μM, and 22.3 (± 2.8) μM, respectively. Interactions of AP-5 with glutathione and other sulfur-containing biological ligands are also studied for assessing the potential for Pt-S-complex formation and understanding possible mechanisms of action.

FRI - 908 Synthesis of Gadolinium (III) Catecholates for Lanthanide Separations

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Ngu Phan*, *Cypress College* and Chantal Stieber, *Cal Poly Pomona*

Abstract: Nuclear power now provides 11% of the world’s electricity and is expected to be a main alternate energy in the near future. The process is highly efficient, but the fuel rod efficiency could be improved. During fission of the fuel rod, lower-mass elements including lanthanides are produced. The separation of lanthanides from actinides would improve energy generation and increase the lifespan of the fuel rod. Separation is challenging because of similar chemical properties of lanthanides and actinides, so there is interest in developing new separation methods. This work investigated the effects of redox-active ligands bound to lanthanides to tailor electronic properties for separation. The synthetic and structural chemistry of gadolinium and holmium catecholates were previously reported, but were synthesized under argon and with water as a solvent. For this research, the synthesis of gadolinium catecholates was tested under oxygen (tabletop) or under anaerobic conditions (argon) and with varying the solvent from water to methanol. Toluene-3,4-dithiol and benzene dithiol were also investigated as potential ligands. Initial findings indicated that different products were synthesized when the reaction was carried under air as opposed to argon.

FRI - 909 DI Water Contamination at Los Angeles City College

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Stephanie Jimenez*, *Los Angeles City College* and Terry Boan, *Los Angeles City College*

Abstract: Chemical water analysis is an essential tool that is often the groundwork of studies pertaining water quality, pollution, hydrology, and contamination. In all cases, the outcome of the analysis contributes information to administer the reassurance that conditions are as expected. An experiment conducted in a biochemistry class discovered that deionized water in the lab had a pH level of 4.8. Because deionized water should be at a neutral pH level of 7, the use of analytical chemistry can help determine the explanation to why the pH level is on the acidic side. It is hypothesized that contamination, like impurities coming from the building’s plumbing, air pollution, mold, or algae growth could be from a source of tainted water in the supply tank. In addition, various samples of water from different classrooms will be analyzed to see if there is a discrepancy betweens the rooms which can prove there may be an issue in the faucets. We plan on performing UV Vis Spectrophotometry to identify possible chlorophyll-a, which is visible between 260 nm and 280 nm, and also freeze drying samples with a rotary evaporator to perform IR analysis. Preliminary results suggest that our DI water is at 4.8 on the acidic side. Following that, our goal is to determine the source that is causing the DI water to be acidic as well as to determine if experiments performed using this DI water on our campus could be affected.

FRI - 910 Ring Closing of Aromatic Alkynes and Gold Cavitand Substrate Selectivity

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Lisa Rusali*, *California State University, Long Beach* and Michael Schramm, *California State University, Long Beach*

Abstract: Like enzymes, gold functionalized resorcin[4]arene cavitands have features that facilitate catalysis: 1) an inwardly directed reactive center and 2) a well defined binding pocket. These provide us with great opportunities to investigate their

applications in molecular transformations. The pocket adjacent to Au is a special characteristic of the cavitand; we find that reactivity is very different when compared to other gold complexes with similar electronic features. The results we present focus on ring closing reactions with aromatic terminal alkynes. To date, 10 analogs have been prepared and screened using the gold cavitands. We have seen that cavitand-mediated cyclization occurs faster and more cleanly than with simpler Au compounds. Limits exist however, and here we find exciting differences: when the guest's features do not pair well with the size of the cavitand interior, reactivity changes. The results of these experiments provide a wealth of information about the advantages and selection rules that cavitands provide when applied to catalytic problems.

FRI - 911 **The Synthesis and Characterization of Polyglutamine Peptides to Better Understand Huntington's Disease**

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Evaudie Paul*, *Stonehill College* and Katharine Harris, *Stonehill College*

Abstract: Huntington's disease is a genetic neurodegenerative disorder that varies in severity. This disease is caused by polyglutamine (polyQ) expansion that affects the huntingtin protein (HTT), specifically causing the proliferation of mutant HTT that is abnormally long. HTT's mutation is due to a trinucleotide repeat (CAG→Gln) in the coding of DNA, causing an extended length of polyQ in the brain. HTT plays an important role in neuronal function in the brain, but the toxic fragments of the elongated mHTT caused by polyQ aggregation disrupt the normal function of brain cells. The purpose of this research is to study the chemistry of polyQ aggregates that occur in people with Huntington's disease. The project focuses on the synthesis of peptides with repeated monomers of glutamine covalently linked together. A method called Solid-Phase Peptide Synthesis is used, where a small resin bead serves as the starting point for the synthesis. Progressively, chains of glutamines are made via an aggregation assay development in order to characterize the structure of the peptides. The effort is invested in synthesizing many segments of peptides (i.e. 6-mer, 7-mer) as a means to quantitatively study the molecular interaction of each chain. A major characteristic of the disease is the glutamine repeat, we, therefore, want to purify and characterize using Ultra Performance Liquid Chromatography, and test the chains using Thioflavin, a fluorescent dye. The expected outcome is to understand the binding characteristics and the insolubility of the peptide aggregates associated with Huntington's disease which may help us to synthesize a treatment.

FRI - 912 **Nitrogen-Containing Derivatives of *O*-Tetramethylquercetin: Synthesis and Biological Profiles in Prostate Cancer Cell Models**

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Pravien Rajaram, *California State University, Fresno*; Ziran Jiang, *California State University, Fresno*; Alyssa Marie Rivera*, *California State University, Fresno*; Alison Phasakda, *California State University, Fresno* and Qiao-Hong Chen, *California State University, Fresno*

Abstract: Prostate cancer is one of the leading causes of cancer deaths in males living in the United States. For 2019, there are about 165,000 new cases of men diagnosed with prostate cancer and roughly about 29,000 result in death. As part of our ongoing research program to develop natural product-based anti-prostate cancer agents, forty-eight nitrogen-containing quercetin derivatives were synthesized from readily available rutin or quercetin for the in vitro evaluation of their biological profiles. The twenty-four 3-O-aminoalkyl-3',4',5,7-O-tertramethylquercetins have been prepared from commercially available rutin through a four-step procedure including global methylation, glucoside hydrolysis, O-alkylation, and N-alkylation. The twenty-four 5-O-aminoalkyl-3,3',4',7-tertramethylquercetins have been achieved from commercially available quercetin through a three-step transformation, including selective tetramethylation of quercetin, O-alkylation with the appropriate dibromoalkane, and N-alkylation. The structures of all these forty-eight derivatives have been characterized by 1H and 13C NMR, as well as HR-MS data. Our WST-1 cell proliferation assay data indicate that thirty-nine out of the forty-eight derivatives possess significantly improved antiproliferative potency as compared with quercetin and fisetin, as well as the parent 3',4',5,7-O-tetramethylquercetin and 3,3',4',7-O-tetramethylquercetin toward both androgen-sensitive (LNCaP) and androgen-insensitive (PC-3 and DU145) human prostate cancer cell lines. 5-O-Aminoalkyl-3,3',4',7-O-tetramethylquercetins were established as a better scaffold for further development as anti-prostate cancer agents. Among them, 5-O-(N,N-Dibutylamino)propyl-3,3',4',7-O-tetramethylquercetin was identified as the optimal derivative with IC50values of 0.55-2.82 µM, being over 35-182 times more potent than quercetin. Our flow cytometry-based assays also demonstrate that 5-O-(N,N-dibutylamino)propyl-3,3',4',7-O-tetramethylquercetin effectively activates PC-3 cell apoptosis.

FRI - 913 **Repurposing an FDA Approved Drug As a Novel Small Molecule Allosteric Inhibitor Against West Nile Virus NS2B-NS3 Protease**

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Shaina Nguyen*, *California State University, Fullerton* and Nicholas Salzameda, *California State University, Fullerton*

Abstract: The West Nile virus (WNV) is a neurovirulent mosquito borne pathogen prevalent worldwide. Upon infection, the viral genome is translated into a genomic polyprotein containing necessary proteins for viral replication and is cleaved by the viral NS2B-NS3 protease. The NS2B is a cofactor that binds to the NS3 to provide the proteolytic activity required for viral replication. The protease is an integral component of the WNV life cycle and an attractive therapeutic target. Zafirlukast, an FDA approved Asthma alleviant, has been discovered as a novel allosteric inhibitor for the NS2B-NS3 protease with IC_{50} value 32µM. The Zafirlukast scaffold consists of three components: a cyclopental carbamate, an *o*-toluic sulfonamide, and a methylated indole core. This research explores the synthesis of third-generation Zafirlukast derivatives by creating analogs of the indole core which included: triazoles, phthalimides, and quinolines. Synthesizing these analogs involved a click chemistry reaction followed by hydrolysis to couple the sulfonamide to produce the triazole core analog. The quinoline and phthalimide were constructed through an alkylation reaction followed by hydrolysis to couple the sulfonamide group. A reduction reaction was performed to couple the phenyl carbamate to the core. Altering the indole core will modify the angle and position of the phenyl carbamate and *o*-toluic sulfonamide within the allosteric site, potentially improving inhibition. Through an enzymatic assay, four analogs have not shown inhibition against the protease and two analogs are currently being synthesized to evaluate inhibition. These third-generation compounds will expand our knowledge of the NS2B-NS3 protease inhibitor molecular scaffold.

FRI - 914 **Coming up with a New Chemistry for Liquid Crystal Elastomers**

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Kaya Sanders*, *Saint Mary's College of California* and Zuleikha Kurji, *Saint Mary's College of California*

Abstract: Liquid crystal elastomers (LCEs) can be used as actuators and materials for artwork. The Yakacki group of the University of Colorado Denver has designed a one-pot synthesis of LCEs using multi-functional acrylate and thiol monomers. Although this framework allows for repeatable and effective material, thiols have a short shelf-life, low-odor threshold, and limited commercial availability. If thiol monomers can be replaced with alcohol-terminated monomers with a suitable catalyst, then a new repeatable, user-friendly, and modifiable LCE platform can be developed. An acid catalyzed Oxa-Michael addition reaction between simple difunctional acrylates and difunctional alcohols was performed under various conditions (temperature, mol % catalyst, etc.), and qualitatively examined by viscosity screening to determine if polymerization occurred. Both solvent-free reactions (60°C, 65°C, 70°C, and 77°C) and reactions with solvent, dimethylformamide, (60°C, 70°C, 77°C) showed an increase in viscosity indicating a reaction transpired. Control reactions containing only acrylate, catalyst and solvent did not show an increase in viscosity, suggesting acrylate and alcohol functional

groups were both necessary. The increased viscosity products from the highest temperature reactions (70°C, and 77°C) did not dissolve in acetone, toluene, methylene chloride, or dimethylformamide indicating cross linking occurred (testing the solubility of lower temperature products is ongoing). TLC and NMR will be used to identify the possible reaction products and mechanism. Decreasing the mol% catalyst may potentially decrease cross linking side reactions. If a new chemistry of LCEs emerges, we will be able to incorporate light responsive properties in order to perform work and integrate in an artistic piece.

FRI - 915 Post-Polymerization Functionalization of Poly(Phenylene-Ethynylene) Type Water-Soluble Conjugated Polymers to Enable Biological Interactability

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Daniel Martinez*, *University of Texas at San Antonio*; Zhiliang Li, *University of Texas at San Antonio* and Kirk Schanze, *University of Texas at San Antonio*

Abstract: Conjugated polymers (CP) are a class of fluorescent macromolecules that are well known for their photophysical applications (e.g. light emitters, energy acceptors/donors, charge transfer, etc.) Making CPs water-soluble enables their capabilities to interact with proteins, cells, and other biological systems. The purpose of this research is to present a common methodology for the synthesis and modification of a water-soluble poly(phenylene-ethynlene) (PPE). The functionality of the polymer was demonstrated by appending complexing agents onto the PPE. One such agent, biotin, was appended to the PPE and its complexation with the protein, neutravidin, was quantified with dynamic light scattering (DLS). It was hypothesized that the biotinylated PPE-neutravidin complex would produce a large aggregate with a much greater diameter than either one of its components. Further investigation into appending fluorescent probes, such as rhodamine, onto the PPE will be carried out to understand the effects on fluorescence lifetimes. Two aryl-based monomers were appended with solubilizing groups and subsequentially polymerized. The resulting polymer was then functionalized with biotin through amidation reactions. The biotinylated PPE had a diameter of about 0.5 nm, neutravidin had a diameter of about 10 nm, and when combined, the aggregated structure had a diameter of about 100 nm. These results indicate that the biotinylated PPE successfully complexed with neutravidin and demonstrates the polymer's functionality and potential as a biological probe.

FRI - 917 Design, Synthesis and Evaluation of 4-Phenylthiazole Based analogs As Novel FAAH Enzyme Inhibitors

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Adrian Salas*, *Cypress College* and Stevan Pecic, *California State University, Fullerton*

Abstract:
Endocannabinoids, anandamide (AEA) and 2-arachidonoylglycerol (2-AG) are endogenous lipids that activate cannabinoid receptors. Activation of these receptors produces anti-inflammatory and analgesic effects. Fatty acid amide hydrolase (FAAH) is a membrane enzyme that hydrolases endocannabinoids, thus inhibition of FAAH represents an attractive approach to develop new therapeutics for treating inflammation and pain. Our hypothesis is that inhibition of FAAH will elevate levels of endocannabinoids which would lead to retention of the beneficial effects of cannabinoid activation. Previously, potent FAAH inhibitors containing 4-phenylthiazole scaffold were identified, but up to the present time very little structure-activity relationship (SAR) studies have been performed on this moiety. The goal of this project is to synthesize various 4-phenylthiazole analogs and to identify functional groups which are required for FAAH inhibition. These FAAH inhibitors could be used in experimental *in vivo*models of pain and inflammation. Our synthetic and biological investigations to date will be presented.

FRI - 918 Synthesis of Novel Linear-Dendritic Block Copolymers and Their Directed Self-Assembly in Breath Figure Arrays

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Tina Monzavi*, *University of South Carolina* and Ivan Gitsov, *The Michael M. Szwarc Polymer Research Institute*

Abstract: For the last decade, amphiphilic linear-dendritic block copolymers (LDBCs) have been at the focus of extensive scientific interest, due to their unique properties and numerous potential applications. Their technological potential comes from their ability to self-assemble into different, morphologically diverse nanostructures. These diverse nanostructures are perfect for the delivery of therapeutic agents due to their unique chemical composition, which is characterized by a hydrophilic block that is chemically tethered to a hydrophobic block. Once the nanostructures are formed, the hydrophobic core regions serve as reservoirs for hydrophobic drugs.

Within this project, we report the formation of films with controlled honeycomb patterns by a static "breath figure" (BF) technique using novel amphiphilic linear-dendritic block copolymers (LDBCs) composed of hydrophilic dendritic poly(ether-ester), PEE, blocks and hydrophobic linear poly(styrene), PSt. The LDBCs are synthesized via atom transfer radical polymerization (ATRP) initiated by a PEE macroinitiator. The obtained LDBCs are utilized to fabricate honeycomb films. The copolymer composition strongly affects the film morphology. LDBCs bearing acetonide end groups produce honeycomb films when the PEE fraction is lower than 20%. Pore uniformity increases as the PEE content decreases. Knowledge of the relationships between polymer composition and film structure is beneficial to design and prepare hierarchically porous films with desirable structures and properties.

FRI - 919 Determination of the Binding Affinity of the RNA Aptamers to B-Cell Activating Factor Receptor Proteins

Discipline: Chemistry
Subdiscipline: Other Chemistry

Thanh Blade*, *Sonoma State University* and Monica Lares, *Sonoma State University*

Abstract: Non-Hodgkin lymphoma (NHL) is a cancer that often originates from lymphocytes, such as, B-cells.The binding of numerous *B-cell Activating Factor* proteins (BAFF) to their receptor proteins (BAFF-R) on the surface membrane of malignant B-cells is responsible for an increase in the survival and proliferation of these cells. Nevertheless, RNA aptamer, a specific nucleic acid sequence with 81 nucleotides, specifically binds to BAFF-R to deliver a cancer drug that knocks down oncogenes while competing with BAFF. Our goal is to confirm their high-affinity between the RNA aptamer and BAFF-R. A constant volume and concentration of the ^{32}P-labeled RNA aptamer was allowed to bind to a constant volume with various concentrations of BAFF-R (purchased from PROSPEC) at room temperature. *Electrophoretic Mobility Shift Assay (EMSA)* was used to separate the free RNA aptamers from RNA-aptamer-BAFF-R complexes in a 5% native polyacrylamide gel, which was later exposed to a film. Typhoon FLA 7000, a phosphoimager, converted the film into a software image. ImageJ, a software (download from National Institute of Health), transformed the image into quantitative data. Our K_D value of 532.6 nM was higher than the published value of 47.1 nM. Our K_D value suggested that half of the RNA aptamer was saturated at a higher concentration of BAFF-R. Therefore, additional EMSAs must be done to investigate the difference of these two K_D values. Once the high affinity of the RNA aptamer and BAFF-R is established, we will move on to investigate their binding mechanism.

FRI - 920 Self-Assembling Peptides (KFE8) As a Platform to Create HPV Vaccine

Discipline: Chemistry
Subdiscipline: Other Chemistry

Claira Glaser*, *Northern Arizona University* and Naomi Lee, *Northern Arizona University*

Abstract: HPV vaccinations administered today do not cure all HPV infections nor are they robust in structure. Researchers are exploring the use of self-assembling peptides as novel vaccines to overcome these limitations by broadening protection and prolonging vaccine storage. Self-assembling peptides are common in nature and comprise alternating hydrophobic and

hydrophilic amino acids forming beta-sheet fibrils. The self-assembling peptide KFE8 (Ac-FKFEFKFE-NH$_2$) was previously shown to induce an immune response displaying peptide antigens. Thus, we hypothesize that the KFE8 fibrils with HPV antigens and a PADRE epitope may induce B-cell and T-cell responses. The KFE8 peptide will be co-assembled with KFE8 displaying HPV antigen along the fibrils. After fibril formation, the PADRE epitope will be conjugated to the fibril lysine side chains using a bifunctional crosslinker. Characterization of peptides and fibrils will be conducted using MALDI-TOF, HPLC, TEM, and circular dichroism. The project was started in January 2019. Thus, at this time, preliminary data includes peptide synthesis using standard Fmoc peptide synthesis. In addition, peptide purification using HPLC and MALDI-TOF mass spectroscopy. Throughout summer 2019, peptide and fibril characterization studies will continue. In addition, vaccine candidates will be tested in a murine model in collaboration with the University of New Mexico. Finally, anti-IgG titers will be assessed using ELISA assays. In conclusion, self-assembling peptides could be used more frequently in the future for vaccines, due to the fact they are robust in structure, they are broad in their protection, and they can also last in storage for a prolong period of time.

FRI - 921 Development of Microbial Fuel Cells Using Wastewater for Potential Applications in Wastewater Treatment Facilities

Discipline: Chemistry
Subdiscipline: Other Chemistry

Aris Rubio*, *Los Angeles City College* and Terry Boan, *Los Angeles City College*

Abstract: Climate change and fossil fuel pollution have produced a need for green energy. Specialized fuel cells, such as microbial fuel cells (MFCs), have been increasingly investigated to find new energy sources that will provide for the growing energy demand and reduce society's carbon footprint. An MFC is a fuel cell that uses bacteria to produce electricity from organic matter. MFCs can be powered by any biodegradable material, including wastewater. Bacteria in wastewater are known to produce electricity when used as substrates. In an oxygen-free chamber, wastewater generates electrons collected onto an anode then transfers onto a cathode inside an oxygen-rich chamber. The electrons then react with oxygen to produce water, and a membrane facilitates proton exchange to complete the cell. Wastewater treatment facilities utilize similar conditions in their digestion process that MFCs use to produce electricity, but it is not optimized. If MFCs become more optimized, the potential applications in wastewater treatment can result in wastewater treatment plants producing water and electricity. The renewability of MFCs with wastewater is limitless, and it has the potential to generate electricity for homes while simultaneously treating wastewater. This study focuses on the energy potentials of MFCs using wastewater as substrate, a Nafion membrane for proton exchange, and the potential applications of MFCs in wastewater treatment facilities. Preliminary results show voltage production is capable of reaching 0.350 V and greater. Concentrations of wastewater and temperature manipulation are used to determine if greater power and consistency can be achieved from MFCs with wastewater.

FRI - 922 Tamoxifen Efficacy Is Dependent on Insulin-like Growth Factor 1 Receptor Expression in Estrogen Receptor Positive Breast Cancer Cells

Discipline: Chemistry
Subdiscipline: Other Chemistry

Marie Angelli Ruiz*, *New Mexico State University*; Siem Goitom, *New Mexico State University* and Kevin D. Houston, *New Mexico State University*

Abstract: Estrogen receptor alpha (ERa) and insulin-Like Growth Factor 1 Receptor (IGF-1R) cooperate to enhance survival and increase proliferation in ERa-positive breast cancer cells. Tamoxifen (Tam), a selective estrogen receptor modulator and ERa antagonist in breast tissue, is the most commonly used adjuvant treatment for patients with ER-positive breast cancer. In addition to antagonism of ERa, inhibition of IGF-1R signaling mediated by the accumulation of IGF Binding Protein 1 (IGFBP-1) is a critical component of Tam efficacy in breast cancer cells. Tamoxifen resistance occurs in many patients subsequent to treatment, however, the molecular mechanisms associated with Tam resistance are not well understood. We hypothesize that alterations in IGF-1R expression and signaling in ERa-positive breast cancer cells is sufficient for Tam resistance. siRNA was used to decrease the expression of IGF-1R in ERa-positive breast cancer cells and Tam efficacy was determined using a cell survival assay. The accumulation of IGFBPs 1 and 3 in Tam resistant breast cancer cells was observed demonstrating that these IGF-1R modulators are increased in Tam resistant breast cancer cells. Next, a flow cytometer was used to measure IGF-1R expression in a single cell manner to identify a subpopulation of cells with relatively low IGF-1R expression in a culture of ERa-positive breast cancer cells. Future work will include isolating cells from the culture with lower expression of IGF-1R and measuring the sensitivity to Tam. These data provide evidence that dysregulation of IGF-1R signaling is a key component of Tam resistance in breast cancer cells.

FRI - 923 Synthesis of [3,3-$^2H_2$]-Dihydroartemisinic Acid to Measure the Rate of Non-Enzymatic Conversion of Dihydroartemisinic Acid to Artemisinin

Discipline: Chemistry
Subdiscipline: Other Chemistry

Kaitlyn Varela*, *University of Texas at San Antonio*; Hadi Arman, *University of Texas at San Antonio* and Francis Yoshimoto, *University of Texas at San Antonio*

Abstract: Artemisinin is a plant natural product that contains an endoperoxide bridge, which gives it anti-malarial properties. Dihydroartemisinic acid is the precursor in the formation of artemisinin. The conversion pathway of dihydroartemisinic acid to artemisinin is often speculated to be either non-enzymatic or enzymatic. Although there have been many efforts to understand the mechanism of this process, the rate of this transformation has never been reported. The purpose of this project was to investigate the spontaneous, non-enzymatic conversion of dihydroartemisinic acid to artemisinin by developing a method to quantify the conversion in the presence and absence of light. It was hypothesized that the use of a dideuterated version of dihydroartemisinic acid would allow for the measurement of the rate of non-enzymatic conversion to artemisinin using a non-deuterated version of artemisinin as an internal standard. A deuterated isotopologue, 3,3-dideuterodihydroartemisinic acid, was synthesized from dihydroartemisinic acid in seven steps. This isotopologue was used to quantify the non-enzymatic formation of 3,3-dideutero-artemisinin using liquid chromatography mass spectrometry (LC-MS) and d_0-artemisinin as an internal standard. The non-enzymatic rates of formation of 3,3-dideuteroartemisinin from 3,3-dideuterodihydroartemisinic acid were 1.4 µg/day with light and 32 ng/day without light. These results suggest that the non-enzymatic rate of formation of artemisinin from dihydroartemisinic acid is faster in sunlight. In addition, the formation of non-deuterated artemisinin from 3,3-dideuterodihydroartemisinic acid was detected with LC-MS in the presence and absence of light, suggesting an alternative mechanistic pathway. These data reflect how the endoperoxide bridge in artemisinin is being formed in nature.

FRI - 924 Characterizing the Impact of Extracellular DNA in Biofilm Formation

Discipline: Chemistry
Subdiscipline: Other Chemistry

Hector Herrada*, *University of San Diego* and Anthony Bell, *University of San Diego*

Abstract: Biofilms are biomolecular matrices composed of polysaccharides, proteins, and extracellular DNA (eDNA). Biofilms form a protective layer that harbors bacteria from antimicrobial and host cell immune response(s). Studies confirm that eDNA from *Staphylococcus aureus* is required for biofilm growth. Research indicates that eDNA facilitates the attachment of *Staph aureus* to basement membranes (cell surfaces, biomedical devices, etc.) to promote biofilm formation that may ultimately lead to infection. Despite clear evidence that eDNA is necessary for biofilm development, the biomolecular mechanisms that define this process are not clear. *We hypothesize that eDNA forms stabilizing binding interactions with host cell factors (i.e. proteins, cations, heme) to form a nucleation center to promote biofilm growth.* Circular Dichroism (CD) and Ultraviolet (UV) Spectroscopy are

used to analyze the nucleic acid profile and thermal stability of eDNA derived from *Staph aureus* biofilms. Two strains of eDNA analyzed are wildtype (WT) *Staph aureus* eDNA and msaABCR eDNA. msaABCR eDNA is a mutant strain that generates defective biofilms. CD data indicates both WT and mutant eDNA are composed of A-form and B-form helices. The data suggests eDNA serves as a binding platform for DNA and RNA binding proteins. The UV data indicates that in the presence of divalent cations (i.e. Mg^{+2}, Ca^{+2}) the gross structure of eDNA is more compact – a feature that may enhance sequestering of metals to boost antimicrobial resistance.

FRI - 925 Investigating the Heterogeneous Catalysis of Volatile Organic Compounds By Environmental Metal Oxides

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Jesus Rincon*, *Humboldt State University* and Chris Harmon, *Humboldt State University*

Abstract: Oxidation degradation of acetone was studied in real-time using the Diffuse Reflectance Infrared Fourier Transform Spectroscopy (DRIFT) technique. Ozone, an atmospherically relevant oxidant was passed over a sorbent bed of Titanium Oxide impregnated with Acetone. The reaction between the irreversibly bounded Acetone and the strong oxidizing agent was studied for 105 minutes *in-situ* while being recorded with the DRIFT apparatus. The formation of functional groups is utilized to explain the molecular interactions and chemistry at the surface. Due to using the DRIFT technique, changes in the surface as well as the environment are recorded simultaneously.

FRI - 926 Crystallization of *Paracoccus Denitrificans* H-Nox Protein

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Fred Serrano*, *New Mexico State University* and Erik Yukl, *New Mexico State University*

Abstract: The H-NOX protein from *Paracoccus denitrificans* is related to a family of heme-containing nitric oxide/oxygen sensor proteins involved in biofilm formation but has not yet been characterized *in vitro*. Biofilm formation is of relevance to many medical applications due to the association of biofilm with bacterial pathogenesis and resistance. In order to have a more complete understanding of this protein, we aim to solve its crystal structure using X-ray crystallography. During the initial purification process, stabilizing *P. den* H-NOX was difficult and would result in immediate precipitation. A detergent (Tween20) was introduced to the purified protein solution. Although this solved the precipitation issue of the purified sample, it posed another during crystallography. Using an under-oil crystal tray filled with paraffin oil, harvestable crystals were obtained during a precipitant concentration screen. 10 mg/mL of purified protein were added to different crystal conditions that contained various concentrations of precipitant and incubated over a span of four months. Crystals were checked once a week for growth until reaching an optimal size. Crystals that were optimal for harvesting grew in 62% precipitant solution, which was the highest range tested. Based on these results, a new set of conditions were made with a new precipitant concentration ranging between 58% and 69%. The long-term goal of this experiment is to obtain a protein structure of *P. den* H-NOX to better understand its function. This will be the first crystal structure obtained for *P den.* HNOX.

FRI - 927 An Alternative Approach to Drug Discovery: Drug Repurposing through Cheminformatics

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Ngima Sherpa*, *Caldwell University* and Melek Ucisik, *Baylor College of Medicine*

Abstract: Drug repurposing discovers new therapeutic applications for existing drug candidates or FDA approved drugs. At present, it takes 10-15 years and costs over $2.5 billion for a new drug to be developed from scratch. This high cost and long development process of traditional discovery method make drug repurposing very attractive. It has served as an alternative approach among pharmaceutical companies for quickly putting new drugs on the market. At the Center for Drug Discovery (CDD) of the Baylor College of Medicine, we have 1300 synthesized molecules from the medicinal chemistry pipeline that are shelved because they did not fulfill the requirements for binding to intended biological targets. Our goal is to repurpose these molecules into novel therapies. Through cheminformatic techniques such as chemical fingerprints, Tanimoto similarity evaluation, and K-means clustering, we clustered the 1300 compounds. Using Tanimoto-similarity, we compared the reference compound from each cluster with 2777 investigational drugs from the DrugBank database. We identified a few good matches, and are currently exploring whether our reference compound can bind to the exact biological targets of investigational drugs. We are using molecular docking to evaluate if and how the reference compounds bind to their new targets to structurally validate them. Then, the targets will be physically assayed for their ability to bind to the identified matching reference compounds. Through this alternative approach of drug discovery, we hope to develop new drugs at a much-reduced cost and time, making therapies accessible to all patients globally.

FRI - 928 N-Mode Convergence of the Hamiltonian Operator in Curvilinear Coordinates

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Walter Quintanilla*, *Los Angeles City College* and Olaseni Sode, *California State University of Los Angeles*

Abstract: Vibrational spectroscopy is a powerful experimental tool to discover the shape of the potential energy surface of chemical systems. However, since the experimental spectra can be complicated, computational and theoretical approaches often prove necessary. Yet, the main challenges of theoretical vibrational methods are the high dimensionality of the potential energy surface and the complex expression of the kinetic energy operator when curvilinear coordinates are used. To overcome these challenges, a hierarchical *n*-mode expansion of the molecular Hamiltonian was recently proposed and applied to the H_2O_2 molecule. We have continued this evaluation of the many-body expansion for the water molecule and the carbon dioxide dimer. In both cases, the vibrational self-consistent field (VSCF) and vibrational configuration interaction (VCI) methods were used to evaluate the excited state energy levels of the truncated expansion and compare them to reference values such as experimental frequencies and the complete expansion. It is predicted that along with the potential energy surface, the coordinate-dependent reduced masses of the kinetic energy are the most important Hamiltonian terms.

FRI - 930 3Dπ: Three-Dimensional Positron Identification with a Liquid Argon Target and Cryogenic Silicon Photomultipliers for Time-of-Flight Positron Emission Tomography

Discipline: Physics & Astronomy
Subdiscipline: Physics

Alejandro Ramirez*, *University of Houston*; Xinran Li, *Princeton University* and Andrew Renshaw, *University of Houston*

Abstract: Positron Emission Tomography (PET) is a diagnostic imaging technique used to observe metabolic processes within patients. This technique works by reconstructing the annihilation origin of incident gamma rays produced by a positron emitting tracer within the patient. However, the inefficiencies of current PET technology, such as low sensitivity and long scan times, can result in poor image reconstruction. To rectify these issues, we propose 3Dπ: a full body, Time of Flight (TOF) PET scanner that employs Silicon Photomultipliers (SiPM) coupled with a Liquid Argon (LAr) scintillator.

We simulated this new design using the Geant4 simulation tool kit while following the National Electrical Manufacturers Association's sensitivity, spatial resolution, and image quality evaluation tests to assess the performance of the scanner. Furthermore, we tested two variations of the LAr scintillator: (1)-LAr with Tetraphenyl-Butadiene, a wavelength shifter, and (2)-LAr doped with xenon atoms. We found that both variations, on average, offer a 200-fold gain in sensitivity, and a timing resolution below 100ps leading to an increase in image quality. Thus, with these advantages, a patient could theoretically undergo 15-30-second scans instead of the average 30-45-minute scan. Additionally, the

dosage of the radioactive tracer ingested by patients can also be reduced while still extracting decent quality scans.

With the LAr scintillator and SiPMs of $3D\pi$, we can use the precise TOF info of gamma rays to improve the localization of individual positron annihilations and provide low-dose PET scans for patients who may be at high risk for exposure to radiation.

FRI - 931 Phase Change Materials for Space Technology

Discipline: Physics & Astronomy
Subdiscipline: Physics

Michelle Marrero-García*, *University of Puerto Rico at Mayaguez*; Armando Rua, *University of Puerto Rico - Mayagüez Campus*; Edwin Pacheco, *University of Puerto Rico, Mayagüez* and Camilo Verbel, *University of Puerto Rico at Mayaguez*

Abstract: Advances in space technology are largely based on the development of new materials. Importance is given to those that serve as practical active thermal controllers because they are capable of maintaining the temperature of a spacecraft within the required limits, regardless of thermal loads imposed from operations. This research focused on studying Vanadium Dioxide (VO_2), a correlated electron material with a metal insulator transition at 67^{O}C (340K), suitable for regulating the temperature inside spacecrafts, while also decreasing its power needs by avoiding the use of electrical or mechanical devices. The reactive sputtering DC method was used to prepare VO_2 and deposit the material on silica substrates. Structural, optical and electrical properties were studied using X-ray diffraction, infrared transmission and electrical resistivity techniques to analyze the effect of growth parameters on the properties of VO_2. In addition, an assessment of the effects on structural and optical properties of the post annealing temperature and annealing time for VO_2 samples was made.

FRI - 932 Updating the Core Imaging Software and Algorithms Used for Thermoreflectance Imaging

Discipline: Physics & Astronomy
Subdiscipline: Physics

Arianna Maxwell*, *Pomona College* and Janice Hudgings, *Pomona College*

Abstract: Charged Coupled Device (CCD)-based thermoreflectance microscopy is a high-resolution, non-contact imaging technique for thermal mapping and evaluating the performance and reliability of numerous electronic and optoelectronic devices at the sub-micron-scale. Thermoreflectance imaging measures the fractional change in relativity of a sample material or device in response to a modulation of the sample temperature. This technique is used for thermal imaging of lasers, integrated circuits, solar cells, and other components. Although thermoreflectance imaging is a powerful method of obtaining high spatial and thermal resolution images, the technique is relatively slow, limiting broader commercial adoption. To improve the experimental system and solve these issues, I am currently working on modifying the 4-bucket algorithm and speeding up the hardware. The algorithm performs pixel-by-pixel lock-in averaging to determine the magnitude and phase of the thermoreflectance signal $\Delta R/R$ at each pixel of the CCD camera. The LabVIEW-based platform used to process the thermoreflectance images runs on an outdated version of Windows, and so I am aiming to modernize the image processing by implementing the 4-bucket algorithm in Python , which is compatible with modern operating systems. I am also working to install a higher speed camera and drivers and interfacing them with the laboratory equipment and existing software.

FRI - 933 ν_e Charged Current Event Identification Based on Shower Energy Profiles in LArTPC

Discipline: Physics & Astronomy
Subdiscipline: Physics

Diego Lopez Gutierrez*, *Macalester College* and Wanwei Wu, *Fermi National Accelerator Laboratory*

Abstract: Liquid Argon Time Projection Chamber (LArTPC) detectors are at the forefront of neutrino research. Their exceptional calorimetry and tracking capabilities let us study neutrino interactions with high precision, thus probing questions such as why there is more matter than antimatter, the nature of neutrinos, among others. However, neutrinos are elusive and they hardly interact with anything. One type of interaction—the charged current (CC) interaction—occurs by exchanging a $W^{\pm}$ boson via the weak force. CC interactions are important because their products let us identify the incoming neutrino (e.g. if an electron neutrino (ν_e) interacts via CC, then we get an electron (e^-) as a result.) However, identifying neutrino interactions is challenging. In this work, we investigate the ν_e CC identification using shower energy profiles. When neutrinos interact with argon nuclei, they release secondary particles such as electrons, photons and pions. Some of those particles may produce shower-like profiles. By studying the shower profiles of different particles, we can calculate the likelihood that a shower was produced by an electron. This likelihood is then used for prediction of ν_e CC interactions. The relevant algorithms are developed using C++ under the LArSoft framework. To test our results, we use Monte Carlo simulations of neutrino events at the Deep Underground Neutrino Experiment (DUNE) far detector. In summary, our project will allow us to study neutrino interactions by identifying the ν_e CC events. While this technique was tested on DUNE simulations, it can also be applied to other LArTPC neutrino experiments such as MicroBooNE.

FRI - 934 Electronic Spin PT System Dynamics

Discipline: Physics & Astronomy
Subdiscipline: Physics

Ekram Towsif*, *Wesleyan University* and Fred Ellis, *Wesleyan University*

Abstract: Parity-Time (PT) symmetry describes systems that are balanced with their environments, where the flow of energy is dictated by the geometric relationship between the elements in the system including gain and loss. Inducing a gain-loss parameter within the constituent equations allows us to observe the boundaries between balanced, unbalanced, and chaotic motion. Such a parameter is implemented in various ways such as electronically via negative resistors and feedback loops. Previous work on PT symmetry include PT-lasers, PT-superconducting wires, and PT-NMR. However, the behavior of large-scale magnetic PT symmetry is unknown experimentally in terms of electronics. Here we address the equations of motions corresponding to magnetic dipole coupled to feedback inductors for implementation of PT NMR gain or loss. We analytically solved the preliminary system parameters relating the normal modes to position and orientation of the feedback inductors, permanent magnets used for the biasing field, and the dipole oscillator. Experimental results demonstrate these various orientational possibilities for a macroscopic permanent oscillating magnet dipole at a resonant frequency near 38 Hz. Optimization of the oriental positions allows us to maximize the gain (or loss) that govern the system. We anticipate that our study will indicate a strategy for implementing PT symmetry for a pair of coupled dipoles. Ultimately, the findings of our investigation should enable the development of novel technology for incorporating PT dynamics into magnetic systems, with possible applications for NMR instrumentation.

FRI - 935 Classification of Solar System Minor Bodies through Precision Astrometry

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Allan Alonzo-Ault*, *Los Angeles City College* and William M. Owen, Jr., *NASA Jet Propulsion Laboratory*

Abstract: Astrometry is the study of the precise positions and movements of celestial bodies. Scientists at NASA's Jet Propulsion Laboratory rely heavily on the high-precision astrometry of minor planets (asteroids) and natural satellites to assist in the navigation of space craft. Measuring and constantly updating the exact position of these bodies allows for the determination of each object's ephemeris, or predicted future positions. Using the astrometric techniques developed by scientists at JPL to obtain the positions and movements of minor planets in our solar system, we set out to determine whether we could use this information to classify minor planets by shape and size. Knowing the exact position and trajectory of minor bodies allows us to predict events known as occultations when a distant object (such as a star) is hidden from sight by another object passing in between it and the observer. Through the observation of these events from different locations and angles, we are able to piece together the profile of a minor body which reveals to us its approximate shape and size. We obtained 519 positions of minor

planets using the 0.6m telescope at JPL's Table Mountain Observatory during the summer of 2018. These positions, published online by the International Astronomical Union's Minor Planet Center, are used by astronomers around the world to predict the timing of and observe stellar occultations by minor planets. We show that through this simple process, even amateur astronomers are able to assist in the classification of minor bodies within our solar system.

FRI - 936 Phase-Resolved Spectra of Millisecond Pulsars with Nicer X-Ray Observations

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Lauren Lugo*, *Haverford College*; Dominick Rowan, *Haverford College*; Zaynab Ghazi, *Bryn Mawr College*; Elizabeth Spano, *Haverford College*; Renee Ludlam, *University of Michigan, Ann Arbor* and Andrea Lommen, *Haverford College*

Abstract: Pulsars are Neutron stars, which are massive stars that have collapsed, that spin in very fast intervals. Millisecond pulsars (MSPs) are a distinct class of rotation powered pulsars with spin periods $P \leq 10$ milliseconds. Despite the detection of approximately 325 MSPs, no unified emission theory describes the population of these highly energetic objects. The pulsed high energy emission can either be thermal from the polar caps or non-thermal in the magnetospheric origin. We present two years of the Neutron star Interior Composition ExplorerR (NICER) X-Ray observations of three millisecond pulsars PSRs B1821−24, B1937+21, and J0218+4232. Our goal is to suggest a model of best fit for the X-ray emission spectra of each observed pulsar to further understand the emission mechanisms. Since NICER includes both timing and energy measurements, we conduct phase resolved spectroscopy to model the emission spectra at narrow phase selections. Additionally, since the X-Ray emission occurs in the primary and interpulse we use the off-pulse region to model the X-Ray background. We use computational X-Ray astrophysical analysis tools such as FTools, Xselect, and Xspec to construct spectra and fit theoretical models. Analysis of NICER data for each pulsar reveals that the best fit model is an single absorbed power law, accounting for the hydrogen absorption, and shows no evidence for a thermal emission component. Therefore, our results suggest that X-Ray emission is dominated by synchrotron radiation in the magnetosphere.

FRI - 937 Galaxy Cluster Membership with Machine Learning

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Suchitra Narayanan*, *University of California, Berkeley* and Michelle Ntampaka, *Harvard University*

Abstract: Galaxy clusters are the most massive gravitationally bound objects in the Universe, and contain hundreds or even thousands of galaxies. Because they are so massive and rare, cluster abundance as a function of mass and redshift is useful to constrain cosmological models. However, when using optical observations, galaxies that are actually in the fore- or background of the cluster look as though they belong in the cluster. These interloping galaxies add both scatter and bias to dynamical cluster mass estimates which introduce error to cosmological constraints. Therefore, it is imperative to develop methods that can accurately identify these interlopers. We use ~38,000 simulated clusters from the MultiDark *N*-body simulation consisting of dark matter only. For these clusters true membership is known. We then use this catalog to develop a data vector of engineered features containing galaxy and galaxy cluster properties which is used to train a machine learning model. We present our technique for determining cluster membership that uses a Random Forest, a machine learning classification algorithm.

2:30 PM – 3:45 PM

Astronomy and Astrophysics & Environmental Science

Room 304AB

Hyporheic Zone Microbiome Assembly Is Linked to Dynamic Water Mixing Patterns in Snowmelt-Dominated Headwater Catchments.

Discipline: Life Sciences
Subdiscipline: Environmental Science

Casey Saup*[1]; Savannah Bryant[1]; Amelia Nelson[1]; Kira Harris[1]; Audrey Sawyer[1]; John Christensen[2]; Malak Tfaily[3]; Kenneth Williams[2] and Michael Wilkins[4], *(1)The Ohio State University, (2)Lawrence Berkeley National Lab, (3)University of Arizona, (4)Colorado State University*

Abstract: Terrestrial and aquatic elemental cycles are tightly linked in upland fluvial networks. Biotic and abiotic mineral weathering, microbially-mediated degradation of organic matter, and anthropogenic influences all result in the movement of solutes (e.g., carbon, metals, nutrients) through these catchments, with implications for downstream water quality. Within the river channel, the region of hyporheic mixing represents a hotspot of microbial activity, exerting significant control over solute cycling. To investigate how snowmelt-driven seasonal changes in river discharge affect microbial community assembly and carbon biogeochemistry, depth-resolved pore water samples were recovered from multiple locations around a representative meander on the East River near Crested Butte, CO, USA. Vertical temperature sensor arrays were also installed in the streambed to enable seepage flux estimates. Snowmelt-driven high river discharge led to an expanding zone of vertical hyporheic mixing and introduced dissolved oxygen into the streambed that stimulated aerobic microbial respiration. These physicochemical processes contributed to microbial communities undergoing homogenizing selection, in contrast to other ecosystems where lower permeability may limit the extent of mixing. Conversely, lower river discharge conditions led to a greater influence of upwelling groundwater within the streambed and a decrease in microbial respiration rates. Associated with these processes, microbial communities throughout the streambed exhibited increasing dissimilarity between each other, suggesting that the earlier onset of snowmelt and longer periods of base flow may lead to changes in the composition (and associated function) of streambed microbiomes, with consequent implications for the processing and export of solutes from upland catchments.

Finding Light in the Dark: Detecting and Decoding Multi-Wavelength Variability in Active Galactic Nuclei

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Anna Payne* and Benjamin Shappee, *University of Hawai`i, Institute for Astronomy*

Abstract: With the advent of all-sky surveys that image the sky every night, transient behavior is discovered in galaxies throughout the universe. The compact region at the centers of galaxies called active galactic nuclei (AGN) that appear to brighten over time are undergoing changes in their accretion onto the supermassive black hole (SMBH) at their centers. As part of the All-Sky Automated Survey for Supernovae (ASAS-SN) team, we are working toward discovering AGN flares at their earliest sign of novel activity, to fully characterize their behavior from the X-ray to optical wavelengths. The presentation will report our work on a recent AGN flare from the galaxy NGC 1566 that began in July 2018. We led an intensive photometric and spectroscopic observing follow-up campaign to analyze this event by measuring the flux at different wavelengths at the time of the flare and the subsequent months following the flare. Deciphering how and why those changes occur over the entire electromagnetic spectrum on the timescales of months to years reveals important aspects of the physics occurring at the galactic centers of galaxies outside our own Milky Way. Monitoring AGN flares such as NGC 1566 allows us to achieve our goal of either supporting or not supporting proposed accretion disk models around SMBHs, in addition to measuring the mass of the SMBH. Ultimately, first discovering and then observing these extragalactic flares provides golden opportunities to characterize the structure of AGN, and, therefore, the physical processes occurring in the environment surrounding the central SMBH.

Machine Learning Models Predicting Amphibian Occupancy in the Novel Ecosystem of the Palouse Prairie

Discipline: Life Sciences
Subdiscipline: Environmental Science

Erim Gómez* and Rod Sayler, *Washington State University*

Abstract: The vast majority of southeastern Washington's Palouse Prairie has been converted to tilled agriculture. The ecosystem has lost an estimated 97% of its original wetland habitat due to intensive farming. This makes the Palouse a useful system for studying conservation of biological diversity within a novel ecosystem. We hypothesized that amphibian occupancy is primarily influenced by 1) introduced or non-native species, 2) ecological features characterizing wetlands, and 3) landscape features. We used machine learning techniques to develop ecological models predicting the occupancy of 7 species of amphibians using data collected from 93 wetlands along a geographic gradient extending from the eastern edge of the Palouse Prairie bioregion to Moses Lake, in central Washington. All study wetlands were artificially constructed as reservoirs, conservation habitats in agricultural lands, or were associated with human development. We used both wetland and landscape scale variables to predict amphibian occupancy. Our models revealed that relatively few ecological variables are needed to predict occupancy of different amphibian species with high accuracy, including a) presence of non-native fish, b) wetland permanence, and c) broader biogeographic factors. We found that Palouse Prairie has retained its historical amphibian diversity despite intensive farming and loss of wetland habitat. The ecological models we developed help inform conservation strategies that would most beneficially impact amphibian species of conservation concern. Our models further demonstrate the adverse effects of non-native fish on pond-breeding amphibians and the ecological importance of seasonal wetlands for amphibians breeding in novel ecosystems.

Investigating Red Giant Stars with Abnormal Carbon to Nitrogen Ratios

Discipline: Physics & Astronomy
Subdiscipline: Astronomy and Astrophysics

Erica Molnar-Bufanda*; Jamie Tayar and Daniel Huber, *Institute for Astronomy, Universtiy of Hawaii at Manoa*

Abstract: Astronomers are currently trying to understand and reconstruct the history of the Milky Way. Giant stars are optimal for this because their intrinsic brightness allows them to be observed at large distances. Additionally, their short lifetimes in evolved stages make it possible to infer a precise age using evolutionary models if the mass and metallicity of the star is known. Recent work has suggested a correlation between the mass of a red giant star and its carbon to nitrogen ratio [C/N], which would enable the estimation of ages of stars across the galaxy using only spectroscopy. However, in our study, we have shown that at least 13% of core-helium burning red clump stars and 10% of red giant branch stars do not follow the relationship between [C/N] and mass, calling into question the reliability of their inferred ages. We identify these outliers in a sample of over 6000 stars with both spectroscopic data from the Apache Point Observatory Galaxy Evolution Experiment (APOGEE) and photometry from the Kepler mission. From analyzing the stellar parameters from these surveys, we infer a history of stellar interaction from larger-than-expected rotation rates, radial velocity differences, or specific identified chemical tracers of past or present merging events. Our results indicate that stellar interaction plays a prominent role in shifting evolved stars off the expected [C/N]-mass relation. Therefore, we recommend that when using the [C/N]-mass relationship as a tool to measure masses/ages for large stellar populations, stars with any indication of binarity should be excluded.

2:30 PM – 3:45 PM

Chemistry: Physical Chemistry

Room 319AB

High Resolution Vibrational Sum Frequency Generation Spectroscopy of Thermally Treated Clay Minerals

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Ariel Nessl*; Sabrina Falcon; Angelo Montenegro; Erica Howard; Muhammet Mammetkuliyev; Brent Melot and Alexander Benderskii, *University of Southern California*

Abstract: Over 90% of industrial chemical products use catalysts in at least one step of synthesis. Despite their utility, catalysts and their processes have not been thoroughly explored. Understanding the catalytic process is crucial for catalyst design. One such catalyst is nickel phyllosilicate which can catalyze the oxidation of alcohols and also perform other reactions. Thermal treatment of nickel phyllosilicate induces defects, modifying the catalytic activity of the material. We seek to characterize the defect sites on the surface to understand the change in catalytic activity. Since catalysis on nickel phyllosilicates occurs at the surface, we are using vibrational Sum Frequency Generation (SFG) spectroscopy, a surface specific technique that can be used to determine the orientation of vibrating species. High-resolution SFG of nickel phyllosilicate and the thermally treated nickel phyllosilicate show significant changes to the orientation of the surface hydroxyl groups. By studying the orientation of the hydroxyls on the surface of these catalysts, the defects causing the changes in catalytic activity can be explored.

Two's Company, Three's a Crowd: How Ions Tag Along for the Ride with Soaps and Polymers on a Nanoemulsion Surface

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Emma Tran* and Geraldine Richmond, *University of Oregon*

Abstract: Oil/water nanoemulsions are nanoscale oil droplets dispersed in water, capturing the attention of scientists and industry alike due to their application in oil spill remediation. Oil dispersants work to break down large oil slicks into tiny oil droplets, very similar to nanoemulsions, that are then naturally engulfed by microbes. During this process, we rely on a mixture of polymer/surfactant (PS) systems to stabilize the nanoemulsion and prevent coalescence. The surface structure of the PS system can influence specific interfacial behavior and properties important for the development of more effective oil spill dispersant systems that are also ecological and nontoxic to marine life. However, determining structural information at a buried interface has been limited due to the experimental difficulty of selectively probing the curved surface. We have overcome this hurdle by employing vibrational sum frequency *scattering* spectroscopy to measure the vibrational spectrum of only species adsorbed to nanoemulsion surfaces. This allows us to determine structural information about the PS system at the molecular level. This study determines how pH governs interfacial behavior and structure of polyethylenimine (PEI) and sodium dodecyl sulfate (SDS) mixtures to elucidate how nanodroplet surfaces respond to different environmental conditions. Interestingly, there is a stark contrast in PEI/SDS adsorption behavior and structural orientation between acidic and basic conditions, which suggests an interplay between electrostatic and hydrophobic forces dictating the way PEI and SDS interacts at the surface. This work provides insight for the design and development of safer dispersant systems with important implications for large-scale ecological applications.

Relaxation Dynamics of Neutral Iron Oxide Clusters with CO_2 Observed Using Femtosecond Pump-Probe Spectroscopy

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Jacob Garcia*; Ryan Shaffer and Scott Sayres, *Arizona State University*

Abstract: Iron oxides have been used in a number of societally important catalytic processes; however, the molecular-level details behind their reaction mechanisms have been a challenge to observe. Molecular clusters have gained experimental attention due to their ability to model bulk materials, ease of production, and direct application for gaining atomic level insights. Using laser ablation combined with femtosecond pump-

probe spectroscopy, the gas-phase dissociation and excitation-relaxation dynamics of neutral iron clusters in the presence of molecular oxygen and carbon dioxide are observed. Dissociation/fragmentation time of neutral iron oxide clusters from $(FeO)_n$ (n = 1-10) decreases with increased molecular size from >300 fs to ~150 fs. Clusters deviating from the 1:1 stoichiometry are generally seen to increase in relaxation time, owing to an increased stability induced by a caging effect from atomic oxygen. A notable example of dissociation stability is observed with the addition of O atoms as Fe_2 grows to Fe_2O_2 which decreases in relaxation time from >650 fs to <250 fs. In the presence of CO_2 the stable neutral Fe_nO_m cluster distribution shows marked differences indicative of CO_2 reactions. Relaxation dynamics of these clusters and bound CO_2-FeO clusters provide crucial information to understanding the interactions that occur between CO_2 and iron oxide molecules. The molecular-level insights from these cluster studies provides a more comprehensive understanding for the design of future catalysts, leading to iron oxide materials with increased reactivity and decreased impact.

2:30 PM – 3:45 PM

Computer & Information Sciences, Mathematics (general)

Room 301A

Rank Problems for Homogeneous Polynomials in Several Variables

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Kevin Palencia Infante* and Jennifer Brooks, *University of Montana*

Abstract: Many important and interesting problems in mathematics are extremal problems. Perhaps the easiest example arises in calculus when we seek the rectangle of maximum area with a fixed perimeter. Other less trivial extremal problems include the problem of finding the orthogonal projection of an element of a Hilbert space onto a closed subspace or the problem of finding the largest number of edges for a graph with n vertices that has no k-cycles.

We consider an extremal problem about homogeneous polynomials in several variables. We define the rank of a polynomial p to be the number of distinct monomials appearing in p with nonzero coefficient. Consider the class H of all homogeneous polynomials p in n variables of degree d such that p= SQ, where Q has degree d-1 and maximal rank and $S=x_1 + x_2 +...+ x_n$. We ask: for fixed d, what is the minimum rank for p in the class H?

This problem was solved in the three-variable case by D'Angelo, Kos, Riehl, and a related problem was solved by Lebl, and Peters for four or more variables. Their solutions use a graph-theoretic approach. Our approach is to reformulate the problem as a question about homogeneous ideals and to address it by studying the Hilbert functions and the graded Betti numbers of certain ideals. We have recovered the known result in 3 variables and have a nontrivial lower bound in the four variable case that is not sharp.

Text Extraction from Images to Detect Cyber Bullying

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Latha Saradha*; Rachel Adler; Salah Latif; Rachel Trana and Sarah Dezetter, *Northeastern Illinois University*

Abstract: This research concentrates on extracting text from images posted on Social Networking Sites (SNSs) in order to detect and classify those that contain cyber bullying. Prior research on cyber bullying has primarily focused on examining text-based comments to determine whether they are considered cyber bullying. However, many images can contain harmful text as well.

Text extraction is an important research problem in image processing and this work has many diverse applications. Our research focuses on ideal algorithms for extracting text from SNS images in order to prevent harmful content from being posted. We have examined multiple algorithms and methods for text extraction, such as text localization, dilation, erosion, morphological transformations, gray scale manipulations, as well as manipulated image resolutions in order to best retrieve the text. We have tested our algorithms on images with varying degrees of complexity in terms of backgrounds, colors, and text styles. Rather than relying on one technique, our code is unique in that it merges existing tools and algorithms, as well as our own, to produce a tool that can extract text from SNS memes with more accuracy.

The goal for this research project is to create a tool that SNSs could use to extract text from memes in order to detect cyber bullying. Automatic flagging of this content on SNSs will not only help victims of cyber bullying, but can be useful for those posting messages to recognize cyber bullying as many may be unaware of the harmful ramifications of their words.

Design of a Unified Single-Instruction Multiple-Data/Threads Model for Parallel Computations in Modern Processors

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Eduardo Ponce* and Gregory Peterson, *The University of Tennessee, Knoxville*

Abstract: Modern processors are equipped with hardware that operates on both scalar and vector computations in order to support a variety of programming and algorithmic paradigms. The use of vectorization and single-instruction multiple-data (SIMD) instructions are necessary techniques to achieve near-peak performance on a single processing core. Programs make use of SIMD features by either using explicit instructions or by leveraging automatic compiler vectorization. Compilers tend to automatically employ vector transformations when code blocks have regular access patterns and minimal data dependencies. For cases where hand-tuning vectorization is effective, programmers use explicit vectorization via either inline assembly or compiler-specific intrinsic functions, thus reducing software portability and maintenance. For multiprocessor systems, performance also depends on efficient implementation of multiple execution threads. This work presents a programming model and software library that provides a generic interface for performing explicit vector operations from high-level languages such as C and C++. The vector library provides common function-based and object-oriented interfaces across compilers and microprocessor architectures. The SIMD model is extended to multicore systems following the single-instruction multiple-threads (SIMT) approach which is also mapped to general-purpose graphics processing units. Hybrid parallel implementations of pseudo-random number generators are presented as case studies that benefit from the SIMD/SIMT model.

2:30 PM – 3:45 PM

Earth Science, Marine Science & Other Geoscience

Room 306AB

Gut Microbes and Diet: Testing Phylosymbiosis in Closely-Related Prickleback Fishes (Family Stichaeidae) with Different Diets.

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Michelle Herrera* and Donovan German, *University of California, Irvine*

Abstract: Gut microbiomes are affected by many characteristics, including diet, habitat, and host genetics. The concept of “phylosymbiosis” predicts that host genetics shapes the gut microbiome, more so than diet. Thus, closely related, sympatric animals with different diets should be investigated to test phylosymbiosis and to examine whether dietary perturbations change microbial community diversity and function. We examined four closely-related, sympatric prickleback fishes that vary in diet: *Xiphister mucosus* (herbivore), *X. atropurpureus* (omnivore), *Phytichthys chirus* (omnivore), and *Anoplarchus purpurescens* (carnivore). We compared enteric microbial diversity amongst

wild-caught individuals of the four species, and among the wild-caught individuals and those fed different diets in the laboratory within a species. I used 16S sequencing to determine hindgut microbial diversity. I hypothesize that microbial diversity will match with host phylogeny and more closely related species (e.g. the *Xiphister* taxa) to have more similar microbial communities. To match microbiome with community function, I will measure by-products of fermentation, short-chain fatty acids (SCFA), and the activity of algae- and chitin degrading enzymes (β-glucosidase and N-acetyl- β-D-glucosaminidase (NAG), respectively). SCFA concentration and β-glucosidase activity are expected to correlate with algal concentration in their diet (herbivore>omnivores>carnivore), whereas NAG activity should not. Preliminary results show that the microbiomes of wild prickleback fishes do not group significantly by host phylogeny or diet, with *X. atropurpureus* forming its own statistical group that is different from the other species. Overall, this is one of the first studies to combine DNA sequencing with functional data to test phylosymbiosis on a broader evolutionary scale.

The Influence of Lava Channel Constrictions and Bends on the Lengths, Dimensions, and Morphologies of Lava Flows

Discipline: Geoscience
Subdiscipline: Other Geoscience

Alyssa Anderson*[1]; Sarah Fagents[1] and Stephen Baloga[2], *(1)University of Hawaii at Manoa, (2)Proxemy Research*

Abstract: The factors controlling the dimensions and morphologies of lava flows are important for understanding the potential volcanic hazards for communities at risk. In the case of a channelized lava flow, changes in channel width and lateral changes in flow path direction can disrupt the flow surface crust and cause enhanced cooling, which can significantly impact the distance the flow can travel. Thermal models have been developed and applied to examples of surface crust disruption observed in images of active Hawaiian lava flows. The model estimates the evolution of core temperature of the flow along its length due to changes in surface crustal coverage caused by (i) channel constrictions (narrowing) and (ii) channel bends. For constrictions, conservation of volume requires a combination of changes in flow depth and velocity to accommodate the decrease in channel width. The width decrease is found to result in a velocity increase, which also increases the surface shear stresses. The primary result is that the narrowing channel increases the surface area of exposed incandescent lava along the channel walls, where shear stresses are greatest. For channel bends, the fraction of exposed hot lava is related to the angle through which the flow turns by a constant of proportionality. The results from both cases are used in the thermal models to calculate changes in core temperature with distance, showing that even small changes in lava core exposure can have significant influences on flow rheology, and ultimately the final dimensions of the flow.

Evolution of Basal Channels in Antarctic Ice Shelves and Implications for Ice Shelf Stability

Discipline: Geoscience
Subdiscipline: Earth Science

Allison Chartrand* and Ian Howat, *Byrd Polar and Climate Research Center, The Ohio State University*

Abstract: Antarctic ice shelves provide a buttressing force against the flow of ice from the continent, effectively slowing Antarctica's contribution to sea level rise. This buttressing effect may be impacted by the presence of basal channels, but very little is known about the evolution of basal channels. Basal channels are deep, longitudinal grooves that extend up into the bottom of the floating ice, formed by concentrated melt. The buoyancy of ice causes surface depressions to form above basal channels, which can be measured using surface elevation data. We study the evolution of basal channels over time using the Reference Elevation Model of Antarctica Digital Elevation Models (DEMs) in conjunction with NASA satellite (ICESat and ICESat-2) and airborne laser altimetry (surface elevation) and radar (ice thickness) data, and surface velocity data. We measure rates of change in surface elevation to examine how basal channels change over time. We have found that several basal channels around Antarctica are actively lengthening, and that several basal channels migrate toward shear margins, sometimes moving perpendicular to the direction of ice shelf flow at rates of 70 m/year. We expect that the resultant thinning of shear margins is the primary mechanism by which basal channels impact ice shelf stability. It is imperative to characterize basal channels and their impact on ice shelf stability so that ice shelf buttressing can be more accurately accounted for in ice sheet and climate models to ensure more accurate predictions of Antarctica's contribution to sea level rise as the global climate warms.

2:30 PM – 3:45 PM

Engineering: Mechanical Engineering

Room 301B

Investigating Viscoelastic Properties of Marine Mussel Byssal Threads

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Marcela Areyano*; Eric Valois; Robert M. McMeeking and J. Herbert Waite, *University of California, Santa Barbara*

Abstract: Marine mussels possess superb adhesive and mechanical properties allowing them to remain adhered to surfaces despite a hostile environment where pH levels vary drastically, predator encounters occur, and cyclic loading occurs due to wave motion. They remain adhered to a number of surfaces including rock, metal, and wood through bundle filaments they secrete called byssal threads. Mussel byssus have spawned many bioinspired adhesives by incorporating chemical moieties found in the natural material into synthetic systems. Despite the abundance of knowledge about adhesion, little is known about the mechanical properties of the threads, particularly the viscoelastic properties. Developing a deeper understanding of the viscoelastic properties could provide insight into the ability for the byssal threads to self-heal. In recent experiments it has been observed that native byssal threads under constant strain will relax as much as 40%, by altering the natural system and treating the byssal threads with different chemical treatments we seek to understand what components contribute to the stress relaxation of the material. Through modeling of the viscoelastic properties, we further seek to characterize these properties, as well as more accurately quantify how varying chemical treatments can change the mechanical properties. We anticipate that these results can lead to advancement of bioinspired materials with superior properties including self-healing properties.

The Effect of Surface-Obstacle Geometry on Maximizing Rough Surface Drag

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Simone Stewart* and Paolo Luzzatto-Fegiz, *University of California, Santa Barbara*

Abstract: The fluid dynamics of a large turbine array are radically different from those of a single turbine. The kinetic energy in the air ahead of the turbines is harvested by the first few rows, but for most of the array, the kinetic energy in the air is replenished through turbulent exchanges with the flow above the farm. Wind turbine arrays are not currently optimized for this exchange, so their maximum power is almost certainly not being extracted. To improve power extraction from wind farms, we investigate how utilizing rough surfaces with various obstacle arrangements works to increase exchanges of kinetic energy with the overlying flow. This project exploits the well-established notion that atmospheric flow over wind turbines in a wind farm is analogous to flow over obstacles that comprise a rough surface. The equivalent roughness ratio, k_s/k, compares obstacle height k to the "effective" roughness heights of the obstacles k_s, which can be used to measure the effects of the surface structure on the drag of the flow. When k_s/k is maximized, drag is also maximized. Due to the spacing between 2D-bars, recirculation regions form, which can isolate the flow from the roughness and result in mutual sheltering. By utilizing 2D-bars as obstacles with "sub-obstacles" at half of the distance between two bars—a process that can be repeated to yield "fractal surfaces"—recirculation regions will be disrupted, producing in a continual ejection of eddies into the

larger outer flow, which will ultimately result in higher drag over the surface.

Performance Characterization of Wood-Fueled Camp Stoves

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Juan Loaiza[*1]; Nelson Granda[2]; Hayri Sezer[2] and Wes Stone[2], *(1)WESTERN CAROLINA UNIVERSITY, (2)Western Carolina University*

Abstract: Biomass fueled camp stoves allow users to harness readily available sustainable fuel, such as wood, to use in their stove during camping; Stoves can be used to boil water for dehydrated foods eliminating disease-causing pathogens prior to consumption. The user does not have to carry any conventional liquid fuels; however, the challenge is to design a wood-fueled camp stove with a small mass that also has a reasonable durability that can satisfy user needs. In the present study, 8 solid-fuel (wood) camp stoves were tested for performance to determine their thermal efficiency, specific fuel consumption, burning rate and firepower. Fire tests were performed in an open environment to simulate campsite aerodynamic conditions and the wood-fuel used was kiln-dried yellow pine with 9% moisture. Efficiency values were calculated using data gathered during water boil tests. Results have determined the stoves that were tested have thermal efficiencies ranging from 4.74 to 36.09%. Preliminary research determined that users tend to avoid using wood-fueled stoves because they create soot. If an efficient stove that can achieve complete combustion can be designed, it would reduce the amount of smoke and emissions released during the burning process. Biomass energy accounts for roughly 9% of the primary energy consumption today; over half of this is connected to cooking and heating, often using inefficient fires with adverse impacts on health. Therefore, an improved stove design would result in reduced health impacts on users, as well as decreased deforestation due to lessened fuel consumption.

2:30 PM – 3:45 PM

Life Sciences: Biochemistry

Room 316C

Biochemical Features of the Amylosome from *R. Bromii*: A Keystone Species of the Gut Microbiota

Discipline: Life Sciences
Subdiscipline: Biochemistry

Filipe Cerqueira[*]; Aric Brown; Ryan Kibler and Nicole Koropatkin, *University of Michigan*

Abstract: Modulation of the human gut microbiota is a promising therapy for individuals with diseases such as Crohn's Disease, obesity, and *C. difficile* infection that are linked to an altered gut community. One way to manipulate the gut community towards improved health is via diet as carbohydrates drive community assembly. *Ruminococcus bromii*, a keystone species in the human gut, degrades dietary resistant starch (RS) and cross-feeds other gut bacteria that produce butyrate, a metabolite with anti-inflammatory and anti-tumorigenic properties. *R. bromii* has an amylosome, a complex of starch-specific enzymes and binding proteins, that is predicted to be responsible for its rare ability to degrade RS. However, the molecular determinants within this complex that confer RS degradation and downstream alteration of the gut bacterial community are poorly understood. Using the amylosome as a model for RS-degradation, I aim to elucidate distinct molecular features required for RS processing. Doc20, a recently discovered component of the amylosome, contains two previously uncharacterized domains. I have purified Doc20 and its domains and confirmed via isothermal titration calorimetry that Doc20 domains 1 and 2 bind to starch substrates. I have determined the crystal structure of Doc20 domain 1 with substrate which revealed a novel starch binding fold suggesting that Doc20 recognizes linear but not helical starch. While community correlation studies have pointed to the importance of the RS-degraders and butyrate-producers axis, my proposed studies will be the first to delve beyond community correlations with RS and explore the molecular basis of RS degradation.

High-Throughput Methods of Analyzing Beta-Sheet Protein Stability

Discipline: Life Sciences
Subdiscipline: Biochemistry

Allyson Langley[*] and Thomas Magliery, *The Ohio State University*

Abstract: Numerous diseases are caused by loss-of-function or destabilizing mutations in a protein, leading to the disruption of a biological pathway. From a drug-discovery perspective, stabilization of these mutant proteins seems like a logical solution. Unfortunately, how the amino acid sequence influences a protein's structure, function, and stability remains a fundamental, unanswered question in biochemistry. We present research using protein GB1 as a model beta-sheet protein because it is well-characterized, highly stable, and binds Immunoglobulin G allowing affinity changes to be studied. We have developed high-throughput (HT) methods to increase the efficiency of purifying and characterizing two libraries; namely, how do constraints in two loops or beta-strand side chain interactions influence stability and binding. These libraries were cloned by randomizing four positions in the respective areas. Stabilities were then measured with fluorescence and circular dichroism experiments to find the changes in Gibbs free energy. Both libraries produced variants that were up to 6 kcal/mol destabilized, but more wild-type-like stability variants were seen in the loop-library. We were surprised to see increased destabilization overall with the beta-strand library, indicating this structural element may be of greater importance to the overall stability. These HT experiments have also been coupled with phage display to increase the size of the library that can be screened. By looking at a larger number of variants, we can start to gain more insight into what factors control beta-sheet protein stability and make advancements toward answering this question that is crucial to the advancement of biochemical research.

Specificity in Mitogen-Activated Protein Kinase Signaling Cascades

Discipline: Life Sciences
Subdiscipline: Biochemistry

Jaylissa Torres-Robles[*] and Benjamin Turk, *Yale University*

Abstract:

Alterations in MAPK signaling pathways contribute to diseases including immune diseases, diabetes and cancer. Despite their high sequence similarity, the three major mammalian MAPK subfamilies (ERK1/2, JNK1/2 and p38a-d) are activated in response to different stimuli and mediate distinct cellular responses. Docking sites know as D-sites, are thought to play key roles in MAPK interaction specificity. These motifs bind to the D-site recruitments site (DRS), a common docking groove outside of the MAPK catalytic cleft. However, known D-site sequences conform to a common consensus sequence irrespective of its specific MAPK interaction partner. We thus lack fundamental information about how MAPKs achieve specificity. Our objective is to understand how binding specificity is encoded within D-site sequences and to discover new MAPK interaction partners. Thus, we developed and executed a yeast two-hybrid screening platform to identify sequences that specifically interact with individual MAPKs. Hits selected from screening a library of ~12,000 sequences from the human proteome with the MAPKs ERK2 and p38α revealed known and novel binding partners for each kinase. Alignment of the top hits uncovered strikingly distinct novel motifs selected by ERK2 and p38a. In ongoing work, we are investigating the capacity of these motifs to discriminate between MAPKs, and to investigate the structural basis for selective interactions. We are further validating novel binding partners for their capacity to act as MAPK substrates in vitro and in cells. The findings from these studies will provide a greater understanding of MAPK signaling networks and their roles in cell physiology and disease.

Towards a Comprehensive Understanding of the MAP Code

Discipline: Life Sciences
Subdiscipline: Biochemistry

Brigette Monroy[*]; Tracy Tan and Kassandra Ori-McKenney, *University of California, Davis*

Abstract: Within cells, numerous motor and non-motor microtubule-associated proteins (MAPs) simultaneously converge on the microtubule. How the binding activities of non-motor MAPs are coordinated and how this contributes to the balance and distribution of microtubule motor transport are open questions. Here, we examine the individual and collective behaviors of recombinant full-length MAP2c, tau, MAP7, MAP9, DCX and DCLK1 on the microtubule lattice using TIRF microscopy. We combine these data with ex vivo imaging of localization patterns of these MAPs in primary neuronal cultures in order to determine if and how these MAPs cooperate or compete for binding to the microtubule. While we find that certain MAPs can bind simultaneously on the microtubule under saturating conditions, most MAPs exclude one another into patches. MAP7 is the only MAP analyzed thus far that spreads along the microtubule to displace another MAP (tau) from the microtubule lattice. We also assess how individual MAPs as well as different MAP combinations affect the accessibility and motility of the microtubule motors, kinesin-1, kinesis-2 and kinesin-3. Together, these data indicate that certain MAPs form barriers to dictate access to the microtubule lattice, while other MAPs facilitate the binding and motility of motors. Overall, these data provide general principles for how the MAP code dictates access to the microtubule to determine the correct distribution and balance of motor activity.

2:30 PM – 3:45 PM

Life Sciences: Cancer Biology

Room 317AB

Characterization of HLA-G, ILT2 and ILT4 Expression on Human Head and Neck Squamous Cell Carcinoma Samples

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Gabriel Rodriguez-Garcia*; Michael Korrer and Young Kim, *Vanderbilt University*

Abstract: Checkpoint blockade of CTLA-4 and PD-1 have provided a new therapeutic approach with great success for certain types of cancer. However, a better understanding of other immune inhibitory receptors will lead to new treatments for cancers that are currently unresponsive to checkpoint blockade. HLA-G, a non-classical HLA molecule, is the ligand of the inhibitory receptors ILT2 and ILT4, which are expressed by granulocytes, macrophages, dendritic cells, B cells, T cells and natural killer cells. HLA-G expression is upregulated in multiple tumors and is associated with increased invasiveness and metastatic potential. We hypothesize that HLA-G expression in the tumor microenvironment inhibits the anti-tumor immune response through these inhibitory receptors. To determine this, we performed multiparameter flow cytometry of human head and neck squamous cell carcinoma (HNSCC) and matched blood samples to determine the expression of HLA-G and its receptors. Our results showed that HLA-G is not only expressed by tumor cells, but also by CD11b$^+$ CD14$^+$ monocytes and CD11b$^+$ CD15$^+$ granulocytes in the tumor. Monocytes present in the blood and tumor express ILT2 and ILT4, while granulocytes only express ILT4. Tumor infiltrating lymphocytes express ILT2 and, surprisingly, a high proportion of T cells in the blood also express this inhibitory receptor. In summary, our data shows that both HLA-G and its receptors are expressed on immune cells in the blood and tumor microenvironment of HNSCC patients. This suggests that HLA-G plays a major role in the inhibition of the anti-tumor immune response and could provide a new therapeutic target in HNSCC.

The Role of Mitochondrial AK4 in AMPK Signaling: An Energy Sensing Approach to Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Jocelyn Rodriguez* and Nathan Lanning, *California State University, Los Angeles*

Abstract: Recently, AMP-Activated Protein Kinase (AMPK) has been linked to tumorigenesis through cell proliferation and responses to cellular stress. Concurrent with its role as a tumor suppressor, LKB1, the upstream activator of AMPK has also been shown to be mutated in many cancers. While it's known that AMPK and LKB1 are involved in tumorigenesis, the mechanism by which these proteins initiate this process remains unclear. Adenylate Kinase-4 (AK4), a mitochondrial phosphotransferase, is unique in its role in cellular bioenergetics. AK4 regulates ATP levels, has lower levels of expression in glioma patients, and impacts AMPK activation. This suggests that elucidating AK4's function could serve as a mechanistic link between AMPK, LKB1 and cancer and may aid in better understanding both normal and cancer cell biology. We hypothesize that altered expression of AK4 will affect the upstream activation of AMPK via the LKB1 kinase and that phosphorylation of AMPK by LKB1 at Thr172 will not occur when AK4 expression is reduced. To test the effects of altered AK4 expression on AMPK levels via LKB1, a series of siRNA knockdowns, CRISPR/Cas9 knockout experiments and cDNA over-expression will be performed in healthy and cancer cell lines. Activation of AMPK and other targets was validated using Western blot analysis. We have shown that loss of AK4 expression robustly activates AMPK signaling in human kidney cells (HK2) and HeLa cells and demonstrates a dysregulation in the AMPK metabolic pathway. We are currently determining if AK4 activates AMPK directly through LKB1.

GP130 Cytokines Regulate Breast Cancer Dormancy Signaling Pathways

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Tolu Omokehinde*[1]; Alec Jotte[1] and Rachelle Johnson[2], *(1)Vanderbilt University, (2)Vanderbilt University Medical Center*

Abstract: Breast cancer cells frequently metastasize to bone, where they may reside in a dormant state. Our lab previously showed that breast cancer cell expression of leukemia inhibitory factor (LIF) receptor (LIFR), part of the glycoprotein130 (GP130) cytokine family, promotes tumor dormancy in bone. The GP130 cytokines LIF, oncostatin M (OSM) and ciliary neurotropic factor (CNTF) all signal through LIFR and can induce JAK/STAT, AKT, and ERK signaling. Of these pathways, only STAT3 is known to promote tumor dormancy, but it is unclear which GP130 cytokines stimulate STAT3 through LIFR. We hypothesized that LIF/OSM/CNTF stimulate STAT3 signaling through LIFR on breast cancer cells. Treatment (50ng/ml) with recombinant LIF or CNTF robustly stimulated pSTAT3 (up to 26-fold, $p<0.001$-0.0001), but not pAKT or pERK, in MCF7 breast cancer cells, and induced no signaling in MDA-MB-231 breast cancer cells, which have a non-functional LIFR. OSM robustly stimulated pSTAT3, pAKT, and pERK (up to 37-fold, $p<0.05$-0.0001) in MCF7 and MDA-MB-231b cells, suggesting OSM may signal through OSM receptor (OSMR), not LIFR. Accordingly, LIF no longer induced pSTAT3 in MCF7 LIFR knockdown cells, while OSM robustly stimulated pSTAT3, pSTAT1 and pERK (up to 63-fold, $p<0.01$-0.0001). Since GP130 cytokines promote stem cell pluripotency, we investigated whether LIF/OSM/CNTF alter the CD44^{Hi}/CD24^{Lo} cancer stem cell (CSC) population. CSC percentage was unchanged after 24 hour treatment, but OSM increased the CD44+ population by 5%, suggesting OSM may promote stemness, which is linked to dormancy. Together, these data suggest GP130 cytokines robustly stimulate signaling pathways through LIFR that promote tumor dormancy.

2:30 PM – 3:45 PM

Life Sciences: Cell/Molecular Biology

Room 323A

From Mother to Bud: Vacuole Inheritance and Biogenesis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Angeline Chemel*, *San Francisco State University*; Rachel Porter, *University of Saint Mary* and Mark Chan, *San Francisco State University*

Abstract: Organelles are key components of all eukaryotic cells, thus it is necessary that daughter cells receive the proper amount of organelles during cell division. In *Saccharomyces cerevisiae*, commonly known as budding yeast, organelles are dragged from the mother cell to its daughter cell in a process called inheritance. Since the mother cell is losing its organelles to its bud (daughter cell), it must make up for that loss through organelle biogenesis (the synthesis of organelles). In yeast, vacuoles are the largest organelle and are used for storage and degradation. Previous research showed vacuoles are crucial for cell cycle progression and suggests that the mammalian lysosome (yeast vacuole equivalent) may also play a crucial role in mammals. Although vacuole inheritance and biogenesis are required for cell cycle progression, it is unclear in which pattern they occur. Using a combination of fluorescence with 3-D microscopy and image analysis software, vacuole inheritance and biogenesis will be measured over time in live cells to determine the pattern of the two processes. As hypothesized, data is suggesting that inheritance may occur in a steady progressive pattern. Additionally, three mutant strains with varying vacuole phenotypes: Apl5Δ (reduced vacuole size), Atg18Δ (enlarged vacuole size), and Vps11Δ (fragmented vacuoles), were examined and preliminary data suggests that vacuole morphology may affect the pattern of vacuole inheritance. Understanding vacuole inheritance may shed light onto elucidating the role organelles play in the cell cycle, thus providing insight into cell cycle arrest for cancer treatment.

A Genetic Strategy to Identify Lipid Droplet Protein Degradation Pathways

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Melissa Roberts*[1]; Dara Leto[2]; Julian Stevenson[1]; Kartoosh Heydari[1]; Lawrence Bacudio[1]; Ron Kopito[2]; Michael Bassik[2] and James Olzmann[1], *(1)University of California, Berkeley, (2)Stanford University*

Abstract: Nearly all cells store lipids in endoplasmic reticulum (ER)-derived organelles called lipid droplets (LDs), which consist of a hydrophobic core of lipids encircled by a phospholipid monolayer with a unique proteome of regulatory proteins and enzymes. Although LD-resident proteins have essential roles in maintaining cellular lipid homeostasis, their regulation – in particular, the degradative pathways that control their abundance – is poorly understood. Previous studies report that LD proteins are degraded by the ubiquitin-proteasome system; however, the specific machinery required (e.g. E3 ligases and E2 conjugating enzymes) remains unclear. To address this question, we performed a genome-wide, fluorescence-based CRISPR/Cas9 screen to identify the degradation pathway of the LD protein perilipin-2 (PLIN2) in human hepatoma cells. We genomically tagged PLIN2 with GFP and confirmed that PLIN2-GFP localizes to LDs and undergoes proteasomal degradation. We then pharmacologically induced lipolytic clearance of LDs to promote PLIN2-GFP degradation and screened reporter cells with a whole-genome sgRNA library. Cells with PLIN2-GFP degradation defects were isolated by fluorescence-activated cell sorting and deep sequencing was used to identify genes required for PLIN2 degradation. Our preliminary data identified the E2 conjugating enzyme Ube2j2 and E3 ligase MARCH6, which have been implicated in the degradation of proteins from the early secretory pathway via a process known as ER-associated degradation. This suggests an intriguing model in which ER protein quality control machinery regulates LD protein abundance and lipid homeostasis. Future studies will elucidate how aberrations in LD protein degradation contribute to dysfunctions in cellular lipid metabolism and metabolic disease pathogenesis.

Testing the Effects of Implanted Depleted Uranium Oxide Particles on Cell and Tissue Integrity in Zebrafish Larvae.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Ronald Allen*; Phillip Kalaniopio and Matthew Salanga, *Northern Arizona University*

Abstract: A consequence of modern combat for many veterans and civilians is exposure to depleted uranium (DU) from armor piercing munitions that disperse uranium oxide (UO) particles and metal fragments upon striking hard targets. Exposure to UO can come in many modes that can result in a persistent chronic chemical burden. Research on uranium chemical toxicity raises uncertainty as to the risks associated with exposure and potential mechanisms of action. In these studies, we use zebrafish larvae subjected to UO or sham implantation to evaluate localized cytotoxic and genotoxic damage attributable to DU. We leverage the humanized zebrafish line, *Tg:mitfa:BRAF*^{V600E}, that reliably form melanoma when combined with chemical, environmental or genetic modifiers, to assess physiological outcomes - such as cell neoplasia. This unique *in vivo* system provides a methodology to test whether DU exposure induces cancer. Our prediction is that DU acts as a positive modifier for neoplasia formation in a dose dependent manner. In the presented studies, we test the feasibility for using zebrafish to examine localized tissue disruption as a consequence of DU embedment. Preliminary results show zebrafish larvae tolerate implantation with no difference in immediate mortality or attrition between the implantation and sham treatments. Furthermore, the DU particles persist for months following implantation and can be visualized by light and electron microscopy providing an excellent test subject to determine if DU causes genotoxic and cytotoxic outcomes in adjacent tissue. To our knowledge, our research represents the first intentional study of melanoma as a consequence of uranium chemical toxicity.

2:30 PM – 3:45 PM

Life Sciences: Cell/Molecular Biology & Developmental Biology

Room 313A

Applying Orca to Understand How Insulators Regulate Enhancers' Activity in *Drosophila* embryos

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Leslie Mateo* and Alistair Boettiger, *Stanford University*

Abstract: Many of the differences in cell types arise from specific interactions between distal enhancers and their target promoters. Although the three-dimensional (3D) genome organization is believed to regulate cell-type specific enhancer-promoter interactions, our understanding of what these interactions look like and how they relate to the transcriptional state within a complex tissue remain limited. I will describe Optical Reconstruction of Chromatin Architecture (ORCA), a super-resolution microscopy approach to follow the nanoscale DNA path in steps as small as two kilobases, giving an unprecedented view of chromatin organization at the single-cell level. Our method allows measurement of 3D trajectories from thousands of cells to compute the pairwise contact frequencies between any two loci and quantitatively recapitulates measurements from high read-depth Hi-C. Simultaneous imaging of nascent RNA transcripts and mature cytoplasmic RNAs allows for correlation between DNA folding and gene expression in single cells. I applied our method to examine the 3D organization of the Bithorax-Complex (BX-C) in *Drosophila* embryos. I find cell-type-specific boundaries between active and Polycomb-repressed DNA, and also observe Polycomb-independent boundaries. These boundaries contain non-coding elements known as insulators and I demonstrate that insulator site deletion leads to ectopic enhancer-promoter interactions, aberrant gene expression, and developmental defects. I will present the data and analyses as well as the genetic perturbations I am using to investigate the functional role of insulators regarding cell-type-specific enhancer activity in the 3D genome and gene expression in embryogenesis.

Analysis of Bidirectional Transfer of Mitochondria between Adipose-Derived Stem Cell and HEK293 Tumorigenic Cell.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Shalise Burch* and Carlos Luna Lopez, *California State University, San Marcos*

Abstract: Stem cell mitochondria transfer (SCMT) to injured cells has been shown to rescue oxidative phosphorylation as well as promote tissue growth and repair. However, if directed at tumorigenic cells, SCMT could enhance tumorigenesis and pose a high oncological risk. In the presence of non-tumorigenic cells, this action was activated by the transfer of injured cell mitochondria through direct-contact. Our preliminary results indicate bidirectional mitochondria transfer (MT) between adipose-derived stem cells (ADSC) and uninjured HEK293 tumorigenic cells. **We hypothesize that direct-contact and bidirectional signaling are necessary to maintain long-term mitochondria transfer.** We propose two specific aims: *Specific Aim 1:* To analyze the rate of bidirectional MT between ADSCs and HEK293. Rho0 cells depleted of mitochondria will be created for both ADSC and HEK293 to determine the dependence of bidirectional MT during short-term and long-term culture. We anticipate long-term MT occurring only between control ADSC and control HEK293 cells. *Specific Aim 2:* To measure and compare the rate of MT through direct-contact and distance-sharing between ADSCs and HEK293. Cells will be cultured in two wells separated by a removable permeable membrane to measure direct-contact and distance-sharing. We will use fluorescence microscopy and flow cytometry to quantify MT rates. We expect that TNT inhibition and distance-sharing will have lower rates than direct-contact sharing. Determining whether bidirectional sharing and direct contact is necessary for tumor growth could allow for the injection of EV rather than whole SC to potentially decrease the risk of tumorigenesis.

Mechanisms of *H. Pylori*-Induced Neutrophil Nuclear Hypersegmentation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Stephanie L. Silva-Del Toro*, *University of Iowa* and Lee-Ann Allen, *University of Iowa Inflammation Program*

Abstract: *Helicobacter pylori* is a human pathogen that resides in the gastric mucosa, eliciting a neutrophil (PMN) dominant inflammatory response that can progress to peptic ulcer disease or gastric cancer. PMNs exhibit significant functional and phenotypic plasticity, and we recently demonstrated that these cells undergo N1-like-subtype differentiation *in-vitro* following *H. pylori* infection. This phenotype is notable for profound nuclear hypersegmentation and a proinflammatory and cytotoxic phenotype. Our objective is to define the underlying mechanisms with a focus on nuclear hypersegmentation. We have shown that direct infection and both host and bacterial transcription and protein synthesis are essential. Recent studies using nocodazole and taxol identified an additional requirement for microtubule (MT) dynamics. Moreover, STED-super-resolution microscopy analysis showed that MTs are longer and more abundant following *H. pylori* infection. Inhibition by Brefeldin A and Exo1 suggested an additional role for anterograde transport, and to our surprise revealed unexpected effects of Brefeldin A on PMN microtubule dynamics. Finally, we used antibodies against lamin B receptor and STED-super-resolution microscopy imagining to analyze PMN nuclei in unprecedented detail. These data demonstrate that the volume of the *H. pylori* infected PMN nucleus is significantly increased and the PMN nuclear volume is altered when cells were treated with MT disruptors. The uniformity of distribution of lamin B receptor in the nuclear membrane was also evaluated and it is altered by drugs that manipulate MT dynamics. Altogether, our data provide fundamental insight into the mechanisms that regulate PMN nuclear morphology as well as the consequences of *H. pylori* infection.

2:30 PM – 3:45 PM

Life Sciences: Ecolocy/Evolutionary Biology

Room 313B

Physiological and Reproductive Responses of an Intertidal Rockweed to Conditions Associated with Sea Level Rise: Assessing the Potential for Local Adaptation to a Changing World.

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Ariel Heyman* and Jennifer L. Burnaford, *California State University, Fullerton*

Abstract: Organisms in the intertidal zone experience terrestrial conditions during low tide emersion and are submersed in seawater during high tide. These organisms are threatened by sea level rise (SLR) which could reduce emersion time by over 50% within the next 100 years. Using a manipulative field experiment, we are assessing the impacts of SLR conditions on the canopy-forming seaweed *Pelvetiopsis californica*. We hypothesized that individuals would perform more poorly under SLR conditions than normal conditions. At two southern California sites, we established three treatments: marked in place individuals (transplant controls: MP) were not moved; middle-zone transplant individuals (MZ) were relocated at the same tidal elevation; and below-zone transplant individuals (BZ) were moved to a lower tidal elevation, exposing them to shorter emersion times (= SLR conditions). We assessed health through monthly measurements of length, branch number, cover of epiphytic seaweeds (which grow on the host and block it from gaining light and nutrients) and Maximum Quantum Yield, a measure of photosynthetic potential. After four months, we saw reduced performance in the SLR condition treatment relative to the non-SLR treatments. The proportion of individuals infected with epiphytic seaweeds in the BZ treatment was over three times the proportion in the MZ or MP treatments, and individuals in the BZ treatment were reduced, on average, to 75% of their original length: 8.75% greater loss than in the MZ treatment. These data indicate substantial risk of SLR to seaweed populations and may help managers develop mitigation efforts for this important intertidal producer.

Revelations from a Monarch: Elucidation of Butterfly Perceptual Range to Facilitate Habitat Restoration

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Alex Mullins*; Thomas Sappington; James Adelman and Steven Bradburry, *Iowa State University*

Abstract: Monarch butterfly populations have declined precipitously over the last 20 years, largely as a result of lost breeding habitat across the U.S. Therefore, major efforts to conserve monarch populations call for the restoration of this habitat. To focus habitat restoration efforts in optimal locations, managers need better data about the distance at which monarch butterflies detect habitat. To this end, the purpose of this study was to elucidate the monarch butterfly's perceptual range, or the distance at which these butterflies detect food and oviposition resources, particularly nectar-bearing prairie plants and milkweed species. Using tethered flight experiments, we tested the perceptual range of wild-captured, non-migratory monarch butterflies by presenting resource patches at 10, 25, 50, 75 and 100 meters away. As a probe for perceptual range, we asked whether butterflies oriented toward these resource at varying distances. Videos from overhead cameras were analyzed using circular statistics to quantify orientation direction during tethered flight. Here, we present data on individual variability in orientation direction and additional factors, such as wind, butterfly size, and butterfly gender that may affect this behavior. This information will provide an understanding of the intrinsic perception abilities and landscape-level factors that affect monarch butterfly movement patterns, habitat selection, and reproductive success. These data will facilitate management decisions for placement of monarch habitat and provide a methodology for further exploration of the perceptual abilities of insects.

Do Birds Control Agricultural Pests in the Marianas?

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jerilyn Jean Calaor* and Haldre Rogers, *Iowa State University*

Abstract: Birds are thought to be important biocontrol agents in agricultural systems as their diets often include many invertebrates considered to be pests. The effectiveness of birds in pest management, however, is influenced by several factors, including mesopredator presence, leading to varying degrees of effectiveness across systems. Understanding which systems birds are effective in may help predict consequences associated with declining bird populations. Thus, we asked whether birds are effective biocontrol agents on Rota and tested the hypotheses that (1) birds control herbivorous insects, leading to reduced plant damage and increased crop productivity, but that (2) spiders respond to bird presence, influencing plant damage and productivity. We planted long beans and eggplants on three

working farms and set up bird exclosures. We surveyed the number of spiders, estimated herbivory, and counted fruits. We found that the influence of birds on plant damage and productivity varied between crops and farms. Herbivore damage did not differ between treatments, but spider abundance and fruit production did. Spider abundance was higher in the exclosure than in open treatment at one farm, but the opposite is true for the other two farms. More fruit was collected from long beans in the open treatment than the exclosure, but this difference was only significant in the farm where greater spider abundance was observed in the exclosure. This farm had a larger pest outbreak than the other two, which may drive our observed results. Overall, our findings suggest that birds are effective biocontrol agents in systems with greater pests.

Biomechanics of Terrestrial Locomotion in *Alligator Mississippiensis*

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Adrien Arias*; Angelina Ball and Emanuel Azizi, *University of California, Irvine*

Abstract: Crocodilians (e.g. alligators, crocodiles, gharials) offer a unique animal model to study the evolution of terrestrial locomotion in limbed vertebrates. Their semi-erect posture and massive tail (~28% total body mass) not only increases the overall force requirement of their limb muscles, but also shifts their center-of-mass (COM) caudally toward their hindlimbs. However, it remains unclear how these factors affect the limb joint mechanics of crocodilians during terrestrial locomotion. Here we use high-speed videography and force-plate ergometry to develop an inverse dynamics model for the limb joints in the American alligator (*Alligator mississippiensis*). We test how mechanical energy production (propulsion) and dissipation (braking) are distributed amongst forelimb (FL) and hindlimb (HL) joints during steady-state walking. Our preliminary results show the wrist and elbow spend larger percentages of stance phase flexing, whereas the ankle and knee spend more time extending. We also find a greater braking impulse in the FLs and greater propulsive impulse in the HLs, and no significant difference in mediolateral or vertical impulses between limb pairs. Furthermore, the transition from braking to propulsion occurs later in the FLs when compared to the HLs. These results highlight the disparities in limb joint mechanics between corresponding distal joints in the fore- and hindlimb of alligators and will serve as a first step in quantifying joint moments during walking. This work will improve our overall understanding of skeletal muscle function in the context of the whole-organism and will serve as a foundation for future studies investigating muscle specializations in quadrupedal walkers.

2:30 PM – 3:45 PM

Life Sciences: Ecolocy/Evolutionary Biology & Plant Sciences/Botany

Room 313C

Integrative Metabolomic, Proteomic and Lipidomic Analyses Revealed Stomatal Molecular Responses to Long-Distance Signals to Strengthen Arabidopsis Immunity to Bacterial Pathogen

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Lisa David*; Sixue Chen; Jianing Kang; Angelica Ortega and Ivan Grela, *University of Florida*

Abstract: Systemic Acquired Resistance (SAR), a plant immune response, improves immunity of systemic tissue after prior exposure to a pathogen. Stomata, pores on leaf surfaces, are formed by guard cells that recognize pathogens via recognition receptors. We found that *Arabidopsis thaliana* plants that have been previously exposed to the pathogenic bacteria *Pseudomonas syringae* pv. tomato DC3000 (*Pst*) have an altered stomatal response compared to control plants when systemic leaves are later exposed to the bacteria. *Arabidopsis* knockout mutants defective in SAR response differ in stomatal responses to the pathogen when compared to wild type plants. Altered stomatal responses lead to increases in the number of bacteria that enter the apoplastic space of the leaves, impacting bacterial growth. We hypothesize that SAR signals including metabolites, lipids, and chaperone proteins enhance stomatal immunity in systemic leaves. We used *Arabidopsis* wild type and a knockout mutant of chaperone protein DIR1 (defective in induced resistance 1) to examine SAR systemic signals in whole leaves and guard cell-enriched samples. We developed a 3-in-1 extraction method to obtain proteins, metabolites, and lipids from the same sample and used a newly developed untargeted metabolomics, proteomics, and lipidomics strategy for identification of SAR signaling components. Preliminary results have identified hundreds of molecules in SAR response in whole leaf and guard cell-enriched samples. An improved understanding of SAR immune signals can aid biotechnology and marker-based breeding for crop improvement.

Impact of Extrinsic Incubation Temperature on Flavivirus Population Structure in Mosquito Hosts

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Reyes Murrieta* and Greg Ebel, *Colorado State University*

Abstract: Arthropod-borne viruses (arboviruses) continue to emerge as major threats to public health. In part, the process of arbovirus emergence has been driven by the emergence of new virus genotypes that alter key transmission phenotypes. The conditions that lead to new virus genotypes are, however, not fully understood. Accordingly, we sought to (1) define the impact of temperature on transmission dynamics of ZIKV and (2) determine whether temperature affects virus population structure during extrinsic incubation (EI) in the mosquito. We exposed *Aedes aegypti* and *Aedes albopictus* mosquitoes to a bloodmeal containing a Puerto-Rican strain of Zika virus (ZIKV, *Flaviviridae,* flavivirus) and held them for 7 and 14 days at 25°C, 28°C, 32°C and 35°C. We also exposed them to fluctuating temperatures that varied from 25-35°C diurnally. We found that transmission of ZIKV in both *Aedes* mosquitoes is most efficient at 28°C and 32°C (P-value <0.05). Using RNAseq to characterize virus genetic diversity, we have identified consensus changes found in both *Aedes* mosquitoes associated with high temperature (28°C & 35°C) and show that EI temperature increases, so does the number of consensus changes to the ZIKV genome (25°C = 7, 28°C = 20, 25°C-35°C = 14, & 35°C = 18). We then assess the variant frequency during systemic ZIKV infection of four minority variants (frequency of 0.12-0.35) found in the input ZIKV population and show that there are temperature and mosquito dependent affects to intrahost variant frequency. Collectively, our data indicate that temperature has multiple impacts on ZIKV biology within mosquitoes.

The Mitigating Effects of Biodiversity on Drought Stress in Plants

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Beatriz Aguirre*, *California State University, Los Angeles* and Alexandra Wright, *California State University Los Angeles*

Abstract: The frequency of drought is expected to increase within the next twenty years. While some plants are adapted to withstand hot and dry weather, other plant species are more sensitive to drought. Biodiversity may mitigate some of the negative effects of drought on plant communities and help maintain ecosystem services and functions. The negative effects of drought on plant growth are due to both: a reduced water supply below ground and an increased water demand in the microclimate (VPD). We hypothesize that drought affects plant growth equally through reduced soil moisture and increased vapor pressure deficit. The negative effects of reduced soil moisture on plant growth in biodiversity field experiments are well documented; however, the negative effects of reduced air humidity and vapor pressure deficits have been neglected. We assessed the mitigating effects of biodiversity on surface soil moisture and VPD by manipulating biodiversity at two levels (8 species and monoculture), soil moisture at two levels (wet and dry), and relative humidity at three levels (ambient, desiccated, and humidified). We applied humidification treatments using the Ideal-Air Pro Series Ultra Sonic Humidifier (Vancouver, W.A.) and applied dehumidification treatments using 10-gram Dry & Dry

silica gel packets. Our approach allowed us to reduce relative humidity of the microclimate by 15% and experimentally increase relative humidity of the microclimate by 35%. Future work will assess plant responses to these increases in RH in low diversity plots and compare them with similar levels of RH found naturally in higher diversity plots.

2:30 PM – 3:45 PM

Life Sciences: Genetics & Physiology/Pathology

Room 314

The Role of Estrogen Signaling in the Sexually Dimorphic Adipose Tissue Expansion

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Rocio Saavedra* and Matthew Rodeheffer, *Yale University*

Abstract: Mammalian white adipose tissue (WAT) distribution and expansion is sexually dimorphic, with males preferentially accumulating visceral WAT (VWAT) and females exhibiting a subcutaneous WAT (SWAT) accumulation bias. Interestingly, females switch to a male-like pattern of WAT distribution after menopause when estrogen levels decline, indicating sex hormones play a role in the distribution of WAT mass, yet the molecular mechanisms governing these processes *in vivo* are not well understood. WAT expansion can occur via adipogenesis, where adipocyte precursors (APs) form new adipocytes. We have shown that indeed the activation pattern of APs in mice in on a high fat diet (HFD) is also sex-dependent, with males having robust AP activation in the VWAT and females having activation in fat depots. Interestingly, the sex-specific AP activation pattern observed occurs in an estrogen-dependent manner. Therefore, estrogen appears to be crucial for AP activation and expansion of SWAT but not VWAT. To identify the role of estrogen signaling in this process, we generated an AP-specific Estrogen Receptor alpha (ERa) knockout mice (ERa-KO), using the AP-specific PdgfRa-Cre line. Using flow cytometry proliferation assays we have found that ERa-KO males and females have AP activation in both depots and gain more fat mass on a HFD than Cre negative littermates. This indicates that ERa is not required for AP activation in WAT and perhaps is playing an inhibitory role in male SWAT expansion. Identifying how estrogen is inhibiting SWAT expansion in males will set precedent on elucidating distinct sex-dependent molecular pathways governing WAT mass expansion.

Tiger FISH - a Computational Pipeline to Design Genome-Scale Hybridization Probes to Visualize Novel Tandem Repeats

Discipline: Life Sciences
Subdiscipline: Genetics

Robin Aguilar* and Brian Beliveau, *University of Washington Seattle*

Abstract: More than half of the human genome is comprised of repetitive sequences, including tandem repeats (TRs). TRs have been implicated in shaping 3D genome organization and play a critical role in the maintenance of genome stability. Despite the biological importance of TRs, studying TRs has remained a challenge, because they are not generally accessible to sequencing-based assays and it is difficult or impossible to unambiguously map reads to TRs, which has resulted in TRs being amongst the least-studied regions of the genome. Fluorescent *in situ* Hybridization (FISH) enables researchers to visualize the distribution of RNA and DNA in fixed samples and has been employed successfully on some TRs, potentially providing an alternative to sequencing-based methods. However, to the best of our knowledge, no dedicated computational utility exists for the design of FISH probes against TR regions. Here, we present TigeR FISH – a computational pipeline that allows for the design of FISH probes for TRs on a genome-wide scale. TigeR FISH seamlessly integrates existing computational tools including Tandem Repeat Finder and OligoMiner to identify TR regions, conduct k-mer based enrichment analysis to assess specificity, and perform thermodynamic simulations to determine binding energy under a range of conditions. We will harness the design capabilities of TigeR FISH and high-throughput microscopy at the single cell level to gain insight of the role these repetitive regions play in genome organization. Furthermore, the TigeR FISH workflow may be used more broadly to facilitate the design of hybridization probes for a variety of applications genome-wide.

Gene Duplication, Pathogenicity, and Genome Plasticity of *Phytophthora ramorum*

Discipline: Life Sciences
Subdiscipline: Genetics

Nicholas Carleson*[1]; Brian Knaus[1]; Meredith Larsen[2]; Caroline Press[2] and Niklaus Grünwald[2], *(1)Oregon State University, Department of Botany and Plant Pathology, (2)Horticultural Crops Research Laboratory, United States Department of Agriculture, Agricultural Research Service*

Abstract: Clonally reproducing plant pathogens, that do not exhibit recombination to increase or maintain genetic diversity, must rely on genome plasticity and other mechanisms to adapt to environmental changes, such as different hosts. The oomycete pathogen *Phytophthora ramorum* has emerged repeatedly over the last 30 years, infecting woody hosts in forests and nurseries of North America and Europe, resulting in extensive management costs and losses despite clonality. In 2006, the Joint Genome Institute (JGI) sequenced the *P. ramorum* genome (isolate Pr-102) and reported that effectors, genes that suppress host immune response and contribute to pathogenicity, were localized in repeat-rich genomic regions, while housekeeping genes were located in separate, gene-dense regions. To explore this unique genome compartmentalization, we re-sequenced the Pr-102 genome using PacBio long-read technology. RXLR-class effectors from each genome were predicted and clustered to identify orthologous genes. We report a gapless *P. ramorum* assembly (Ns: 0, length: 75,183,546 bp, N50: 1,287,631), substantially improving the previous assembly (Ns: 12,227,865, length: 66,652,401 bp, N50: 308,042). We found 475 RXLRs in the PacBio genome, 410 of which align to all 322 RXLRs found in the JGI genome (BLAST e-value: $1e^{-4}$), leaving 65 novel RXLRs in the PacBio genome. Orthology analysis determined there were more than double the number of orthogroups with at least three genes compared to the JGI assembly, and more than triple the number with four-copy paralogs. PacBio sequencing revealed duplication of known RXLR-class effectors as well as novel effectors, evidence for contributions of genome plasticity to pathogenicity.

Mistranslation Mutagenesis: Tools for Identifying the Biological Consequences of Protein Mistranslation at the Proteome Scale

Discipline: Life Sciences
Subdiscipline: Genetics

Bianca Ruiz*[1]; Stephanie Zimmerman[1]; Judit Villen[1]; Ricard Rodriguez-Mias[1]; Stanley Fields[2]; Christopher Brandl[3] and Matthew Berg[3], *(1)Department of Genome Sciences, University of Washington, (2)University of Washington School of Medicine, (3)Department of Biochemistry, University of Western Ontario*

Abstract: Many methods exist to study the functional consequences of protein-altering mutations, but they are often limited to one protein of interest per experiment. In order to extend functional studies of protein-altering mutations to the proteome scale, the Fields and Villén labs are developing a technology called Mistranslation Mutagenesis. Our collaborators in the Brandl Lab at the University of Western Ontario have developed mistranslating tRNAs expressed in *S. cerevisiae,* which we use to introduce proline to serine substitutions across the proteome. Functional selections will be applied to the mistranslated proteome to identify destabilizing, stabilizing, or functionally neutral substitutions. I will apply selections that probe protein stability by subjecting the proteome to a gradient of temperature or pH conditions. After selection, I will analyze the soluble fractions of the proteome by mass spectrometry and determine the extent to which particular substitutions impact protein stability under selective conditions. Functional scores will be derived from stability selection datasets and will reveal the effects of substitution on proteins with respect to structure, complexing and subcellular localization. I will further process selection datasets with machine learning models, to use our data to understand how amino acid substitutions affect protein stability, and impute scores for mutations that were not experimentally measured.

2:30 PM – 3:45 PM

Life Sciences: Microbiology I

Room 315

High-Throughput Screening of Microbial Interactions Using a Photodegradable Hydrogel

Discipline: Life Sciences
Subdiscipline: Microbiology

Priscila Guzman*; Niloufar Fattahi; Ryan Hansen and Thomas Platt, *Kansas State University*

Abstract: Microbial interactions influence the structure and function of microbiomes but are often hard to study. We have developed a high-throughput strategy to screen microbe-microbe interactions using a photodegradable hydrogel. The poly(ethylene glycol) hydrogel we have developed confines bacterial cells, permits continuous cell monitoring, and allows nutrient exchange and cell growth. In order to screen microbial interactions, we grow mixtures of strains or genotypes within a hydrogel and use fluorescence microscopy to simultaneously observe the impact of thousands of strain pairings on the growth of fluorescently labeled cells. The retrieval of micro-colonies in which the growth of the focal strain is promoted or antagonized allows subsequent validation and identification of strains or mutant genotypes that influence the growth of the focal strain. We developed and illustrate the utility of this strategy with the antagonistic interaction between the plant pathogen *Agrobacterium tumefaciens* C58 and the biocontrol strain *Rhizobium rhizogenes* K84. K84 produces a bacteriocin that strongly antagonizes the growth of C58, however preliminary screens using our approach have identified C58 mutants that grow in the presence of K84. We are currently identifying the mutations that underlie C58's resistance to K84's inhibition. This new technology allows us to efficiently screen over a hundred thousand microbial interactions in order to not only identify the genetic factors influencing microbial interactions, but also the strains influencing the performance of a focal individual.

2:30 PM – 3:45 PM

Life Sciences: Microbiology II

Room 316A

Partitiviruses with Characteristics of Mutualistic Symbionts Are Extremely Common in Wild *Drosophila Melanogaster*, and Have Relatives in Mosquito Vectors

Discipline: Life Sciences
Subdiscipline: Microbiology

Shaun Cross*[1]; Bernadette Maertens[1]; Joseph Fauver[2]; Alissa Williams[1]; Brian Foy[1]; Greg Ebel[1] and Mark Stenglein[1], *(1)Colorado State University, (2)Washington University School of Medicine*

Abstract: Here, we describe our initial characterization of partitiviruses that are exceptionally common in wild populations of the model organism, *Drosophila melanogaster*. In fact, infection rates are comparable to those of the well known bacterial endosymbiont *Wolbachia*. We hypothesize that partitivirus infection is beneficial to their fruit fly hosts, which produces an advantage in relative fitness and the observed high global prevalence of infection. We have found that related partitiviruses are also common in wild mosquitoes, including vectors in the *Anopheles*, *Aedes*, and *Culex* genera. We are therefore motivated to study these viruses to test the hypothesis that they are indeed mutualists and to help us better understand arthropod biology. Partitiviruses are segmented, multipartite dsRNA viruses (family *Partitiviridae*) that until recently were only known to infect fungi, plants, and protozoans. Partitiviruses have been found a variety of arthropods and in nearly every wild population of *Drosophila* that has been examined, but little is known about their biology. We identified partitiviruses in wild *Drosophila* from Colorado and Haiti and established lab colonies of infected flies. We confirmed that partitiviruses actually replicate in *Drosophila* cells, and identified sites of virus replication in larval and adult flies. We quantified transmission routes and efficiencies, and found that these viruses can be transmitted both horizontally and vertically. In both cases, transmission from infected females was more efficient than transmission from infected males. We are pursuing additional studies to directly test the hypothesis that these viruses are mutualists, and to further understand their impact on arthropod biology.

Understanding the Synergistic Effect of β-Lactam Antibiotics and FtsZ Inhibitors Against Methicillin-Resistant *Staphylococcus aureus* (MRSA)

Discipline: Life Sciences
Subdiscipline: Microbiology

Edgar Ferrer-González* and Daniel Pilch, *Rutgers, Robert Wood Johnson Medical School*

Abstract: Antibiotic resistance is a rising global threat that needs to be addressed. According to the CDC, an estimated 2 million people per year in the United States acquire an infection caused by a resistant pathogen. Infections caused by pathogens such as methicillin-resistant *Staphylococcus aureus* (MRSA) have become difficult to treat, as resistance to current standard-of-care antibiotics (e.g., vancomycin) rises. Given the substantial morbidity and mortality associated with MRSA bacteremia along with our limited options for treating such infections, new treatments and better public health policies are needed. In order to address this problem, we have developed a promising novel anti-MRSA agent (TXA707) that targets the cell division protein FtsZ. Here we demonstrate that FtsZ inhibitors synergize with β-lactams antibiotics to which MRSA is intrinsically resistant, thereby reactivating the β-lactams. Significantly, those β-lactams antibiotics with a high affinity for penicillin binding protein 2 (PBP2) have the greatest degree of synergy with TXA707. To understand the basis of this synergy, we used fluorescence microscopy to evaluate the impact of TXA707 on FtsZ and PBP2 localization in MRSA. Toward this end, we developed two MRSA cell lines expressing FtsZ-mCherry with either PBP1-sfGFP or PBP2-sfGFP fusion proteins. Our studies reveal that TXA707 induces the co-mislocalization of both FtsZ and PBP2, while PBP1 and FtsZ do not demonstrate this co-mislocalization effect. This behavior may give rise to the synergy between TXA707 and PBP2-targeting β-lactam antibiotics that effectively lowers the resistance barrier to the β-lactams.

A Role for the SETD1B Histone Trimethyl Transferase in HIV Replication

Discipline: Life Sciences
Subdiscipline: Microbiology

Vanessa Montoya*, *University of Washington* and Michael Emerman, *Fred Hutchinson Cancer Research Center*

Abstract: At different points in the HIV life cycle, host cellular proteins are hijacked by the virus to establish and enhance infection. To identify genes that encode these dependency factors, the Emerman Lab has developed a virus-packageable HIV-CRISPR screen that targets the entire human genome. We screened for HIV dependency factors with two viral strains, one isolated late in disease progression, that uses CXCR4 as a co-receptor, and another isolated early in infection that uses CCR5 as a co-receptor. In addition to the receptor CD4, and the respective co-receptors that came through the screen as expected dependency factors, the SETD1B, scored as one of the highest hits for both strains (ranked #4thand 5th). SETD1B is a component of a histone methyltransferase complex known to produce trimethylated histone H3 at Lys4, a marker for transcriptional activation. However, its role in HIV has not been described before. To validate this observation, I knocked out SETD1B in a T cell line and consistently observed an average 5.7-fold decrease of HIV infection. During the viral life cycle, the HIV genome integrates into the cellular chromosome at transcriptionally active sites of chromatin. Therefore, I hypothesize that during HIV infection, SETD1B plays a role in regulation of HIV transcriptional activation, or alternatively that it actively methylates one of the viral proteins in a manner that favors virus replication. Experiments are underway to distinguish these two hypotheses and describe the role of SETD1B in virus replication.

2:30 PM – 3:45 PM

Mathematical Biology & Other Life Sciences

Room 316B

Med2Mech: Leveraging Neural-Symbolic Representation Learning to Estimate Molecular Mechanisms Underlying Pediatric Disease

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Tiffany J. Callahan*[1]; Adrianne L. Stefanski[1]; Michael G. Kahn[2] and Larry E. Hunter[3], *(1)Computational Bioscience Program, University of Colorado Denver Anschutz Medical Campus, (2)Department of Pediatrics, University of Colorado Anschutz Medical Campus, (3)Computational Bioscience Program, University of Colorado Anschutz Medical Campus*

Abstract: Personalized medicine requires an understanding of the molecular mechanisms underlying disease. Unfortunately, molecular data are not available for most patients. Linking knowledge from generalized molecular data to clinical patient observations would provide a solution until every patient is sequenced. We present Med2Mech, a method that employs neural-symbolic representation learning to generate patient-level embeddings of molecular mechanism. As a proof-of-concept, we compared the performance of Med2Mech to clinical concept embeddings on a subphenotyping task. *We hypothesized linking each patient's unique clinical concepts to molecular mechanisms would improve subphenotyping*. We evaluated Med2Mech using a subset of rare disease and control patients from the Children's Hospital of Colorado. First, clinical concept embeddings were generated using Doc2Vec. Then, a knowledge graph was built to generate and link mechanism embeddings to each patient. A One-vs-the-rest multiclass classification strategy, with five cross-fold validation, was used to evaluate the discriminatory ability of the mechanism and clinical concept embeddings. Precision and recall were used to evaluate performance. Finally, rare disease patient embeddings were investigated using K-Means and reviewed with a clinician. Clinical concept embeddings were built for 2,464 rare disease and 10,000 control patients using 6,382 conditions, 2,334 medications, and 272 laboratory tests. Mechanism embeddings were generated from our knowledge graph (116,158 nodes/3,593,567 edges). On classification, the mechanism embeddings (precision/recall=0.95/0.95) out-performed all parameterizations of the clinical concept embeddings (precision/recall=0.83/0.82). Clustering rare disease patient mechanism embeddings captured clinically relevant subphenotypes. These promising preliminary results suggest Med2Mech may provide a reasonable mechanism proxy in the absence of patient-level molecular data.

Analyzing Genomic Data Using Tensor-Based Orthogonal Polynomials

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Saba Nafees*; Sean Rice and Caleb Phillips, *Texas Tech University*

Abstract: Rapid increases in the availability of genomic data for diverse organisms has spurred the search for better mathematical and computational methods to investigate the underlying patterns that connect genotypic and phenotypic data. Large genomic datasets make it possible to search for higher order epistatic interactions, but also highlight the need for new mathematical tools that can simultaneously represent sequences and phenotypes. We propose a multivariate tensor-based orthogonal polynomial approach to characterize nucleotides or amino acids in a DNA/RNA or protein sequence. Given phenotype data and corresponding sequences, we can construct orthogonal polynomials using sequence information and subsequently map phenotypes on to the space of the polynomials. This approach provides information about higher order associations between different parts of a sequence, and allows us to identify both linear and nonlinear relationships between phenotype and genomic or proteomic sequence data. We use this method to assess the relationship between sequences and transcription activity levels in a large raw mammalian enhancer dataset downloaded from NCBI. We provide insights into the bioinformatics and computational pipeline necessary to curate and translate large-scale genomic data to extract and quantify complex genome-phenotype interactions.

Avian Malaria & Hawaiian Honeycreepers: Modelling of the Effectiveness of Vector Control, Captive Propagation, and Translocation for Long-Term Population Viability

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Kyle Dahlin* and Zhilan Feng, *Purdue University*

Abstract: Avian malaria, a mosquito-borne parasitic disease of birds, has been identified as a cause of the drastic decline of Hawaiian forest birds, in particular the endemic Hawaiian honeycreepers (family: *Drepanididae*). We formulated a mathematical model of the transmission dynamics of avian malaria between mosquitoes (*Culex quinquefasciatus*) and three species of honeycreeper—‘i‘iwi (*Drepanis coccinea*), ‘apapane (*Himatione sanguinea*), and Hawai‘i ‘amakihi (*Chlorodrepanis virens*)—as a system of ordinary differential equations. Reproduction numbers as well as criteria for the existence and long-term stability of disease-free and enzootic equilibrium population sizes are derived. The basic reproduction numbers exceed one for low-elevation honeycreeper populations as well as mid-elevation ‘apapane, indicating that these populations are likely partly responsible for the maintenance of active avian malaria transmission in other honeycreeper populations. We then consider the population and disease control impacts of source reduction of larval mosquito habitat and captive propagation and translocation of honeycreepers. It is shown that the elimination of enzootic avian malaria is likely impossible through the application of these management strategies alone. However, the long-term densities of honeycreeper populations residing at higher elevations may be returned to "healthy" levels through application of these strategies at appropriate intensities. Further work will determine the population impacts of management scenarios that incorporate modern forms of vector control such as sterile-insect techniques or *Wolbachia*-based methods.

Distributional Patterns and Variation in the Microbiome of *Aedes albopictus* (Diptera: Culicidae) on Maui, Hawai'I

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Priscilla Seabourn*; Helen Spafford and Matthew Medeiros, *University of Hawaii at Manoa*

Abstract: The mosquito microbiome alters the physiological traits of medically important mosquitoes, influencing its ability to sustain disease transmission. The microbiome is defined as a community of microorganisms that live on or within a host organism. The composition of the mosquito microbiome varies significantly across mosquito populations. However, the factors that contribute to this variation are poorly understood. To further understand the factors that influence variation and diversity of the microbiome of mosquitoes, a survey of the mosquito microbiome was conducted in the medically important mosquito, *Aedes albopictus.* Adult mosquitoes were sampled on the island of Maui across an entire sampling year at nine sites that differed in climate. Microbial diversity was assessed by next generation sequencing technologies that enabled us to identify bacterial taxa and measure their abundance and diversity in mosquitoes. The results indicate that the microbiome of *Aedes albopictus* on Maui was dominated by *Wolbachia* and several genera within *Enterobacteriaceae*. *Wolbachia* live within host cells and are inherited from the mother very early in development, whereas the bacteria *Enterobacteriaceae* are acquired from the environment during development. The diversity of other bacteria varied between sampling sites. These results give a snapshot of the influence that the environment has on the microbial diversity and variation of mosquitoes. Future analyses will reveal how other organisms influence microbiome variation of *Aedes albopictus*. To our knowledge, this is the first study that has assessed the diversity and variation of the microbiome of a medically important mosquito in Hawai‘i.

2:30 PM – 3:45 PM

Organic Chemistry, Biochemistry & Other

Room 323B

Determining the Active Site Base of F_{420} Cofactor Dependent Glucose-6-Phosphate Dehydrogenase from *Mycobacterium Tuberculosis* using Steady-State, Pre Steady-State and Kinetic Isotope Effect Methods

Discipline: Chemistry
Subdiscipline: Other Chemistry

Lindsay Davis*[1]; Mercy Oyugi[1]; Ghader Bashiri[2]; Edward Baker[2] and Kayunta Johnson-Winters[1], *(1)University of Texas at Arlington, (2)University of Auckland*

Abstract: F_{420}-dependent Glucose-6-Phosphate Dehydrogenase (FGD) is vital to the existence of *Mycobacteria tuberculosis*, the causative agent of TB disease. FGD catalyzes the conversion of glucose-6-phosphate (G6P) to 6-phosphogluconolactone, using F_{420} cofactor, which becomes reduced during catalysis (Figure 1). The cofactor is necessary for *Mycobacteria* to exist and proves to be mechanistically important for activating pro-drugs that treat tuberculosis disease. This reaction is the first step of the pentose phosphate pathway, which creates precursors for nucleic acid biosynthesis. A previous crystal structure of wild-type FGD led to a proposed mechanism, suggesting that the conserved His40 residue served as the active site base, while Glu109 served as the active site acid. Our previous work using pH dependence profiling has suggested that Glu109 is the active site acid, while His40 does not serve as the active site base. The goal of this present work is to determine which active site amino acid could serve as the active site base. Our results from pH dependence profiling studies reveals that Glu13, Lys259, Arg283, and His260 do not serve as the active site base. Recent global analysis studies from pre-steady state kinetic experiments reveal an intermediate is present in wtFGD during catalysis.

Catalytic Oxidation for Recycling Carbon Fiber Reinforced Polymer Composites

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Carlos Navarro*; Katelyn Michael; Yijia Ma and Travis Williams, *University of Southern California*

Abstract: There is no efficient recycling method for polymer-carbon fiber composite material scrap or end-of-life waste. The strong chemical bonds of thermoset polymers hold the carbon fibers rigid and form the backbone of these strong, lightweight materials, but it also complicates their recycling. Current recycling procedures utilize physical processes (pyrolysis, solvolysis) that are energy-intensive, destructive, and fail to recover the maximum value from these highly engineered and expensive materials. We believe that if the resin chemistry is the problem, the chemistry can also be the solution.

To this end, we have synthesized small molecule analogs of the overall resin structure and studied how they decompose under acidic peroxide conditions. We report that dealkylation of these anilines proceeds through formation of an *N*-oxide species, followed by imine formation and hydrolysis to cleave the carbon - nitrogen bond formed during curing. Unfortunately, applying these conditions to a composite sample reveals these reagents are too harsh and lead to over-oxidation, destroying the valuable resin.

With this knowledge, we are developing manganese and aluminum catalysts that can perform this depolymerization under milder conditions using air as the terminal oxidant. Applying our aerobic catalysts to model resin systems for 24 hours completely homogenizes the sample and derivatized organics can be recovered for re-use – an industry first! We continue to develop and optimize these catalysts to maximize their efficiency. We have since patented this technology and hope to apply this in industry.

Nickel-Substituted Rubredoxin As a Model Protein Scaffold for Hydrogen Production: A Handle for Understanding Catalysis

Discipline: Chemistry
Subdiscipline: Other Chemistry

Regina Trevino*; Jeffrey Slater and Hannah Shafaat, *The Ohio State University*

Abstract: Nature's hydrogenases are exemplary examples of efficient bi-directional catalysts for hydrogen production and oxidation, while utilizing earth abundant metals, nickel and iron, in their active sites.[1,2] However, the study and utilization of these enzymes is challenging due to their sensitivity towards oxygen and mutagenesis and lack large scale production. Using nature as inspiration, replicating the active site of these enzymes while conserving the control and selectivity of the secondary sphere within a protein construct should result in similar activity seen with the enzyme. Rubredoxins (Rd) are robust electron transfer proteins with a tetrathiolate, mononuclear metal center that natively binds iron (FeRd); however, this active site metal can be exchanged for a variety of different metals without compromising the oxygen tolerance. Previous reports have demonstrated that nickel-substituted rubredoxin (NiRd), with an identical primary sphere coordination at the nickel center as the native enzyme, is a structural, functional and mechanistic mimic of the [NiFe] hydrogenase. This model is active for proton reduction, both electrochemically and in solution.[3–5] Covalent attachment of Rd directly onto graphite electrodes shows outstanding electrochemical stability for over 30 days. Ongoing work focuses on the careful tuning of the primary coordination sphere to correlate changes in structure and electronics to changes observed in catalysis. Optical and vibrational spectroscopy are employed along with the electrochemical characterization of these artificial enzymes to relate structure and catalytic performance. Understanding the mechanism of NiRd during catalysis allows for further modification of the catalyst, while also providing a handle towards next-generation catalyst optimization.

Differential Effects of Etoposide-Polyamine Derivatives on Topoisomerase IIα- and IIβ-Mediated DNA Cleavage

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alexandria Oviatt* and Neil Osheroff, *Vanderbilt University*

Abstract: Etoposide is a widely-prescribed antineoplastic agent that induces cell death responses by enhancing and stabilizing DNA cleavage mediated by human topoisomerase IIα and IIβ. Though the drug has been useful in many cancer treatments, the high rate of secondary leukemias that result from etoposide administration highlight the need for increased drug specificity. The relative roles of the two isoforms in promoting either cell death or recombination pathways upon drug treatment are unclear. To increase the specificity of etoposide, a derivative that replaces the C4 sugar moiety with a spermine substituent on the etoposide core was synthesized [Barret et al. (2008) Cancer Res. 68, 9845-9853]. This compound, F14512, exhibits increased potency and efficacy against multiple cancer cell lines that encode active polyamine transport systems. However, the respective contributions of the α and β isoforms to F14512 activity are also ill-defined. In order to assess the effect of the polyamine moiety on drug specificity, we analyzed the activity of etoposide-polyamine hybrids toward topoisomerase IIα and IIβ. All derivatives enhanced enzyme-mediated DNA cleavage to an extent equal to or greater than that of etoposide. In particular, the hybrids dramatically induced double-stranded DNA scission mediated by topoisomerase IIβ when compared to the parent drug. The difference was more moderate with topoisomerase IIα. Modeling studies suggested that this difference is a result of key contacts that the polyamine tails are able to make with a glutamine residue in the drug binding site in topoisomerase IIβ that the analogous methionine in topoisomerase IIα does not support.

2:30 PM – 3:45 PM

Professional Fields, STEM Education & Learning, Animal Sciences/Zoology

Room 318AB

How Teacher Practices and Students' Perceptions Intersect Via Adolescents' Mathematics Identity: Effects on Mathematics Achievement

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Luis Fernandez*; Damon Gaddis and Rebecca Callahan, *The University of Texas at Austin*

Abstract: In response to recent interest in adolescents' mathematics identity formation and its implications for achievement, this quantitative study explores teachers' mathematical pedagogies and students' perceptions of teacher equity as they relate to mathematical identities and achievement. Using a nationally representative dataset, HSLS:2009, multiple linear regression analyses reveal that students' mathematics identity is strongly associated with mathematics achievement, even after accounting for prior achievement and other covariates. Moreover, teachers' use of abstract-thinking mathematics pedagogy (i.e., developing problem-solving skills, learning how to reason mathematically, and exploring logical structures in mathematics) and students' perceptions of teacher equity show a strong association with mathematics identity. Our results suggest that teacher instructional practices, both pedagogical and equity-oriented, merit further research with respect to the development of mathematics identity and overall mathematics achievement.

Review of Mobile Applications for the Detection and Management of Atrial Fibrillation

Discipline: Other
Subdiscipline: Other Professional Fields

Victoria Jimenez*; Samuel Isaac; Munther Alshalabi; Ruth Masterson Creber and Meghan Reading Turchioe, *Weill Cornell Medical College*

Abstract: **Introduction**: Atrial Fibrillation (AF) is a cardiac arrhythmia affecting an estimated 6 million people.[1] Advances in mobile health (mHealth) have made it possible for patients to monitor and manage cardiac conditions at home.[2] However, there is little guidance for patients and clinicians on which commercially available mHealth applications (apps) to choose for managing AF.

Objective: This review aimed to investigate commercially available applications and assess their functionalities for monitoring and managing AF.

Methods: We used a previously established methodology for this review.[3] Relevant apps from three major app marketplaces were identified using patient-related search times. We screened apps based on pre-specified inclusion/exclusion criteria. The final list of included apps were evaluated using the Mobile Application Rating Scale (MARS), IMS Institute for Healthcare Informatics functionality scores, and consistency with general AF management guidelines, in absence of patient-specific self-management guidelines.[4,5]

Results: Our review identified 1,473 potentially relevant apps; 13 met final inclusion criteria for evaluation. Nine of 13 apps had MARS scores of 3.0 or greater, which is the minimum acceptability score. There was high interrater reliability among the four reviewers (IRR=0.75-0.83). Of the apps evaluated, Afib Companion had the highest overall MARS score (4.1). None of the apps adhered to all the evidence-based guidelines for AF management.

Conclusion: A review of current literature reveals promising avenues for clinically validated apps that leverage native smartphone capabilities. Future app development should aim to engage with clinician expertise and offer greater functionality to better meet the self-management needs of this patient population.

Evaluating the Impact of an Animal Ambassador Program on African Penguin Welfare

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Sana Saiyed*, *Department of Anthropology, University of Notre Dame*; Lydia Hopper, *Lester E. Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo* and Katherine Cronin, *Animal Welfare Science Program, Lincoln Park Zoo*

Abstract: Animal ambassador programs, which allow people to be in close contact with wildlife while learning about animal care, biology, and conservation, are increasingly prevalent in zoos due to their popularity with guests. Yet, few studies have investigated their impact on animal welfare. We assessed the effects of an ambassador program on a colony of 15 African penguins (*Spheniscus demersus*) at the Lincoln Park Zoo in Chicago, Illinois. We used affiliative and aggressive interactions between penguins as a proxy for *S. demersus* welfare. Behavioral data were collected for 16 weeks and included 43 'Penguin Encounters' during which zoo visitors entered the penguins' enclosure. We compared colony behavior preceding and following encounters to behavior during matched control periods lacking an encounter. We found no significant differences between affiliative or aggressive behaviors during these times, suggesting that the encounters did not disrupt interactions in the colony. We also measured penguin temperament on the shy-bold continuum by recording the birds' response to novel objects and found that temperament, age, and sex predicted voluntary participation in the program. We conclude that 'Penguin Encounters' had a neutral or positive impact on penguin welfare, and consider this in relation to aspects of the program that provide penguins' control over their individual involvement.

"Visit, Meet, and Walk the Land Together": A Policy Analysis & Case Study on Tribal Nation and US Forest Service Relationships

Discipline: Other
Subdiscipline: Other Professional Fields

Jessica Lackey* and Mae Davenport, *University of Minnesota Twin Cities*

Abstract: In 1988, Chief of the United States Forest Service F. Dale Robertson affirmed the agency's dedication to working towards a mutually beneficial relationship with Native American peoples and appointed its first tribal relations coordinator. However, such formal relationships between Native American tribes and the US Forest Service have not always been present. In fact, it was during the formation of the US Forest Service Agency and the National Forest System that the 1887 General Allotment Act was at its peak; while the National Forest System grew extensively, tribal nations were losing overwhelming amounts of land. The past 30 years has seen a number of Federal policies created in support of the active involvement of tribal nations in the management of public lands. Furthermore, there has been an increase in the assertion of Native American voices and powers in the decision-making processes involved in National Forest management plans. My research focuses on how Federal Indian Policy and Federal policies that formed the US Forest Service have interacted and shaped tribal nation and federal government relationships within our National Forests. An analysis of public policies and historical documents on a broad scale were utilized to inform this research. A case study site, the Medicine Wheel/Medicine Mountain National Historic Landmark in the Bighorn National Forest in Wyoming, was focused on in order to illustrate how national policies and tribal assertion have affected the decision-making and management of a specific site within the National Forest System.

2:30 PM – 3:45 PM

Public Health, Medicine & Pharmacology

Room 323C

Community Engaged Participatory Approaches to Improve STD Screenings in Vulnerable Populations

Discipline: Health
Subdiscipline: Public Health

Nixon R. Arauz* and Dina Garcia, *Virginia Commonwealth University*

Abstract: **Background**

Community engaged (CE) participatory approaches help address systemic disparities exacerbated by the persistent social determinants of health (SDH) affecting vulnerable populations. Identifying and addressing these prominent determinants maximizes intervention effectiveness and sustainability. The Community Approaches to Reducing Sexually Transmitted Diseases (CARS), is a Centers for Disease Control and Prevention (CDC) funded project that utilizes CE participatory approaches to

design and implement STD prevention interventions to address the SDH to improve STD screening in vulnerable communities, and to examine the relationship between STD screening and STD/HIV positivity rate.

Methods

Four sites across the U.S. implemented the CARS program from 2011 to 2014. At each site, CARS grant recipients established a community advisory board (CAB) that used mixed methods approaches (i.e. focus groups, town halls, street surveys, key informant interviews, site visit reports, and quantitative evaluation) to identify the prominent SDH to reduce STDs and to develop interventions to address them.

Results

The significant determinants of health identified by CAB members included: education, gang and domestic violence, community physical environment, and incarceration. To address these determinants, CAB members designed interventions like GED classes, health fairs, STD screening services, resume workshops, and a felony friendly employers list. A total of N=1300 people were screened, which resulted in an average of 17.6% STD/HIV positivity rate.

Conclusion

CE participatory approaches to address STD disparities can be used to improve the health outcomes of vulnerable populations. These interventions empower communities to take the appropriate actions for policy and structural change to address prominent SDH, improve population health.

Glutathione-S-Transferases Represent a Novel Pathway Contributing to the Metabolic Clearance of the Anti-Cancer Agent and Aromatase Inhibitor, Exemestane

Discipline: Life Sciences
Subdiscipline: Pharmacology

Irina Teslenko*; Gang Chen; Zuping Xia; Christy J. W. Watson and Philip Lazarus, *Washington State University*

Abstract: Exemestane (EXE) is an endocrine therapy used to treat estrogen receptor positive (ER+) breast cancer in postmenopausal women by inhibiting aromatase enzyme in the final step of estrogen biosynthesis. Inter-individual variability exists in overall patient response and adverse events that may be attributed to variation in EXE metabolism. Preliminary studies have demonstrated that cysteine conjugates of EXE and its active metabolite 17β-dihydro-EXE (17β-DHE) comprise 77% of total EXE metabolites in urine of patients. The initial step in cysteine conjugate formation is glutathione (GSH) conjugation catalyzed by the glutathione-S-transferase (GST) family of the enzymes. The goal of the present study was to identify hepatic GSTs active in the metabolism of EXE and 17β-DHE. A total of 12 cytosolic GSTs were found to be hepatically expressed and were either purchased or produced as recombinant histidine-tagged proteins using an E-coli expression system. The GSTs were screened by incubating GSH with EXE or 17β-DHE (125 μM) using 0.5 μg of pure recombinant protein. GS-conjugates of EXE and DHE were detected using UPLC-MS/MS. Results from the EXE-GS conjugation assays indicate that the cytosolic enzymes GSTA1, GSTM3, GSTP1 and GSTT1 are active against EXE and marginally active against 17β-DHE, with GSTA1 exhibiting the highest relative activity. K_M values for human liver cytosol (HLC) (44.6±8.35 μM) and GSTA1 (77.3±25.0 μM) indicate that GSTA1 may be the main driver of EXE conjugation in human liver cytosol and that GSH conjugation by GSTA1 may be an important metabolic pathway contributing to elimination of EXE in patients.

Macrophage Cytological Profiling and Anti-Inflammatory Drug Discovery

Discipline: Life Sciences
Subdiscipline: Pharmacology

Tannia Lau*, *University of California Santa Cruz* and Scott Lokey, *University of California, Santa Cruz*

Abstract: Millions of people are affected by diseases and conditions related to the immune system. Unfortunately, our current supply of approved anti-inflammatory medicine is very limited and only treats a small fraction of inflammatory diseases. Natural product (NP) drug discovery is critical to generate diverse chemical compounds, and developing methods to elucidate their modes of action (MOA) will inspire the next generation of novel therapeutics. However, there are no well established high-throughput screening methods for the direct prediction of compound MOA in an inflammatory context. We have shown that Cytological Profiling (CP) in HeLa cells is a valuable tool to give insights about the potential MOA of lead compounds at the primary screening stage based on a limited staining set that probes the cell cycle, organelles, and the cytoskeleton. However, current CP methods utilize cancer cell lines and only 30% of the reference library showed any discernable phenotypic effect. In order to address this issue, I am developing a high-content screen that utilizes lipopolysaccharide (LPS)- macrophages to capture bioactive compounds that are involved in pathways related to the innate immune response. We expect that with the addition of the LPS stimulus, will refine the ability of CP to cluster compounds that engage and inhibit specific signaling pathways involved in a diseased inflammation state, not seen in resting cells. I anticipate that training the +/- LPS macrophages with the annotated chemical libraries and fitting the NP extract fingerprints to those clusters will dramatically improve our ability to identify novel anti-inflammatories from NPs.