

PR-01

Individual Differences in Talking Enjoyment: The Role of Prenatal Testosterone

Shelia Kennison (Oklahoma State University), Azucena Gonzalez (Bethel College)

Prior research has found conflicting results regarding the extent to which women talk more than men. A recent study failed to observe sex differences in talking, while prior studies observed small differences. In a study published in *Science*, Mehl, Vazire, Ramírez-Esparza, Slatcher, and Pennebaker (2013) collected speech samples using the electronic activated recorder (EAR) and found no significant differences in the number of words used by men and women. In the study, participants wore a recording device during their waking hours of a period of several days. In the present study, we developed the talking enjoyment scale (TES); the six item TES was found to have high internal consistency ($\alpha=.90$). The present research tested the hypothesis that there are individual differences in talking behavior for both men and women and these differences are related to prenatal exposure to testosterone (as reflected in 2D:4D ratio). The results confirmed the hypothesis for men, showing that talking enjoyment was significantly related to 2D:4D digit ratio. Men who were exposed to higher levels of testosterone prenatally reported less talking enjoyment. The results suggest that individual differences in talking enjoyment may have a biological basis.

Key Terms: Sex Differences
Psycholinguistics
Hormone

PR-02

Extremophiles in Biofuel Synthesis

Rajesh Sani (South Dakota School of Mines and Technology)

The Homestake gold mine (8000 ft. deep, Lead, SD) offers a unique opportunity for direct exploration of the deep biosphere environment. This mine is now known as the Sanford Underground Research Facility -SURF. In past seven years, we have collected water, soil, sediment, and biofilm samples from the 300, 2000, 4400, 4850, and 5000 ft. levels below the surface of the earth. Using PhyloChips, clone libraries, and various enrichments results show that SURF harbors a significant microbial diversity including archaea, unclassified (novel) microbes, and unique organic polymer-degrading and -fermentative bacteria. SURF microbial diversity compared well at phylum level with other gold mines. The common bacterial phyla were *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Chlorobi*, *Chloroflexi*, *Firmicutes*, *Gemmatimonadetes*, *Nitrospirae*, *Proteobacteria*, and candidate divisions OP10 and TM7. Extremophiles and their enzymes will likely play important roles in many kinds of bioprocessing including in conversion of non-food biomass into biofuels. Therefore using various enrichments, we have isolated several thermophilic microbial strains having highly thermostable enzymes for lignocellulosic degradation. For example endoglucanase, β -glucosidase, and endoxylanase showed remarkable residual activity (>50%) after prolonged incubation (96, 76, and 288 hours, respectively) at 70°C. Using mine thermophiles and thermostable enzymes, a novel form of consolidated bioprocess which will convert lignocellulosic wastes into bioenergy (e.g. biohydrogen, biopolymers) is currently being developed. The significant and immediate impact of ongoing research will be not only on biofuel research, but also on the national economy through the development of an efficient, economical, and sustainable biofuel production process.

Key Terms: Bioprocessing
Extremophiles
Lignocellulosic biomass

PR-03

University of Kansas particle physics with the CMS experiment at CERN's Large Hadron Collider

Philip Baringer (University of Kansas)

The particle physics group at the University of Kansas works with the CMS experiment at CERN's Large Hadron Collider. One of our data analysis efforts led to the discovery of a new production mechanism for top quarks – the production of a single top quark in association with a W boson. The group is also involved in efforts to improve the innermost part of the CMS detector with a redesigned solid state tracking device that uses silicon pixels to measure precise locations of particles.

Key Terms: Particle physics
Experiment
Hadron collider physics

PR-04

Comparative Analysis of Antibacterial Properties of Three Varieties of *Hibiscus Sabdariffa*

K' Ashley Collins (Huston Tillotson University); Ashlee Washington (Tuskegee University), Willard Collier (Tuskegee University), Mohamed Abdalla (Tuskegee University)

The *Hibiscus sabdariffa* is widely used as a medicinal herb plant for the treatment of various diseases. The objective of this study was to extract and analyze chemical compounds from three varieties of *H. Sabdariffa* for their antimicrobial properties. Three products from three *H. sabdariffa* varieties (Rico Red, Thai Red and a commercial brand) were extracted from 5g of dried calyces using 40 mL of ethanol at 55° C and 80 RPM on a shaking bath for one hour. Each extract was concentrated to 2 mL of ethanol using rotavap at room temperature. The ethanol extract of each hibiscus variety was investigated for its antimicrobial properties on *Staphylococcus aureus* and *E.coli* bacteria using Rapid Diffusion Assay. Inhibition zones were indicated by a lack of bacterial growth into tryptic soy agar culture medium beneath the hibiscus-impregnated disks. The results showed that the most potent hibiscus against *Staphylococcus* bacteria was the Thai Red. In contrast, the zone of inhibition for Rico Red and the commercial brand extracts were smaller in size in comparison to the Thai Red. In the *E.coli* bacteria plates, there were no significant differences among the zones of inhibition for the three extracts. Overall, these results indicated that the three plant extracts from *Hibiscus sabdariffa* are equally effective against most of the common foodborne pathogens. For further analysis, column chromatography was used to separate the natural products from each extract. These fractions are currently being analyzed for their antimicrobial agents using NMR and LC/MS.

Key Terms: *Hibiscus sabdariffa*
Antimicrobial activity
Staphylococcus



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PR-05

Linking Cognitive Impairment to Human Temperament Across Adulthood: Biological Bases of Executive Functioning?

Joseph McFall (State University of New York at Fredonia), Amanda Cocchiara (State University of New York at Fredonia), Hailey Griewisch (State University of New York at Fredonia)

Severe personality changes are anecdotally described as symptomatic of cognitive impairment, especially after diagnosis of dementia; however, little is known about whether there are pervasive systematic personality changes, what mechanisms drive them, and when they would be evident amid the variability of everyday behavior. Ideally, a simple measure of "personality changes" could indicate dementia risk and necessitate follow-up testing for cognitive impairment. A myriad of research has measured personality characteristics, but personality is constrained to social context. Temperament is a more biologically-based approach to defining behavioral patterns, but no research links temperament to adult cognition. We modified Thomas and Chess's classic dimensions of temperament to create an Adult Temperament Rubric. We also administered the Montreal Cognitive Assessment (MoCA). Among Older Adults, Age (73-98 years, $M=87$, $SD=7$) was not correlated with MoCA scores nor the Temperament Rubric total score (high scores=more desirable characteristics). However, the Temperament was positively correlated with MoCA ($r=.74$, $p<.001$), especially the dimensions of Purpose ($r=.82$, $p<.001$), Persistence ($r=.77$, $p<.001$), and Distractibility ($r=.76$, $p<.001$). Moderate correlations were found for Self-Criticism ($r=.49$, $p=.023$) and Activity ($r=.47$, $p=.029$). No correlation was found with Irritability and Mood. Results align with expectations that impaired executive functions would lead to noticeable changes in persistence and distractibility. We also examined a control group of 40 Younger Adults (18-23 years, $M=19$, $SD=1$). Again, Age was not correlated with the MoCA; however, neither was Temperament. There were typical Age-related differences in MoCa among our sample, but Older Adults had more desirable Temperament scores than Younger Adults.

Key Terms: Cognition
 Psychology
 Temperament

PR-06

Histology for the World

Larry Johnson (Texas A&M University)

Knowledge of histology is important in the understanding of cell biological structure and function, disease states, and therapeutic treatment. Digital histologic images, online lessons (PowerPoint presentations), and YouTube videos provide a mechanism to bring high quality histology to the world with visualizations available anywhere and anytime without the need for a microscope. The objective was to make histologic information available worldwide at no cost with the intent to help educate the world. YouTube videos and PowerPoint lessons covering most of the body have been made for three groups of students (freshmen undergraduate, upper-class undergraduate and medical students; <http://www.youtube.com/vibshistology>). PowerPoint lessons covering most of the animal body has been made for veterinary students. The PowerPoint slides have hyperlinks to access the corresponding digital histologic images (<http://peer.tamu.edu/histology.asp>). Students can visualize (on computer, tablet, or phone) these digital images as if they were looking through a microscope themselves. Currently, we have an online histology class for 94 freshmen/sophomore undergraduate students using these resources. As of 9/22/2015, our YouTube channel has enjoyed 3,280 subscribers and received 234,867 views since joining YouTube 1/14/2013. Only one third of these views were from the USA. The videos have received several comments from all over the world. One medical student from South Africa commented that "she needed a histology instructor and now she has a virtual one."

Key Terms: Histology
 Digital
 Video

PR-07

Evolutionary Patterns of an Emerging Pathogen: A Decade of Mutation in the VHS Fish Virus Since Its First Appearance in the Laurentian Great Lakes

Carol Stepien (University of Toledo), Megan Niner (University of Toledo), Lindsey Pierce (University of Toledo), Douglas Leaman (University of Toledo)

The RNA rhabdovirus Viral Hemorrhagic Septicemia virus (VHSV) causes one of the world's most serious fish diseases, infecting >80 species. A new, novel, and especially virulent substrain -VHSV-IVb- appeared in the Great Lakes about a decade ago, with massive fish kills, rapid spread, and diversification. We analyzed its temporal and spatial mutational patterns for the novel non-virion (*Nv*) gene that is unique to novirhabdoviruses, in relation to its glycoprotein (*G*), phosphoprotein (*P*), and matrix (*M*) genes. Results show that the *Nv*-gene has been evolving the fastest ($k=2.0 \times 10^{-3}$ substitutions/site/year), with the *G*-gene at $\sim 1/7$ that rate. Most (all but one) of the 12 unique *Nv*- haplotypes encode different amino acids, totaling 26 changes. The 12 corresponding *G*-gene haplotypes had seven amino acid changes. The *P*- and *M*- genes are more evolutionarily conserved, evolving at just $\sim 1/15$ of the *Nv*-gene's rate. The 12 isolates contained four *P*-gene haplotypes with two amino acid changes, and six *M*-gene haplotypes with three. Patterns of evolutionary changes coincided among the genes for some isolates, but appeared independent in others. New viral variants were discovered following the large 2006 outbreak; such differentiation may have been in response to fish populations developing resistance. Two 2012 variants from central Lake Erie fish lacked classic VHSV symptoms, having genetically distinctive *Nv*-, *G*-, and *M*-gene sequences (with one also differing in the *P*-gene. Such rapid evolutionary differentiation may allow new viral variants to evade fish host recognition and immune responses, facilitating longtime persistence along with expansion to new geographic areas.

Key Terms: Virus
Quasispecies
Host-pathogen coevolution

PR-08

Indoor Environmental and Air Quality Characteristics, Building-Related Health Symptoms, and Worker Productivity

Tee Guidotti (Medical Advisory Services), David Lukcso (Medical Advisory Services), Don Franklin (Building Health Sciences), Allan Burt (Building Health Sciences)

We investigated environmental conditions in a government building complex with a history of persistent occupant complaints by environmental monitoring and an on-line health survey that was completed by 7,637 building occupants (49% response rate). Building environmental measures were within current standards and guidelines, with few outliers. Four environmental factors were consistently associated with group-level building-related health complaints: physical comfort/discomfort, odor, job stress, and glare. Several other factors were frequently commented on by participants including cleanliness, renovation and construction activity, and noise. Low relative humidity was significantly associated with lower respiratory and "sick building syndrome"-type symptoms. No other environmental conditions correlated directly with individual health symptoms. Indicators of atopy or allergy (sinusitis, allergies, and asthma) when present singly or in combination were hierarchically associated with increased absence, increased presentism (presence at work but at reduced capacity), and increase in reported symptom-days, including symptoms not related to respiratory disease. In buildings without unusual hazards and with environmental and air quality indicators within the range of acceptable indoor air quality standards, there is still an identifiable population of occupants with a high prevalence of asthma and allergic disease who disproportionately report discomfort and lost productivity due to symptoms, more closely associated with host factors than with environmental conditions. We conclude that when the building and its work areas are within regulatory standards and industry guidelines, building-related health complaints are best investigated at the work-area level with an occupant-centered medical evaluation to guide environmental investigations.

Key Terms: Indoor air
Work environment
Health

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PR-09

Childhood Lead Poisoning Hot Spots in Tennessee and Hamilton County

Dawn Ford (The University of Tennessee at Chattanooga), Nyssa Hunt (The University of Tennessee at Chattanooga)

Lead exposure can cause serious health problems in children. In 2012, the Centers for Disease Control and Prevention lowered the reference level for childhood lead poisoning from 10 $\mu\text{g}/\text{dL}$ to 5 $\mu\text{g}/\text{dL}$. The purpose of this study was to describe childhood lead poisoning in Tennessee and identify high-risk geographic areas by census tract in Tennessee and Hamilton County associated with low, medium, and high child blood lead levels (BLLs). Archival data were used of 127,627 children under the age of 6 with a detectable BLL reported to the Tennessee Department of Health between 2009 and 2013. Across Tennessee, Memphis and Northeast Tennessee were found to be high-risk areas for all BLLs, and the highest BLLs were characterized by unique high-risk areas in Southeast Tennessee (including Hamilton County) and Northwest Tennessee. In Hamilton County, the high-risk areas were in South Chattanooga and Soddy Daisy for all BLLs. These results can help public health agencies move towards Healthy People 2020 goals for childhood lead poisoning.

Key Terms: Environmental health
 Geographic information systems
 Childhood lead poisoning

PR-10

Updates to *Conflict in History* Book

Dennis Collins (University of Puerto Rico-Mayaguez retired)

The poster presents updates to the 2011 book *Conflict in History, Measuring Symmetry, Thermodynamic Modeling and Other Work* by Dennis G. Collins, Author House, Bloomington, IN. The book and updates show how history is dominated by one pattern, over different scales (wavelets); symmetry is based on counting the number of pairs of equal distances; and social science extends from Josiah Willard Gibbs' thermodynamic models. Attempts to measure "emergy" as developed by H.T. Odum (U of Florida 2014), to make conflict "weather" forecasts (Kewanna, IN 2013-2015), to extend the genetic code to quadruples including metals (U of Southern Indiana 2014), and to explain how a curved space could appear flat (Washington U St. Louis 2014) may be included.

Key Terms: Symmetry
 Quantum History Institute
 Genetic Code

PR-11

Respiratory Syncytial Virus Serum Neutralizing Antibodies in Infants Target the Prefusion Form of the F Protein More Strongly Than the Attachment Protein

Cristina Capella (The Research Institute at Nationwide Children's Hospital), Erin Gorell (The Research Institute at Nationwide Children's Hospital), Supra-nee Chaiwatpongsakorn (The Research Institute at Nationwide Children's Hospital), Zachery Risch (The Research Institute at Nationwide Children's Hospital), Fang Ye (The Research Institute at Nationwide Children's Hospital), Sara Johnson (The Research Institute at Nationwide Children's Hospital), Octavio Ramilo (The Research Institute at Nationwide Children's Hospital and The Ohio State University), Asuncion Mejias (The Research Institute at Nationwide Children's Hospital and The Ohio State University), Mark E. Peeples (The Research Institute at Nationwide Children's Hospital and The Ohio State University)

Respiratory syncytial virus (RSV) is the most frequent cause for hospitalization in infants. Neutralizing antibodies (nAb) play a major role in the defense against RSV infection. The RSV G and F glycoproteins are responsible for virion attachment to target cells and fusion of the virion and cell membranes to initiate infection, as such they are the only targets for nAb. The F protein exists in two configurations. Prefusion F protein is the active form present on the surface of the virion and is responsible for causing membrane fusion to initiate infection. The F protein is in its postfusion form at the end of this process, and cannot return to the prefusion state. No studies have yet quantified the levels of serum antibodies to the prefusion F glycoprotein or to the attachment (G) glycoprotein, or the relative roles of these serum antibodies in neutralizing the virus. We expressed and purified recombinant soluble versions of each of these proteins to characterize the antibodies in serum from acutely infected children ≤ 2 years of age, diagnosed with their first episode of RSV bronchiolitis. We established ELISA assays to quantify antibodies against the prefusion F, postfusion F and the G proteins. We found that serum from acutely infected infants contain at least 3-fold more IgG antibodies against the prefusion form of the F protein compared to the postfusion F and the G proteins. To test the neutralizing function of these

antibodies we pre-absorbed sera with each of these soluble proteins before adding virus and testing its infectivity *in vitro*. Pre-adsorption with the prefusion F protein removed more of the serum neutralizing activity (50-55%). Unexpectedly, G-specific antibodies removed more neutralizing activity (35-40%) than postfusion F-specific antibodies (0-20%). Overall, our data indicate that the prefusion form of the F protein is the most important neutralizing RSV antigen, but that G-specific antibodies also play a significant role in RSV neutralization.

Key Terms: Virology
 Respiratory syncytial virus
 Antibody response

PR-12

Cleavage/Inactivation of the Respiratory Syncytial Virus Attachment Glycoprotein Requires Low pH and Is Prevented by Protease Inhibition

Jacqueline D. Corry (The Ohio State University and Center for Vaccines and Immunity, Nationwide Children's Hospital), Mark E. Peeples (The Ohio State University Biomedical Sciences Graduate Program and The Ohio State University College of Medicine)

No vaccine is available to protect against respiratory syncytial virus (RSV) disease. Live attenuated vaccines are produced in Vero cells, a cell line approved by the WHO that yields the highest RSV titers. We previously found that in Vero cells the RSV attachment (G) glycoprotein is cleaved, reducing its size from 90 kDa to 55 kDa, and reducing the infectivity of produced virus by 10-fold when assessed in primary, well differentiated human airway epithelial (HAE) cultures. Because HAE cultures are an excellent model for airway epithelium, it is likely that vaccine virus produced in Vero cells would be similarly inefficient at initiating infection in the nose and therefore in producing antigen and inducing an immune response. We have found that G protein cleavage in Vero cells can be prevented by cysteine protease inhibitors, and more specifically by a cathepsin inhibitor. Cathepsins are proteases found primarily in lysosomes. In order to test if the protein undergoes endocytic recycling we generated a soluble G (sG) protein that should be released from its anchor by furin in the Golgi and secreted from the cells. The sG protein released from Vero cells was not cleaved, but a portion of the G protein that was not released from its anchor by furin was, suggesting that the G protein is cleaved after its arrival at the cell surface. In addition, RSV-infected Vero cells treated with chloroquine displayed reduced cleavage of the G protein, indicating that an acidic pH such as that found in the lysosome is required for cleavage. Together this data indicates that G protein cleavage in Vero cells occurs during recycling through the lysosome. Virus grown in Vero in the presence of cathepsin L more efficiently, confirming the importance of the intact G protein in HAE infection, and likely *in vivo*.

Key Terms: Virology
 Respiratory syncytial virus
 Vaccine

PR-13

A Prototype Indicators System for U.S. Climate Changes, Impacts, Vulnerabilities, and Responses

Melissa A. Kenney (University of Maryland, College Park)

Indicators are observations or calculations that are used to systematically report or forecast social and biophysical conditions over time. When the purpose of indicators is to, in part, provide complex scientific information that is understood by non-scientists and included in decision processes, the choice of indicators requires a structured process that includes co-production among a range of actors, including scientists, decision-makers, and a range of stakeholders. Here we describe recommendations on a vision and a prototype created for an indicators system, we term the National Climate Indicators System (NCIS). The goal of the NCIS is to create a system of physical, natural, and societal indicators to communicate and inform decisions about climate changes, impacts, vulnerabilities, and responses. The process of generating the indicator system involved input from over 200 subject-matter experts. Organized into 13 teams, experts created conceptual models of their respective sectors to generate an initial recommended set of indicators. A subset of indicators, which could be immediately implemented, were prototyped for the U.S. Global Change Research Program (USGCRP) a Federal program that coordinates and supports integration of global change research across the government. USGCRP reviewed the recommendations (Kenney et al., 2014) and prototypes provided by the scientific experts, and recently launched 14 indicators as proof-of concept in support of a sustained National Climate Assessment and to solicit feedback from the users. Social science research is currently being undertaken in order to evaluate how well the prototype indicators communicate science to non-scientists, the usability of indicator system portal by scientists and decision-makers, and the development of information visualization guidelines to improve visual communication effectiveness. The goal of such efforts would be to provide input into the development of a more comprehensive USGCRP indicator set, building on recommendations from Kenney et al. (2014), and improve our understanding of the comprehension and use of indicators by non-scientists.

Key Terms: Science Policy
 Climate Change
 Indicators

PR-14

Reliability of Diagnostic modalities for Dental caries

Bapanaiah Penugonda (New York University College of Dentistry), Kritika Srinivasan (New York University College of Dentistry), Benjamin Godder (New York University College of Dentistry), Joel Silver (New York University College of Dentistry), Maria Congiusta (New York University College of Dentistry), Xu Sheng (New York University College of Dentistry), David Hershkowitz (New York University College of Dentistry)

Objectives: The aim of this study was to compare three clinical diagnostic modalities: 1) visual-tactile, 2) radiographic, and 3) laser fluorescence (DIAGNODENT).

Methods: This in vitro study utilized 30 extracted premolars and molar teeth. The teeth were brushed with water using a tooth brush to remove debris and mounted in wax for evaluation. Nine clinicians examined each tooth, corresponding radiographic and separately utilized a laser fluorescence device to decide if the tooth was carious. Data was analyzed to yield Cohen's Kappa and intraclass correlation coefficient (ICC).

Results: Across evaluators, 76% of teeth were considered decayed based on visual and tactile examination. For ratings based on such exploration, kappa ranged from 0.20 to 0.87 (Med= 0.49) and the ICC was 0.54. Amidst evaluators, 40.6% of teeth were considered decayed upon examination of corresponding X-ray films. Based on the x-ray data, kappa ranged from 0 to 0.81 (Median= 0.24) and the ICC was 0.24. Finally based on laser fluorescence device readings 91.1% of teeth were considered caried and kappa ranged from 0.14 to 0.78 (Median= 0.52) and the ICC was 0.49.

Conclusion: The laser fluorescence device detected more carious lesions than the visual and radiographic methods. While clinical and laser fluorescence device assessments yielded moderate ICCs of about 0.5, the x-ray data were much less reliable. All three modalities of caries detection are not singularly reliable and reproducible by nine examiners.

Key Terms: Dental
Caries
Diagnosis Reliability

PR-15

Wild Dark-Eyed Juncos (*Junco hyemalis*) Carry Recognized Plant Pathogens and Beneficial Bacteria on Their Feathers

John W. Dille, Christopher M. Rogers, and Mark A. Schneegurt (Wichita State University)

Migratory birds can disperse pathogenic microbes and establish novel disease foci along their ranges. Previous studies of feather microbial communities focused mainly on keratin degradation, finding little bacterial diversity. We have dislodged microbes from composite ventral feathers of overwintering Dark-eyed Juncos (*Junco hyemalis*), after mist-net capture in south-central Kansas. We then measured bacterial loads by serial dilution and collected >300 isolates on R2A medium (with cycloheximide) by repetitive streak-plating. Microbial isolates were characterized with biochemical and physiological tests and identified by 16S rRNA gene sequencing and phylogenetic analysis. Individual bacterial loads from eight juncos varied significantly within a range of 10^5 - 10^6 colony-forming units g^{-1} feather. Gram-positive bacteria dominated the isolates, balanced between low and high G+C clades. *Bacillus* spp. were abundant, as in previous studies, along with *Lysinibacillus*, *Paenibacillus*, and *Staphylococcus*. Remarkably, substantial numbers of Actinomycetes were isolated, with examples of *Clavibacter*, *Curtobacterium*, *Microbacterium*, and *Rathayibacter*, genera recognized as crop plant pathogens. Apposed to these are feather isolates implicated as beneficial to host plants, *Frigoribacterium* and *Kitasatospora*, being antagonists to pathogens or acting as growth promoters. *Proteobacteria* dominated the Gram-negative bacteria, including the recognized plant pathogens *Agrobacterium* and *Sphingomonas*, along with *Aurentimonas*, *Brevundimonas*, *Methylobacterium*, *Pantoea*, *Pseudomonas*, *Rhizobium*, *Rhodobacter*, and *Stenotrophomonas*. This is the first report of abundant helpful and harmful phyllosphere bacteria on wild bird feathers. The clear implication is that migratory birds may act as vectors of plant pathogens and beneficial bacteria.

Supported by NIH NIGMS IDeA KINBRE, KS NSF EPSCoR, and NSF GK-12.

Key Terms: Diversity
Microbiology
Ornithology

PR-16**Matters of Fact and of Method pertaining to Anthropogenic Global Warming/Climate Change**

Laurence I. ("Larry") Gould (University of Hartford)

Many arguments, using a variety of factual claims and methodologies, have been made that — as a result of human activities which emit greenhouse gases (mainly carbon dioxide) — there is a dangerous trend of increasing global temperatures so as to result in events such as melting glaciers, rising sea levels, and increased storms. That served as the basis for the hypothesis that students can — through an analysis of some of those arguments and methodologies — decide whether or not the evidence supports the belief of Anthropogenic Global Warming/Climate Change (AGW). The hypothesis was tested through two semester-long freshman seminars at the University of Hartford. At the first class meeting students briefly wrote their views about AGW. At the end of the semester students gave both an oral presentation and a supporting term paper to argue for their position. (Note: despite being asked several times, the instructor refused to state his position.) A variety of critical-thinking tools involved readings and discussions on fundamentals such as techniques for listening to people and descriptions of the scientific method. Videos exposed students to arguments by those who argued *for* AGW (the "pro" side) as well as those who argued *against* AGW (the "con" side). By the semester's end: (a) some students who were "pro" at the beginning of the semester had changed their position to "con", (b) others maintained and strengthened their "pro" or "con" position, and (c) there were a few who changed their "pro" position to one that was undecided. Small sample size precludes confirmation of to what extent the hypothesis was borne out. More testing is needed over a larger student population in order to isolate which of the arguments used in the course were most significant in altering or bolstering a student's position on AGW. Yet a wider research implication is how curious people may seek a deeper understanding and thus enhance their ability at scientific enquiry. It should be of particular interest to science educators and to students who are at the beginning of their scientific careers.

PR-17**Construction and Immunogenicity Evaluation of Recombinant Influenza A Viruses Containing Chimeric HA Genes From Genetically Divergent Influenza H1N1 Viruses**

Kara McCormick (Sanford School of Medicine, The University of South Dakota), Longchao Zhu (South Dakota State University), Zhiyong Jiang (South Dakota State University), Steven R. Lawson (South Dakota State University), Robert Langenhorst (South Dakota State University), Russell Ransburgh (South Dakota State University), Colin Brunick (Sanford School of Medicine, The University of South Dakota), Victor Huber (Sanford School of Medicine, The University of South Dakota) Ying Fang (South Dakota State University)

Influenza A virus causes highly contagious respiratory diseases in a variety of mammalian hosts, including humans and pigs. To develop a vaccine that can be broadly effective against genetically divergent strains of viruses, in this study, we employed molecular breeding (DNA shuffling) technology to create a panel of chimeric HA genes. Each chimeric HA gene contains genetic elements from four parental viruses that represent major phylogenetic clusters of influenza A H1N1 viruses. Eight shuffled HA constructs were initially evaluated in mice by DNA immunization. The result showed that six HA constructs, HA-111, HA-113, HA-123, HA-116, HA-107 and HA-129, induced broad antibody response against either four or five of the genetically distinct parental viruses. These chimeric HAs were subsequently cloned into the backbone of A/Puerto Rico/8/34 and A/swine/Texas/4199-2/98 infectious clones, and HA-129 recovered viable recombinant viruses using reverse genetics, designated as PR8-129 and TX98-129. The PR8-129-infected mice developed HI antibody titer greater than 1:80 to parental viruses. The broad protective immunity induced by HA-129 was further assessed in a pig challenge model. Pigs were immunized with live or inactivated TX98-129 virus. The result showed all of the immunized pigs developed HI antibody titer higher than 1:40 to four parental viruses at 28 days post immunization, with significant difference between the inactivated TX98-129 immunized group and non-immunized group of pigs. This study established a platform for creating novel HA genes of influenza viruses using molecular breeding approach, which will have important implications in future development of broadly protective influenza virus vaccines.

Key Terms: Influenza
Vaccine
H1N1

PR-18

Biomechanically Relevant Cancer Screening Platform

Jorge I. Rodriguez (Clemson University)

My research activities are focused in cancer biomechanics and cell/drug screening. My long term goal is to develop a cancer screening platform that better resembles the physiology occurred in natural occurring tumors. Current drug discovery screening platforms have limited throughput and high volume reagents usage; thus a need for miniaturization and ultra-high throughput exist. My initial published studies demonstrated that by using inkjet bioprinting we can downsize the screening process down to $180 \pm 30\%$ picoliters per assay. Subsequent work was done to apply the screening platform to the treatment of cancerous cells demonstrating that the developed miniaturized platform provides a more efficient use of valuable drugs in the screening process. During my postdoctoral studies, I had focused on the bio-fabrication of mechanically relevant microtissues to combine them with the previously developed screening platform. The biomechanical properties of cancer cells have been identified as a key element to understand cancer fate. Single-cell analyses had revealed that cellular nanomechanical properties can serve to distinguish between metastatic tumorous and healthy cells. However, tumors conformed in complex shapes and compositions which differ from single-cell or two dimensional analyses. My work has focus on assessing the biomechanical properties of three-dimensional (3D) breast cancer microtissues via atomic force microscopy (AFM). I have elicited the properties of 3D microtumors in the presence of cellulose-based materials that modifies the behavior cells agglomerates. This approach can help us to understand the role of the mechanical properties of cancer cells on their metastatic behavior and in the creation of more relevant screening platform in support of a more personalized and predictive chemotherapy.

Key Terms: Biofabrication
 High throughput
 Cancer

PR-19

Looking for *Macrobiotus americanus* (Packard, 1873)

Emma Perry (Unity College)

In 1873, the first tardigrade was described in America by Packard. This tardigrade was collected by Rev. Cross from New Gloucester, Maine and described by Packard as *Macrobiotus americanus*. By 1938, Mathews had relegated this taxon to the status of *incertae sedis* due to insufficient information. In this same paper Mathews confused the Maine species with a similar second species also described by Packard in the same publication (1873). This second species was sent by Prof. Bessey from Ames, Iowa and Mathews (1938) listed it as *Thulinus augusti*. Here we examine the tardigrade fauna of New Gloucester, Maine and evaluate possible candidates for Packard's *Macrobiotus americanus*. Twenty six samples of moss, and lichen were collected from sites known to exist in Reverend Cross' lifetime. More than 400 tardigrades were found and the twelve species identified were compared to the sparse taxonomic information given by Packard in 1873.

PR-20

Making platelets using bioreactors: *Ex vivo* donor-independent human platelet production

Elise Mochizuki (Jericho Middle School)
Advisor: Jonathan N. Thon (Brigham and Women's Hospital, Harvard Medical School)

Presented by Kenjiro Mochizuki, M.D. (Harvard University) on behalf of the author and advisor

Platelets play a critical role in stopping bleeding, however bacterial contamination, disease transmission from human donors, and short platelet unit shelf-life limit the availability of platelet transfusions. Currently, *in vivo* methods cannot produce yields comparable to donor-derived platelet unit collection. Stem cells produce megakaryocytes, which in turn produce platelets. Superior to embryonic and umbilical cord blood stem cells, human induced pluripotent stem cells can be expanded and maintained in culture, thus providing an unlimited source of stem cells to create megakaryocytes. Until recently, those megakaryocytes were unable to make platelets at a clinically and commercially viable scale. Our hypothesis was those stem cells could be triggered to make platelets outside of the body. Microfluidic devices that selectively trap megakaryocytes to trigger platelet production were developed in order to mimic bone marrow physiology, allowing megakaryocytes to generate human platelets in small numbers. These platelet bioreactors recapitulate bone marrow stiffness, extracellular matrix composition, micro-channel size, hemodynamic vascular shear stress, and endothelial cell contacts. Each megakaryocyte produced roughly 100 platelets. Bioreactor platelets were structurally indistinguishable from, and functionally comparable to, human blood platelets. After tackling the bottleneck of *ex vivo* platelet production, the remaining bottleneck is to trigger megakaryocytes to produce human platelets at clinical amounts. Our next goal is achieving platelet quantities that exceed the 1×10^8 platelets per 300 mL required to perform the pre-clinical regulatory studies required to advance into human clinical trials.

PR-21

Phase 1 results for BIO201: Potential drug for the intermediate dry form of age-related macular degeneration (AMD)

Elise Mochizuki (Jericho Middle School)
Advisors: Stanislas Veillet (Biophytis); René Lafont, (University Pierre and Marie Curie)

Presented by Kenjiro Mochizuki, M.D. (Harvard University) on behalf of the author and advisors

Age-related macular degeneration (AMD) and the lack of any drug to treat the intermediate dry form became more significant with an aging population. Light and oxygen in the human eye causes oxidation of the byproduct A2E, whose accumulation in retinal pigment epithelium (RPE) cells disrupts their phagocytic activity. Deposition of amyloid-like waste products (drüsen) at the basal side of RPE cells initiates an inflammatory process eventually leading to death of RPE cells and associated photoreceptors. Extracted from *Bixa orellana* cultivated in Peru, BIO201 is an agonist of PPAR α , a nuclear receptor that protects the retina from oxidative stress associated with the accumulation of A2E. BIO201 is thought to possess an antioxidant effect as well as anti-inflammatory and anti-VEGF actions. By reducing the accumulation of A2E by RPE cells, BIO201 might protect against apoptosis of retina cells. *In vivo* results of oral BIO201 in animal models showed improved electroretinograms and reduced quantities of A2E in the eyes. Our hypothesis was oral BIO201 would also be safe and effective in humans. Phase 1 clinical trial (double-blind, placebo-controlled) with European healthy volunteers (n=47) assessed chronic oral administration of 35 mg/day of BIO201 for 12 weeks. The results confirmed satisfactory bioavailability, no toxicity, and no serious adverse events. The next step is a Phase 2 clinical trial including U.S. patients from a Harvard affiliated hospital (n=180, 3 cohorts). Using oral administration of 0 or 100 or 350 mg/day for 24 weeks, this multicenter, randomized, double-blind, placebo-controlled study would determine the therapeutic dose of BIO201.

STUDENT POSTER ABSTRACTS

ASNR-01

Rapid Assessment Of Disease Tolerant *Pinus taeda* Families For Strength, Chemical and Bioenergy Applications Using Near Infrared Spectroscopy

Gifty Acquah (Auburn University), Lori Eckhardt (Auburn University), Oladiran Fasina (Auburn University), Nedret Billor (Auburn University)
Advisor: Brian Via (Auburn University)

Over the past fifty years, premature deaths have been associated with *Pinus taeda* (loblolly pine), the most economically important tree species in the USA. As a management strategy, stakeholders are deploying genetically superior families that have been selectively bred to be disease tolerant. Nevertheless, it is vital that we determine an optimum balance between disease tolerance and other properties that affect wood quality for different end users. With the large number of trees involved in tree breeding programs, alternative analytical tools that have high throughput and are cost-effective are needed.

In this study, near infrared spectroscopy (NIRS) coupled with partial least squares regression was used to rapidly and non-destructively predict the density, modulus of elasticity, modulus of rupture, extractives content and higher heating value of loblolly pine families that have been selectively bred to be disease tolerant. Calibration models were developed with 1st treated NIR spectra collected from six positions of solid wood samples. Smaller errors of NIR models compared to larger standard deviations of the conventional methods gave RPD values greater than 2.5. R^2_{adj} values of cross-validated models ranged from 0.81 for MOR to 0.89 for MOE. At 95% confidence level, all models accurately estimated the various properties of at least eleven of the fifteen families studied.

NIRS models developed should also be applicable in the rapid screening of other loblolly pine families for tree improvement programs. This will help make the right feedstocks available for the conventional forest industry, as well as to support the emerging bioeconomy.

Key Terms: Near infrared spectroscopy
Forest products
Bioeconomy

ASNR-02

Effects of Rider Weight on Horse Stride Length: A Preliminary Study

Kylee O. Short (Truman State University), Kelly W. Walter (Truman State University)
Advisor: Kelly W. Walter (Truman State University)

Recommendations for maximum weight-loads carried by horses are commonly used for equine events; however, lack scientific support and vary depending on the source. The objective of this study was to evaluate effects of weight-load (WL) applied at 0%, 15%, 20%, 25%, and 30% of the horse's body weight at the trot using gait analysis software. We hypothesized the heaviest WL would result in a shorter stride length, and altered range of motion (observed as changing angles in the fetlock joint). Eight horses were organized into a replicated 4x4 Latin Square Design, and data for each horse was collected on 4 consecutive days. Each day, horses were filmed at a 0% WL, followed by a randomly assigned WL. EquineTec software program was used for video analysis, and variables analyzed included fetlock angle at maximum flexion and stride length for both front and hind limbs. Data was analyzed using SAS statistical software. Lighter WL tended to cause greater front fetlock angles than heavier WL ($p = 0.10$), suggesting the fetlock joint flexed more with increased WL. For hind stride length, 0% WL tended to differ from all other weight loads ($p = 0.06$) with stride length increasing with increasing weight load. This was unexpected, and suggests horses could have been altering their stride to carry the WL more on the hind-quarters. Further research is needed utilizing more horses and evaluating WL carried over longer durations and distances to elucidate these observations and conclude what loads are appropriate in terms of equine welfare.

Key Terms: Equine
Stride length
Weight-load

STUDENT POSTER ABSTRACTS

BSS-01

Sex-specific Patterns of the Neuroepigenome within the Neocortex are Associated with Sex Differences in Fear-related Learning and Memory

Michael Emami (UC Irvine), Xiang Li (UC Irvine),
Timothy Bredy (UC Irvine)
Advisor: Timothy Bredy (UC Irvine)

Emotionally relevant experiences can generate long-term memories, which may be so strongly associated with that emotional event that they can lead to post-traumatic stress disorder (PTSD). According to the American Psychological Association, women suffer from higher rates of PTSD despite the fact that males are at a higher risk of experiencing a traumatic event. One way by which this might be mediated is through sex-chromosome-specific epigenetic modifiers such as the histone demethylase, ubiquitously transcribed X chromosome tetratricopeptide repeat gene (*Utx*). This histone demethylase acts directly on the histone modification H3K27me₃, which is a repressive chromatin mark. Also, it has been shown that *Utx* is an x-escapee gene, meaning females would express higher levels of *Utx*, which may lead to greater gene activation in response to learning. Indeed, we have observed marked increases in gene expression (i.e. *Rab3a*) in female mice following behavioral training. Our data demonstrate that females retain fear memory significantly more compared to males. Based on this observation, we hypothesize that *Utx* knock-down in females will lead to a behavioral-phenotype similar to that of males. We find there is no difference in the acquisition of fear memory, however, there is a significant resistance to the extinction of cued fear memories in females. Additionally, we find evident mRNA levels for *BDNF* and *Utx* are increased in the prefrontal cortex of female mice. Further experiments are needed in order to elucidate the epigenetic mechanisms involved in the acquisition and extinction of persistent fear memories in the female brain.

Key Terms: Epigenetics
 Fear Conditioning
 Neuroscience

BSS-02

Identification of the Functionality of Bifaces in the Chaney Collection

Emily Tochtrop (University of Central Missouri)
Advisor: Jeffery Yelton (University of Central Missouri)

At the turn of the century and into the twenties, Mr. Walter Chaney collected Native American artifacts as a hobby. In 1995, the children of Mr. Chaney donated his collection to the University of Central Missouri's McClure Archives and University Museum. It is assumed all the artifacts are from Missouri. The Chaney collection includes approximately 106 chert bifaces. For my project, I sorted the bifaces into six categories based on their stem type: corner-notched, side-notched, basal-notched, stem contracting, and stem straight. When I completed categorizing the bifaces, I took measurements for each biface and performed statistical analyses to suggest function. My hypothesis was that by comparing thickness, weight, and stem width, there will be patterns indicating the original function of each biface as either a dart point for an atlatl or an arrow point for a bow. From the graph data, light weight as well as thin points was labeled as possible arrow points, and heavier, thick bifaces were interpreted as possible atlatl or knife points. My work contributes to the methods of identifying functionality and has given me more experience for my future career as an archaeologist.

Key Terms: Anthropology
 Archaeology
 Biface

STUDENT POSTER ABSTRACTS

CBB-01

Nr4a2 Regulates the Formation of Cocaine Drug-seeking Behavior

David Saldana (UC Irvine), Marcelo Wood (UC Irvine)
Advisor: Marcelo Wood (UC Irvine)

Drug addiction is characterized by persistent drug-seeking behavior despite negative consequences. Drug abuse produces pronounced changes in gene expression profiles within the reward pathway. These changes in gene expression drive persistent changes in cell function and plasticity, ultimately leading to sustained drug-seeking behavior. One potential mediator of the changes in gene regulation is NR4A2, a nuclear transcription factor that regulates dopamine neurotransmission in the reward pathway. Studies in human post-mortem tissue have reported that acute versus chronic drug use leads to increased and decreased *Nr4a2* expression, respectively. We hypothesize that this timely phenomenon occurs with cocaine consumption and we propose that NR4A2 is key in mediating the changes in gene expression which drive drug-seeking behavior. In order to address these hypotheses we conducted a week of intraperitoneal injections in mice with three different treatments: saline for 7 days, saline with cocaine on the last day (acute), and cocaine for all days (chronic). We subsequently conducted immunohistochemistry analysis of coronal brain slices of the nucleus accumbens (a brain region involved in addiction), then extracted tissue for gene expression analysis using qRT-PCR. We will also conduct a cocaine conditioned-place preference study using *Nr4a2* knockdown mice to investigate the role of NR4A2 in a behavioral task. Our results suggest that NR4A2 may be a key mediator of cocaine drug-seeking behavior.

Key Terms: Neuroscience
Drug Addiction
Memory

CBB-02

Filamentation Patterns in Protein Repair-Deficient *Escherichia coli* Under Low-Salt

Kailie Briza (North Central College)
Advisor: Jonathan Visick (North Central College)

Protein damage is implicated in aging and is associated with Alzheimer's and some autoimmune diseases. The spontaneous isomerization of the amino acids aspartate and asparagine to isoaspartate can be fixed by a protein-repair enzyme, L-isoaspartyl protein carboxyl methyltransferase (PCM). PCM is essential for the long-term survival of stationary-phase *Escherichia coli* exposed to denaturing stresses such as methanol, heat, and salt; we therefore hypothesize that a key role of PCM is to maintain the folded state of proteins. Preliminary results suggested that PCM-deficient *E. coli* filament and have difficulty disposing of protein aggregates under low-salt conditions. We observed considerable filamentation under low-salt conditions for both wild-type (WT) and a PCM-deficient mutant (Δ pcm). However, by measuring the cell lengths, we found no significant difference in the percentage of filaments between the two. To further understand filamentation, we investigated the septation inhibitor SulA as a possible mechanism for filamentation. To measure *sulA* transcription, we inserted a *sulA* promoter fused to the green fluorescent protein (GFP) gene into *E. coli* at the att λ site and verified this using PCR. Results indicated that only a very small percentage of filamented cells vividly expressed the GFP, and consequently *sulA*, in the first few days of long-term stationary phase. This suggests there are other mechanisms for filamentation under these conditions.

Key Terms: Microbiology/Genetics
Protein-repair enzyme
E. coli

CBB-03

The effect of combined pulsed wave low-level laser therapy and human bone marrow mesenchymal stem cell - conditioned medium on open skin wound healing in diabetic rats

Ramin Pouriran (Shahid Beheshti University of Medical Sciences)

Advisors: Mohammad Bayat (Shahid Beheshti University of Medical Sciences), Abbas Piryaie (Shahid Beheshti University of Medical Sciences)

Pulsed wave low-level laser therapy (PW LLLT) exhibited biostimulatory effects on wounds in diabetic animals. The nobility of this scientific study was to investigate the combined effects of PWLLLT and human bone marrow mesenchymal stem cell-conditioned medium (BM-MSCs CM) on the biomechanical parameters of wounds in an experimental model for diabetes mellitus (DM).

Type I DM was induced in rats by streptozotocin (STZ). Two wounds were made on proximal and distal parts in dorsal region of each rat. They were divided into four groups. First group, were considered as the control group. Second group, received hBM-MSCs-CM. Third group, received PWLLLT. Fourth group, received (hBM-MSCs-CM +LASER). hBM-MSCs- CM were administrated twice intraperitoneally. The proximal wounds in the 3rd and 4th groups were treated with a pulsed laser by 890 nm wavelength, 80 Hz frequency, and 0.2 J/cm² energy densities. On the 15th day, a standard sample from each healing wound was submitted for biomechanical examination.

PW LLLT and hBM-MSCs- CM alone or in combination, significantly increased biomechanical parameters within the healing wounds. In the 3rd and 4th groups, the numbers of wounds closures were significantly enhanced in proximal part, contrariwise to the control ones.

It was clear that PW LLLT, and hBM-MSCs-CM alone or in combination significantly accelerated wound healing process in an experimental model for STZ-induced type I DM. However, PW LLLT was statistically more effective compared to the hBM-MSCs-CM. These treatments could significantly improve severe diabetic foot ulcers in patients. This is the most significant part in our study.

Key Terms: Diabetes mellitus
Low-level laser therapy
Human bone marrow-derived mesenchymal stem cell

CBB-04

Effect of Heat Stress Duration on Root Growth and Development in *Arabidopsis thaliana*

Samantha Sharpe (Kansas State University)
Advisor: Jalean Petricka (Carleton College)

Exposure to elevated temperature can trigger a variety of changes in gene expression, including increased production of heat shock proteins, which stabilize and protect other cellular proteins but are costly to produce. The pathways through which heat stress influences root development are not fully understood, but the transcription factor SCARECROW (SCR), which maintains stem cell identity during root growth, may play a role in this process. We tested the effect of 9 different durations of heat stress exposure on root growth and SCR expression in 5-day-old *Arabidopsis thaliana* seedlings. Periods of exposure lasting 4 hours or less had little effect, but root growth decreased significantly after 6, 12, and 24 hours at an elevated temperature. Oddly, an 8-hour heat stress treatment did not seem to affect root growth at all. Expression of SCR protein in the cortex of the root tip appeared to decrease after 4 hours of heat exposure. These results suggest that a period of between 4 and 6 hours of heat stress is necessary to reduce root growth, and that lower levels of SCR protein in the tips of elongating roots may be involved in this response.

Key Terms: Heat Stress
Development
Root Growth

STUDENT POSTER ABSTRACTS

CBB-05

Yak1p and Ypl247 influence glycogen accumulation and stress resistance in *Saccharomyces cerevisiae*

Cameron Harvey (North Central College), Sidney Schneider (North Central College)
Advisor: Stephen Johnston (North Central College)

Under high stress conditions, the yeast *Saccharomyces cerevisiae* accumulates the storage carbohydrate glycogen. The protein kinase Yak1 is found to work as a growth antagonist and is linked to nutrient accumulation. Protein binding screens have shown Yak1p binds Ypl247p making it important to investigate the relationship between these proteins. The mechanism of glycogen storage regulation by both Yak1 and Ypl247 is unclear, whether the regulation is at synthesis or degradation. In addition, the importance of these proteins in other stress responsive situations such as the presence of acetic acid, hydroxyurea, or nocodazole has yet to be elucidated. We found loss of either Ypl247 or Yak1 increased the amount of glycogen accumulated in either stationary or exponential growth. Yak1 and Ypl247 were not found to have a significant impact on the rate of glycogen degradation. Rather, we found that these two genes play integral roles in regulating the GSY2 promoter for transcription of glycogen synthase 2, the major isoform of glycogen synthase in yeast. Ypl247 is shown to have the most significant role in GSY2 transcription and glycogen accumulation while Yak1 plays a much smaller role and seems to act downstream of Ypl247. Yeast was found to be less resistant to hydroxyurea and nocodazole with yak1 deletion. Yeast was also found to be more resistant to acetic acid treatment with ypl247 Δ and YAK1 overexpression. These results suggest Yak1 and Ypl247 work together as important environmental response mechanisms in yeast.

Key Terms: Molecular Biology
Genetics
Cell Biology

CBB-06

Determination of Medial Habenula Activity and Role During Cocaine Withdrawal

Monica Espinoza (University of California, Irvine)
Advisors: Alberto Lopez (University of California, Irvine), Marcelo Wood (University of California, Irvine)

Drugs of abuse can change the memory formation and reward circuitry of the brain. One region drawing attention with regards to drug-seeking behavior is the medial habenula. Work has implicated the medial habenula in nicotine seeking behavior/addiction (Fowler et al 2011, Gorlich et al 2013), but medial habenula activity remains unexplored in the context of other drugs of abuse, such as cocaine. This research explores the medial habenula's role throughout the phases of addiction. First, medial habenula activity during reinstatement (the resurfacing of drug-seeking behavior and memory after a period of withdrawal through re-exposure to the drug/drug administration context) was assessed. A Conditioned Place Preference (CPP) paradigm was used as a model to study drug-seeking behaviors. Mice were conditioned in the CPP paradigm, their preference extinguished, and reinstated with either cocaine or saline. Post reinstatement, mice were sacrificed and brains were prepared for fluorescent in situ hybridization against *C-fos* (neuronal activity marker). Quantification of intensity data indicate that mice reinstated with cocaine had elevated medial habenula activity. Next, medial habenula activity was explored with the withdrawal-relapse model of drug addiction. Animals underwent chronic exposure to cocaine followed by a withdrawal period and an acute dose of cocaine or saline. Again, medial habenula activity was elevated in animals exposed to cocaine. Current experiments will determine when the medial habenula is engaged by cocaine exposure and withdrawal. Together, all of these experiments will identify a novel node that regulates reward signaling and relapse behavior, ultimately to better understand drug addiction.

Key Terms: Neurobiology
Addiction
Neuronal circuitry

CBB-07**Engineering Capsomers of Hepatitis C for Vaccine Development via Coexpression with Shigella bacteriophage sf6 Capsid Protein**

Annie Lynn (University of Kansas)
Advisor: Liang Tang (University of Kansas), Advisor:
Haiyan Zhao (University of Kansas)

Hepatitis C affects over 150 million people worldwide and is a major agent leading to the development of liver cancer. The core protein of the Hepatitis C virus (HCVC) forms the viral nucleocapsid and plays a crucial role in the viral life cycle. Because HCVC is unstable and fragile, it is difficult to work with and it is unknown how the nucleocapsid assembles. Although there are drugs that can treat Hepatitis C, there is currently no vaccine that can immunize against it. This study investigated the fusion of the HCVC core protein to the C-terminus of the gene product 5 (gp5) capsid protein of Shigella bacteriophage sf6, which spontaneously assembles into a stable procapsid structure. The protein coexpression was hypothesized to promote expression and capsomer assembly of HCVC, which would be the first steps leading to the development of a Hepatitis C vaccine. A plasmid encoding both the HCV core protein and gp5 was successfully engineered, and these proteins were co-expressed in *E. coli* cells and purified. In the resultant engineered viral assembly, gp5 formed a procapsid-like structure with HCVC expressed as small studs around the outside of the gp5 protein. This structure is stable enough for analysis using structural virology analysis techniques including X-ray crystallography and cryo-electron microscopy. The viral complex will also allow isolation of the HCVC capsomers, which can be used to develop a vaccine that immunizes against Hepatitis C via an antibody response to HCVC capsomers that more closely model the wildtype virus structure.

Key Terms: Structural Virology
 X-ray Crystallography
 Protein Crystallization

CBB-08**Association analysis of DISC1 gene polymorphisms with Attention-deficit/hyperactivity disorder in Iranian population**

Khashayar Pouriran (Shahid Beheshti University of Medical Sciences)
Advisor: Dr. Abolfazl Movafagh (Shahid Beheshti University of Medical Sciences)

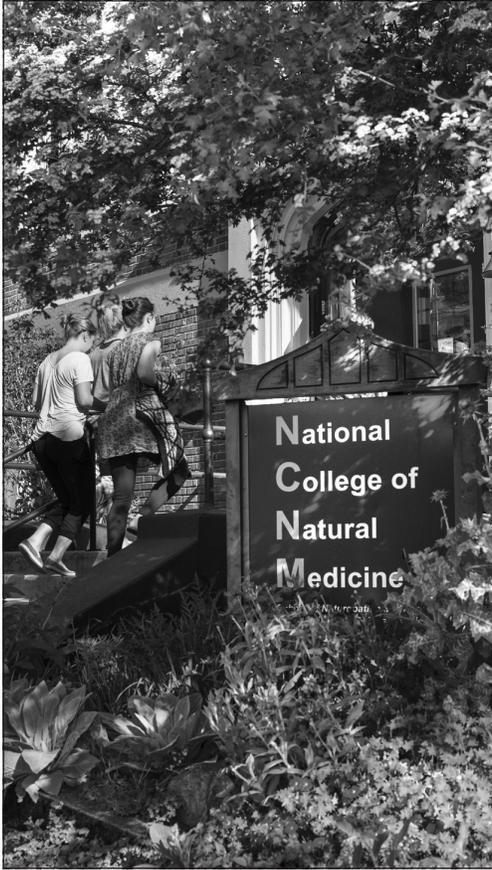
Attention deficit hyperactivity disorder (ADHD) is a common heritable psychiatric disorder with a worldwide prevalence of 5%. The etiology of ADHD is still incompletely understood, but several studies, consistently indicate the strong role of genetic factors on this disorder. ADHD is known to have polygenetic nature with multiple genes involved in its genetic basis. Disrupted-in-Schizophrenia-1 (*DISC1*) has been identified as a susceptibility locus for several psychiatric disorders and some of its polymorphisms are studied in many neurological disorders, but are not included in ADHD studies as much.

In this study we investigated the association of three SNPs (rs11122330, rs6675281 and rs11122319) in the *DISC1* gene with ADHD in Iranian population. 240 subjects composed of 120 patients and 120 normal controls were included and tetra-primer ARMS PCR technique was used for genotyping all SNPs.

We found differences in genotype and allele distributions of rs 6675281 polymorphism between patients and controls.

Our findings strengthens the role of *DISC1* gene as a susceptibility locus for ADHD and indicate that rs6675281 polymorphism is a susceptibility factor for ADHD in Iranian population.

Key Terms: Iranian population
 Disrupted-in-Schizophrenia-1
 Attention deficit hyperactivity disorder



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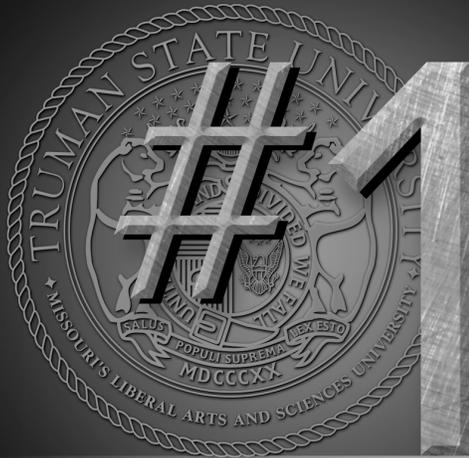
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CBB-09**A Novel Technetium-Based Imaging Agent for the Detection of Occult Thrombus in Left Ventricular Assist Devices**

Krishna Paranandi (Washington University in St. Louis)
Advisor: Gregory Lanza (Washington University in St. Louis)

Left ventricular assist devices (LVADs) are mechanical pumps designed to provide circulatory support in patients with advanced heart failure. Despite the survival benefit of LVADs, they are also associated with adverse events, including intra-pump thrombosis and stroke. In this study, a ^{99m}Tc -labeled peptide was developed to detect occult fibrin deposition within the ventricular assist device. A bifunctional fibrin-specific homing peptide (F1A) conjugated to a ^{99m}Tc radio-label was prepared (^{99m}Tc -F1A) and compared to an analog consisting of four ^{99m}Tc -F1A units coupled to a tetrameric polyethylene glycol backbone (^{99m}Tc -F4A). In vitro, these probes bound to fibrin clots in buffer in the presence of cysteine. Importantly, human plasma interfered with ^{99m}Tc -F1A binding but not ^{99m}Tc -F4A clot targeting. In an LVAD mock loop flowing at 6L/min, the high-avidity ^{99m}Tc -F4A bound to fibrin but ^{99m}Tc -F1A did not. NanoSPECT/CT revealed that mice with carotid thrombus were effectively targeted with ^{99m}Tc -F4A. Unbound ^{99m}Tc -F4A was eliminated from the body via urine. Explanted LVAD pumps from patients undergoing heart transplant or LVAD replacement were rewired and studied in the mock loop. NanoSPECT/CT imaging of ^{99m}Tc -F4A showed thrombus in 17 of 18 pumps. Six of 17 LVADs were from patients suspected of pump thrombosis (SPT) while 12 were from individuals with no clinical evidence of clotting. ^{99m}Tc -F4A imaging revealed thrombus in the inlet and outlet cannulas and bearing-stator assemblies. In summary, ^{99m}Tc -F4A is a high-avidity probe to detect and localize thrombus in LVADs to afford earlier clinical intervention to minimize pump exchange.

Key Terms: Biomedical Imaging
 Nuclear Medicine
 Heart Failure

CBB-10**Methodology for Measuring Protein Aggregates and the Effect of Betaine on Protein Aggregation and Survival in *Escherichia coli***

Christopher Wojcik (North Central College)
Advisor: Jonathan Visick (North Central College)

Damage to aspartate and asparagine residues results in the formation of isoaspartate residues, which result in “kinks” in the protein, affecting protein function. Misfolded proteins expose hydrophobic regions that attract one another, resulting protein clumping, forming a protein aggregate. The L-isoaspartyl protein carboxyl methyltransferase (PCM) repairs these residues to normal. We hypothesize that as PCM restores isoaspartate residues, it will prevent protein misfolding. The previous method of measuring aggregates involved differential centrifugation and protein quantitation by the Lowry assay. Because the protein chaperone IbpA binds to aggregates, we hypothesized that we would be able to use a YFP to IbpA fusion to measure aggregates by fluorometry. To determine the feasibility of this method, we measured aggregation using the Lowry method and then compared the fluorometer results. Fluorescence correlated with the relative amount of aggregates, although with higher experimental error than in the Lowry method. This new method could be useful in determining if a chemical chaperone like betaine could substitute for PCM in reducing aggregates. Chemical chaperones have been shown to reduce the number of aggregates by either preventing the unfolding or facilitating the refolding of proteins. To begin looking at this question, we monitored survival and aggregation using fluorescent microscopy for a nine-day period for wild-type and PCM-deficient *Escherichia coli*. Preliminary results suggested in the wild-type betaine increased survival at day nine. When viewed under a fluorescent microscope, strains at high salt concentrations and with betaine appeared to have less fluorescence than low salt and no betaine.

Key Terms: E. Coli
 Protein Repair
 Protein Aggregation

CBB-11

Antioxidant Activities of Dioecious *Morus alba* Extracts

Paramita Basu (Texas Woman's University)
Advisor: Camelia Maier (Texas Woman's University)

White mulberry, *Morus alba* (*Moraceae*), has been known for its pharmacological, medicinal, nutritional and economical values around the world. In this study, total phenolics, flavonoids, and proanthocyanidins were determined in bud, leaf, and stem of male and female *M. alba* ethanolic extracts. *In vitro* antioxidant activities of male and female extracts were evaluated by 2,2-diphenyl-1-picrylhydrazyl (DPPH), ferric reducing antioxidant potential (FRAP), 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid) diammonium salt (ABTS), nitric oxide (NO) scavenging, and ferric reducing power assays. The highest phenolic, flavonoid, and proanthocyanidin contents were found in male bud (573.03 ± 1.7 mg GAE/g), female stem (111.6 ± 3.7 mg QE/g), and male bud (429 ± 1.2 mg GAE/g) extracts, respectively. Male leaf extract (100 μ g/ml) showed the highest ferric reducing power ($A_{700} = 0.23 \pm 0.0012$). The highest FRAP activity was detected in male stem extract ($A_{593} = 1.6 \pm 0.05$ μ M Fe^{2+} g^{-1}). All extracts exhibited increasing radical scavenging activities with increasing concentrations (20-100 μ g/ml). The highest DPPH, ABTS, and NO radical scavenging activities were displayed by 100 μ g/ml concentrations of male leaf ($A_{517} = 5.23 \pm 0.12$), male stem ($A_{734} = 14.3 \pm 0.211$), and female leaf ($A_{540} = 31.2 \pm 0.3$) extracts, respectively. High correlations between IC_{50} values of DPPH, ABTS, NO of male and female leaf extracts and their total phenolics, flavonoids, proanthocyanidins contents were found. Male plant extracts showed significantly higher antioxidant activities than female plant extracts indicating that *M. alba* male phytochemicals are good candidates for the treatment and/or prevention of oxidative stress-related diseases.

Key Terms: Plant Biochemistry
Molecular Biology
Cancer Biology

CBB-12

Possible Activational Differences of Orexin Neurons in Binge Eating Prone and Binge Eating Resistant Female Rats

Osasumwen Virginia Aimuwu (University Of California, Irvine), Amber D. Kimble (Howard University School of Medicine), James S. Brown (Morehouse College), Allison K. Hester (Howard University School of Medicine), Subramaniam Uthayathas (Howard University School of Medicine), and Kimberlei A. Richardson (Howard University School of Medicine)
Advisor: Kimberlei Richardson (Howard University School of Medicine)

The orexin system is one of the hypothalamic peptide families involved in food intake regulation. Alterations in orexin may lead to a higher propensity of individuals to binge eat. The purpose of this study was to determine whether there are activational differences in orexin neurons of binge eating prone (BEP) versus binge eating resistant (BER) rats in three regions of the hypothalamus (dorsomedial hypothalamus, perifornical area, lateral hypothalamus). Female Sprague-Dawley rats ($n=???$ /group) underwent eight feeding tests to determine their phenotypes based on their consumption of palatable food within a limited time interval (4 hours/test). Ninety minutes after the final feeding test, rats were perfused and brain sections were processed for Fos and orexin-A using double label immunohistochemistry. Preliminary data showed no significant difference in the number of orexin neurons and Fos-activated, orexin neurons in BEP and BER rats. There was a significant difference in Fos neurons in the lateral hypothalamus of the BEP rats. These data could provide a basis for potential pharmacological targets in the treatment of binge eating disorder and other maladaptive feeding disorders.

Key Terms: Neurobiology
Pharmacology
Molecular Biology

CBB-13

Extension-iterative saturation mutagenesis (E-ISM), a novel technique for the directed evolution of proteins

Matthew Dominguez (Eastern New Mexico University)

Advisors: Elliott Stollar (Eastern New Mexico University), Rachel Service (Eastern New Mexico University)

Extension-iterative saturation mutagenesis (E-ISM) is a new method in the directed evolution of proteins. Directed evolution mimics the process of natural selection to evolve proteins or peptides towards a specific goal; the process involves the combination of genetic mutagenesis, expression of the mutant proteins, and screening for the most stable mutant. Extension iterative saturation mutagenesis (E-ISM) is an approach which sequentially extends a protein by adding new amino acids to a growing polypeptide chain at either termini or a specific position. In this study, an SH3 domain was subjected to E-ISM. A four amino acid extension was inserted in at a specific position known to be important for peptide binding. By limiting the four amino acid extension to only four possible amino acids, screening of approximately 400 mutant proteins provides coverage of 75% of the possible mutations. The screening process involves two chemical denaturation assays and circular dichroism temperature melts. Screening results from the mutant proteins have shown mutants with enhanced stability. Once the mutant with the highest stability has been completely characterized, it can be subjected to a second round of E-ISM to further enhance its properties. This study is the beginning of what could become a highly selective way to increase protein stability and protein-protein interactions, both of which could assist in the development of novel therapeutics for protein related diseases.

Key Terms: Directed Evolution
Biochemistry
SH3 Domain

CBB-14

Benchmarking A Bioinformatic Approach To Probe The Structure And Function Of Yeast SH3 Domains

Rajkumar Shevagani (Eastern New Mexico University)

Advisors: Elliott Stollar (Eastern New Mexico University), Rachel Service (Eastern New Mexico University)

The 60 amino acid SH3 domain is one of the most important protein interaction domain in animals and is conserved across more than 1 billion years of evolution from yeast to humans. The study of SH3 domains in yeast is an excellent model for the study of protein interactions in humans. The traditional way to determine important structural and functional regions in a protein is to examine their three dimensional structures in conjunction with data of biochemical assays and mutagenesis studies, which are experimentally intensive to perform. Over the last decade there has been an explosion in sequenced genome data and a growing number of structures solved with no associated biochemical analysis. This has created a need to develop bioinformatic methods to assess the structural and functional importance of residues in a protein. In this study, by taking advantage of the current wealth of protein sequence and structure data, a new method was developed for analyzing sequence conservation for a given domain by comparing the conservation of its ancestors (orthologs) to the conservation within the family (paralogs). By using our new python based program for sequence alignment analysis, specifically conserved residues have been predicted as structurally and functionally important. These residues are unique and are expected to be responsible for the structure or function of the protein such as its binding nature. Overall, this study helps in benchmarking a method to predict new binding surfaces in yeast SH3 family as well as reveal new structurally and functionally important regions.

Key Terms: Bioinformatics
Biochemistry
SH3 Domains

CBB-15**Methods to Elucidate the Role of DSCAM in the Development of the Vertebrate Retinotectal Circuit**

Marc Piercy (University of California, Irvine)
Advisor: Susana Cohen-Cory (University of California, Irvine)

An important aspect of neural development is the formation of functional circuits in the brain. In order for dendrites partner with an axon, several processes need to take place. The dendrite must be able to recognize and make contact with an incoming axon, and must be able to recognize and avoid itself. In *Drosophila*, each neuron expressing a different isoform of the protein Down Syndrome Cell Adhesion Molecule (DSCAM) to recognize and avoid a neuron's own projections. Vertebrates only express two isoforms of DSCAM, DSCAM and DSCAM-L1, and yet the structure and function of DSCAM is conserved from insects to vertebrates. This leads to the interesting question, how do vertebrate neurons recognize self from non-self? To answer this question we must develop tools to investigate the function of DSCAM during critical times in the development of the vertebrate nervous system. Using *Xenopus laevis* as a model, we can observe the development of the retinotectal circuit in a living vertebrate. To these means, I have developed a DSCAM-GFP construct to allow us to observe how overexpression of DSCAM affects dendritic morphology and differentiation during critical times in the development of the retinotectal circuit. I have also optimized a Western blot assay to quantify DSCAM expression over time and to confirm that overexpression or knockdown of DSCAM effectively change levels of the endogenous protein in living tadpoles. With the observations made possible by these tools we hope to elucidate the role of DSCAM in the development of the vertebrate nervous system.

Key Terms: Neuroscience
 Neurobiology
 Neuron Development

CBB-16**Value of Combining SecinH3 with Sphingolipids that Induce Nutrient Transporter Loss to Kill Cancer Cells**

Sergio Serafin (University of California, Irvine),
Manuel Ramirez (University of California, Irvine),
Aimee L. Edinger (University of California, Irvine)
Advisors: Aimee L. Edinger (University of California, Irvine),
Manuel Ramirez (University of California, Irvine)

Cancer cells require continuous access to nutrients due to mutations that constantly drive biosynthetic pathways. In non-transformed cells anabolism is driven by growth factors and pathways sensitive to extracellular nutrients. When normal cells are deprived of nutrients they become quiescent and adapt their metabolism accordingly. Cancer cells continue biosynthesis despite nutrient deprivation due to activated oncogenes which desensitize the cells of environmental cues from the deletion of negative regulators of growth. Depriving cancer cells of nutrients can cause them to enter a bioenergetic crisis. The sphingolipid-based drug FTY720 is an FDA-approved, water soluble, drug for multiple sclerosis. At higher doses required for immunosuppression, FTY720 reduces surface 4f2hc. 4f2hc is a chaperone protein required for surface expression of some amino acid transporters. Our lab has shown that FTY720 down-regulates transporters for both amino acids and glucose. *In vivo* FTY720 selectively killed cancer cells and decreases nutrient transporter surface levels. In addition to reduced 4f2hc, our lab has also shown that total Arf6-GTP is reduced during sphingolipid treatment. SecinH3 is a compound that inactivates one class of Arf6-GEFs and therefore should decrease Arf6-GTP and possibly reduce 4f2hc. I hypothesize that the expression level of Arf6 or the cytohesin family of proteins will correlate with the cell lines' sensitivity to SecinH3. A combined treatment of FTY720 and SecinH3 together induced cell death on SupB15 and CCRF cells without inducing further 4f2hc reduction. This shows that SecinH3 is potentiating cell death independent of 4f2hc reduction.

Key Terms: Cancer Biology
 Cellular Biology
 Cell Metabolism

CBB-17

Formation and Restoration of Adherens and Tight Junction in Hypoxic Retinal Endothelial Cells

Natalie Wardia (Oakland University), Wendy Dailey (Oakland University), Mei Cheng (Oakland University)

Advisors: Kimberly Drenser (Oakland University), Kenneth Mitton (Oakland University)

Hypoxic retinal environments, seen in diabetic retinopathy and retinopathy of prematurity (ROP), can trigger an upregulation of vascular endothelial growth factor, otherwise known as VEGF. The high level of VEGF loosens junction protein connections between human retinal endothelial cells (HRECs). These fenestrated leaky vessels allow leakage, resulting in retinal edema. Previous studies have shown that Norrin, a ligand that activates WNT signaling, increases the integrity of retinal vessels in hypoxic retinal tissue. The purpose of our study was firstly to create an in vitro model that would mimic the loosening of cell-to-cell junction connections and secondly, to evaluate the addition of Norrin in this model. The experimental set of cells was grown in an incubator maintained with low oxygen level (1-3%) while the control cells were grown under normoxic conditions (20% O₂). After various timed incubations, the cells were immunostained for VE-cadherin or claudin-5. Hydrocortisone (2 μ M) was added to some wells as a positive control since it increases junction protein expression. Norrin (50ng/ml) was also added to the culture media in both normoxic & low O₂ conditions. We found that low O₂ incubation depleted levels of both VE-cadherin and claudin-5. However, when hydrocortisone was added to the media the border localization of VE-cadherin and claudin-5 was maintained. Norrin appeared to partially maintain the claudin-5 border localization. Western blot revealed a decrease in the total level of claudin-5 protein after low O₂ exposure for 18 hours. We believe that this model may be used to evaluate possible therapeutics such as Norrin.

Supported by The Vision Research Ropard Foundation.

Key Terms: Hypoxia
Junction Restoration
Pediatric Retinal Research

CBB-18

The *C. elegans* Casein Kinase 2 KIN-3 Acts As A Negative Regulator Of Centrosome Assembly

Megan Kabara (Oakland University), Jeff Medley (Oakland University), Mike Stubenvoll (Oakland University), Mi Hye Song (Oakland University)
Advisor: Mi Hye Song (Oakland University)

Centrosomes play a critical role in establishing bipolar spindles at mitosis. Aberrant centrosomes result in chromosome mis-segregation, leading to genomic instability. Thus, for the maintenance of genomic integrity, each centrosome must duplicate precisely once per cell cycle, only one daughter centriole per mother. While key factors necessary for centrosome duplication have been identified, it has not been fully understood how these factors interplay within the pathway and how they are modulated. Recent efforts have explored how post-translational modifications contribute to the centrosome assembly. Protein Phosphatase 2A (PP2A) has been shown to promote centrosome duplication by stabilizing key regulators (ZYG-1 and SAS-5). However, the counter-acting kinase in this context has not yet been identified. Here, we study *C. elegans* Casein Kinase 2 (CK 2), KIN-3 as a potential kinase in this regard. We observed that KIN-3 localizes to the nuclear envelope, mitotic spindles, and cytoplasm and plays a role in the early cell cycle of *C. elegans* embryos. Further, we found that KIN-3 negatively regulates centrosome assembly by controlling ZYG-1 stability and its recruitment to centrosomes. Our current data suggest that KIN-3 may counter-act PP2A phosphatase to maintain proper levels of key centrosome regulators. We are continuing to examine other factors to determine which proteins are targeted by the kinase KIN-3, and how KIN-3-dependent phosphorylation influences centrosome assembly, by employing both genetic and biochemical tools.

Key Terms: Centrosome
Cell Cycle
Casein Kinase 2



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STUDENT POSTER ABSTRACTS

CBB-19

Evaluation of Inhibitory Potential in Potential New Anti-biotic Compounds Designed Using Computer Modeling to Inhibit Glutamate Racemase

Emily Wells (Ohio Northern University), Olivia Dinsmore (Ohio Northern University), Danny Krall (Ohio Northern University), Amy Stockert (Ohio Northern University), Tarek Mahfouz (Ohio Northern University)

Advisor: Amy Stockert (Ohio Northern University)

Antibiotic resistance is growing problem affecting healthcare. Exploring new targets is essential to continue to combat the resistance. Glutamate racemase, the enzyme responsible for the inter-conversion between D- and L-glutamate in bacteria, is a potential target. Glutamate racemase is essential for viability of several pathogens, making it an ideal target for developing a new class of antibiotics. Using computer modeling, the active site of glutamate racemase from *S. Pneumoniae* was modified to create a docking model, which was used to generate compounds that were hypothesized to act as competitive inhibitors. Various compounds were explored using Kirby-Bauer screening to determine their antimicrobial activity. The gene encoding the enzyme was cloned and expressed in *E.coli* for further testing. We explored that activity of the enzyme in the presence of the potential inhibitors in order to determine the effectiveness of these potential drugs as specifically inhibiting this enzyme.

Key Terms: Enzyme Inhibition
 Kinetics

CBB-20

Methylenetetrahydrofolate Reductase Gene C677T Polymorphisms

Daniel Salatto (SUNY Plattsburgh)

Advisor: Dr. Nancy Elwess (SUNY Plattsburgh)

The Methylenetetrahydrofolate Reductase Gene (MTHFR) was studied to see if there was any correspondence with polymorphisms of a C-T nucleotide change at base 677 (C677T) resulting in the suppression of an individual's health, leading that individual to be more susceptible to a wide range of health concerns. The MTHFR gene produces an enzyme that is essential to the human immune system, which is being studied through single-nucleotide polymorphisms. DNA was collected from volunteers via buccal cells. The experimental group consists of test subjects who have Asthma. The control group incorporated subjects who lack the health characteristics of the experimental group. DNA samples were isolated, amplified and digested using restriction enzyme *HinfI* and then analyzed through gel electrophoresis. A single fragment of the 198 nucleotide base pair (bp) has been identified as homozygous (CC); three fragments of 198, 175, and 23 bp have been identified as being heterozygous (CT) and the nucleotide base pairs that have been found to be homozygous (TT) which has two nucleotide fragments of 175 and 23 bp. Statistical analysis was done to provide researchers quantitative results that compared the control group and experimental groups. Hypothesis: Individuals with Asthma will demonstrate a higher percentage of the C677T single-nucleotide change than the control group.

Key Terms: Genetics
 Molecular Biology
 Biological Science

CBB-21

Functional Analysis of β -hemoglobin gene in *Paramecium tetraurelia*

Feysel Shifa (SUNY Plattsburgh)
Advisors: Nancy Elwess (SUNY Plattsburgh), Sandra Latourelle (SUNY Plattsburgh)

The in-depth analysis of the β -hemoglobin encoding gene in *Paramecium tetraurelia* can provide insight to the functional purpose of the gene to the cell's survival. The genetic expression of the β -hemoglobin gene was examined under Oxidative and Hypoxic conditions. Conventional and real-time quantitative Polymerase Chain Reactions were used to determine levels of genetic expression under different oxygen concentrations. Complementary DNA (cDNA) was synthesized by reverse transcription from mRNA that was isolated from *P. tetraurelia* cell cultures grown under the previous conditions. Amplification of the cDNA was done at different PCR cycles. Both methods of amplification revealed higher rates of genetic expression for cell cultures grown under Hypoxic conditions. Future studies will include bacterially-mediated RNA interference (RNAi) to create a β -hemoglobin gene knockout phenotype. Cells with knockout phenotype can be studied for their response to differences in Oxygen concentration, survival rate, cell morphology and swim speeds. This study aims to better characterize β -hemoglobin gene of *P. tetraurelia* and expand its the role as a model system for other experimental approaches involving microorganisms.

Key Terms: Genetics
 Biological Sciences
 Molecular Biology

CBB-22

Engineering Biotin-Binding Immune Receptors (BBIRs) for Universal Cancer Immunotherapy

James Ham (Carnegie Mellon University), Jason Lohmueller (University of Pittsburgh)
Advisor: Olivera Finn (University of Pittsburgh)

Chimeric antigen receptors (CARs) are artificial T cell receptors that use the specific binding capacity of antibodies to re-direct engineered T cells to lyse tumor cells expressing a tumor-associated antigen (TAA). To create a universal CAR therapy we created a novel CAR that has a monomeric streptavidin targeting domain, creating a biotin binding immune receptor (BBIR). These BBIR cells can then be directed to kill tumor cells by being co-administered with tumor-specific biotinylated antibodies which will "paint" the tumor cells. Upon interaction with the BBIR cells, the biotin on the tumor cells will then lead to T cell activation and target-cell killing. In our experiments we targeted MUC1, a well-studied TAA that is over-expressed and hypoglycosylated on all adenocarcinomas. To optimize the design of the BBIR, we cloned BBIR-expression plasmids to include either CD28z or 4-1BBz T cell signaling domains. The Jurkat T cell line was transduced to express each BBIR construct, and BBIR cells were co-incubated with either MUC1-positive or MUC1-negative target cells stained with a panel of anti-MUC1 antibodies. After overnight incubation, cells were assayed for T cell activation markers CD69 and CD62L by flow cytometry. Several of the antibodies activated these markers in a MUC1-specific manner. Cells expressing BBIR-28z resulted in higher basal T cell signaling making the 4-1BB BBIR the focus of our future experiments.

Key Terms: Immunotherapy
 Immunology
 Cancer

CBB-23

Molecular and expression analysis of maize RNA Binding Motif Protein 48 (RBM48) required for proper development of seed and plant viability

Christian J. Brigolin (Oakland University), Donya Shodja (Oakland University), Federico Martin (University of Florida), Jeffery Gustin (University of Florida), Amy E. Siebert (Oakland University) A. Mark Settles (University of Florida), Shailesh Lal (Oakland University)
Advisor: Shailesh Lal (Oakland University)

The precise recognition and removal of non-coding introns from precursor-mRNA (pre-mRNA) is a complex process. Despite its fundamental importance in eukaryotic gene expression, this process is poorly understood in plants. Of the numerous splicing factors which participate in this process, a highly conserved family of Arginine/Serine Rich (SR) proteins play an important role in splice site selection during pre-mRNA processing. Our group has recently characterized an SR related maize gene, which is homologous to human RNA Binding Motif Protein 48 (RBM48). Our previous work indicates RBM48 is essential for seed development and plant viability (unpublished data). Herein, we determine the subcellular localization of RBM48 by transient expression in tobacco (*Nicotiana benthamiana*) leaves. Our results indicate that RBM48 is localized within nucleoplasmic speckle compartments, and that the SR domain is required for recruitment of RBM48 to those regions. Furthermore, co-localization and Bimolecular Fluorescence Complementation (BiFC) assays suggest RBM48 interacts with other U2AF1, U2AF2, and RGH3 (human ZRSR2), which are other core splicing factors involved in splice site selection during pre-mRNA processing. We have raised peptide antibodies against RBM48, as well as recombinant versions of each protein, for *in vitro* co-immunoprecipitation (Co-IP) assays to investigate whether RBM48 interacts with U2AF1, U2AF2, and RGH3 via direct protein-protein interaction. The data generated from these studies will no doubt provide a better understanding of the mechanisms of pre-mRNA processing in plants. This will lead to improved genetic engineering of plant species for better agronomic traits and yield.

Key Terms: Pre-mRNA Splicing
Colocalization
RNA Binding Protein

CBB-24

Preliminary Study of an Estrogen Receptor Heterodimer Inducing Compound

Shanika Kingston (Barry University), Carlos Coriano (University of Wisconsin-Madison), Taryn James, PhD (University of Wisconsin-Madison), Wei Xu, PhD (University of Wisconsin-Madison)
Advisors: Wei Xu, PhD (University of Wisconsin-Madison), Carlos Coriano (University of Wisconsin-Madison)

Estrogens are the primary female sex hormones responsible for regulation of cell growth and differentiation of the different tissues. The physiological effects of estrogens are primarily mediated by two estrogen receptors: ER α and ER β . In hormone dependent diseases such as breast cancer ER α has been shown to accelerate cellular proliferation, while ER β shows a protective effect. The ligand binding domain of these receptors mediates dimerization where homodimers (ER β / β or ER α / α) or heterodimers (ER α / β) are formed. Although the function of each homodimer is well understood, the biological role of the ER α / β heterodimer is still undetermined due to the lack of selective heterodimer-inducing compounds. Recently, the Xu Lab (University of Wisconsin-Madison) identified a compound that could selectively induce the ER α / β heterodimer and utilized to evaluate the biological response of cell lines that express both receptors. A series of ligand binding, luciferase, and cell viability assays were performed to outline the usefulness of a set of experiments to be used in a larger screening of the cellular effects of the compound that could help us decipher the heterodimer's role.

Supported by DOD ERA of HOPE Scholar Award (W81XWYH-11-1-0237) to Wei Xu and the Molecular and Environmental Toxicology Summer Research Opportunity Program (NIH- R25ES020720-05).

Key Terms: Toxicology
Oncology
Cancer

CHM-01

A Mild and Eco-Friendly Reagent for Deprotection of Phenolic Methoxymethyl Ethers

Ryan Monahan (SUNY at Plattsburgh), Oghale Obaro-Best (SUNY at Plattsburgh), Alya Aisyah Fadil Binti (SUNY at Plattsburgh)
Advisor: Rajesh Sunasee (SUNY at Plattsburgh)

Protection and subsequent deprotection of a hydroxyl group remain a common practice in multi-step synthesis of complex organic molecules. The hydroxyl group is present in many biological molecules such as carbohydrates, steroids, nucleosides, side-chain of amino acids and as intermediates in total synthesis of natural products. While a number of hydroxyl protecting groups have been developed, the methoxymethyl (MOM) group is widely used due to its ease of introduction and high stability under a variety of reaction conditions. Several reagents have been developed for the removal of a MOM group including HCl, BBr₃, pyridinium *p*-toluene sulfonate under strong acidic condition and even Lewis acids such as LiBF₄, ZnBr₂, TiCl₄, etc.. However, most of these methods have different drawbacks such as longer reaction time, low yields, refluxing at high temperature, tedious work-up procedures, toxic reagents and a barrier to acid sensitive substrates. Hence, there is still a scope to develop mild and efficient methods and new reagents for MOM deprotection. Herein, we report the utility of bismuth trichloride (BiCl₃) as a mild and eco-friendly reagent for phenolic MOM deprotection. Phenolic MOM ethers were easily cleaved using a catalytic amount of BiCl₃ in acetonitrile/water (50:1) at 50 °C. Using the optimized reaction conditions, a number of substituted phenolic MOM ethers were deprotected in good to excellent yields.

Key Terms: Eco-Friendly
Deprotection
Ethers

CHM-02

The Purification of Various Porphyrins for Subsequent use in Photochemical Reactions

Shadi Khayyo (College of Mount Saint Vincent), Valerie Khayyo (College of Mount Saint Vincent)
Advisors: Pamela Kerrigan (College of Mount Saint Vincent), Daniel Amarante (College of Mount Saint Vincent)

This research examines the synthesis and purification of porphyrins that are comprised of a heterocyclic pyrrole ring system with substituents in the meso-positions of the ring. The goal of this research is to separate two major isomers in either *p*-anisaldehyde, *p*-tolualdehyde or *p*-pyridinecarboxaldehyde porphyrin preparations. The synthesis of these substituted porphyrins was done using various para-substituted aldehydes and pyrrole. All porphyrins were also made with *p*-acetamidobenzaldehyde and the respective aldehyde in a 3:1 ratio.

The porphyrin isomers of each type are purified and separated through the use of column chromatography. Different silica and chloroform mixtures were used based on the type of porphyrin being purified. For the tolyl and methoxyporphyrin, a 60 Å mesh silica size was used. The tetra-tolyl porphyrin used only chloroform, while the tri-tolyl porphyrin used a 5% methanol to chloroform solvent mixture. The tetra-methoxy was obtained with chloroform and the tri-methoxy porphyrin required a 2% methanol to chloroform mixture. The silica used for pyridine porphyrin was a 150 Å mesh. The tetra-pyridine was obtained with pure chloroform and the tri-pyridine compound required a 2% methanol to chloroform mixture.

Purity was tested by TLC, UV-Vis, and NMR. The tolyl porphyrin purification gave a 5% yield. The methoxy porphyrin percent yield was 4.77% and the pyridine porphyrin was 5.4%. The molecules will next be used in photodynamic therapy. Porphyrin molecules also have photochemical properties and can be used as a ligand with either rhodium or osmium to form complexes that function as light harvesting material.

Key Terms: Porphyrin
Photodynamic
Photochemical

CHM-03

Prussian Green: A High Rate Capacity Cathode for Potassium Ion Batteries

Joseph Thiebes (Portland State University), Prasanna Padigi (Portland State University), Mitchell Swan (Portland State University), Gary Goncher (Portland State University)

Advisor: Raj Solanki (Portland State University)

In the synthesis of non-toxic potassium iron hexacyanoferrate battery cathode materials, the influence of the precursors, namely potassium ferrocyanide and potassium ferricyanide, on the electrochemistry and particle sizes of Prussian Blue (PB) and Prussian Green (PG) respectively, have been investigated under identical reaction conditions. The PB particles, formed by a reaction of potassium ferrocyanide, were on the order of 2–10 microns in size. The PG particles, formed by a reaction of potassium ferricyanide, were on the order of 50–75 nm in size. It was found that the particle size influences the gravimetric capacity utilization of these materials as cathodes for aqueous potassium (K⁺) ion batteries. The PG cathodes demonstrated a reversible capacity of 121.4 mAh/g, with a coulombic efficiency of 98.7% compared to PB cathodes which demonstrated 53.8 mAh/g, with a coulombic efficiency of nearly 100%. The high reversible capacity of the PG cathode is on the order of the same capacity as state-of-the-art cathodes in commercially available lithium (Li⁺) ion batteries. We interpret the increased capacity of PG batteries relative to PB batteries as being a result of the smaller particle size of PG, which results in greater surface area, and therefore greater accessibility of the cathode to K⁺ ions.

Key Terms: Energy Storage
Intercalation Materials
Cathode

CHM-04

The Effects of Alkaline and Acidic Conditions on the Staining and Surface Roughness of Micro-Hybrid Composite Resin

Eshaa Selvam (Freehold High School)

Advisor: Bapanaiah Penugonda (New York University)

Tooth discoloration is a rising concern for many people as it destroys one's aesthetic appearance, and can in turn lead to decay. The purpose of this study is to determine the effects of various alkaline and acidic beverages on the staining of micro-hybrid composite resin. This material was chosen to act as a model to predict the effects on actual teeth. Samples of this composite resin were soaked in beverages such as acid free coffee and regular coffee (both brewed in distilled water and alkaline water), distilled water, and alkaline water. The study was conducted for 45 days, in which measurements were taken every 15 days with a profilometer to observe the staining and decay imposed on the samples. At the conclusion of the study, it was determined that exposure to varying pH increases the surface roughness of dental composites, and increasing surface roughness leads to stain susceptibility of composites. It is hoped that through this study, scientists will be able to understand the effects of alkaline and acidic conditions on composite resin, and advise patients on the effects of these beverages so that consumption of them can be regulated, in turn minimizing surface roughness and on the composites and thus decreasing the susceptibility to discoloration. Using these results, the next step would be to perform the experiment on extracted teeth, in order to confirm the predictions made based on the composite resins.

Key Terms: Dentistry
pH variation
Surface roughness

EEB-01

Macroinvertebrate Ecology of a Southeastern Oklahoma Quaking Bog

Kinsey Tedford (University of Central Oklahoma)
Advisor: David Bass (University of Central Oklahoma)

An unusual wetland pond, known as a quaking bog, is located on the Oka' Yanhali Preserve in Johnston County, Oklahoma. A quaking bog develops when vegetation forms a false bottom below the surface of the water, causing the pond to shake when walked upon. There is little known about these ecosystems, and none have been described in published studies from Oklahoma. Objectives of this study included determining basic water quality, identifying macroinvertebrates present, estimating population sizes, calculating species diversity, and comparing macroinvertebrate samples from different areas of the bog. Physicochemical data and aquatic macroinvertebrates were collected in June and December of 2014. With the exception of low dissolved oxygen concentrations, the water quality was capable of supporting a healthy aquatic ecosystem. A total of 10,917 individuals representing 40 taxa were collected during the warm and cold seasons. Oligochaetes, bivalves, and chironomids dominated the collections, with 75% of all individuals categorized as detritivores. The highest species richness values and greatest number of individuals occurred in the center of the pond where water levels were the most stable.

Key Terms: Aquatic macroinvertebrates
Quaking bog
Ecology

EEB-02

Bacterial Inhibition of Water Mold and Isolation of Inhibitory Molecule from *Bacillus anthracis* and *Aeromonas jandaei*

Jacob Nesemeier (North Central College), Joshua Highsmith (North Central College)
Advisor: Nancy Peterson (North Central College)

Amphibian populations worldwide have seen a decline over the past 40 years. Water mold has a known pathogenic effect on amphibian egg/embryo populations. Bacteria can inhibit the growth of water mold. We hypothesized that bacteria were secreting a molecule that was inhibiting the water mold (*Phytophthora sp.-2014*) growth and these molecules would be isolatable. To test this, we cultured *Bacillus anthracis* and *Aeromonas jandaei* in LB broth and the bacteria was removed through centrifugation and filtration resulting in conditioned media. The conditioned media was shown to inhibit water mold growth in the absence of bacteria. Dilutions show that a 1:2 conditioned media:LB agar inhibited water mold growth more the longer the bacteria was allowed to grow before extracting the molecule of interest. The molecule was also shown to be heat stable up to 64 °C for 30 minutes at a 1:2 dilution factor. Conditioned media was washed using 95% ethyl acetate in a separatory funnel. The ethyl acetate was removed by evaporation in vacuo. The molecule of interest was extracted and was dissolved in ethanol before being added to LB agar plates and was able to exhibit significant inhibition when at a 0.83:1 concentration or higher. This molecule of interest could be an alkaloid because previous research showed that inhibition required protein in the media.

Key Terms: Inhibitory molecule
Bacteria
Water mold

EEB-03

Flexible Reproductive Mode and Offspring Development in Unisexual (All Female) Salamanders

Marisa Hildebrandt (Eastern Michigan University)
Advisor: Katherine Greenwald (Eastern Michigan University)

Unisexual *Ambystoma* salamanders reproduce via kleptogenesis, in which they “steal” sperm from males of one of several sexually reproducing species. Frequently, the sperm triggers asexual reproduction without being incorporated into the resulting (gynogenesis). However, offspring can also be created either by replacing one of the maternal genomes with a paternal version, or by adding the male genome to the full female complement of chromosomes (ploidy elevation). The goal of this study was to determine whether females preferentially use genomes from foreign vs, local males. We conducted a breeding experiment pairing females with males from their own pond versus a more distant pond, with the hypothesis that they would foreign males with dissimilar genomes. We evaluated numbers of gynogenetic or ploidy-elevated eggs and compared offspring and parental genomes to see if the paternal genome was added. We also examined developmental stages, egg and larval survival, to find whether gynogenetic or ploidy-elevated eggs developed more successfully. Contrary to our hypothesis, we found that local males’ genomes were incorporated more frequently than those of foreign males. However, the tetraploidy resulting from genome addition was associated with developmental anomalies and reduced survival during development.

Key Terms: Genetics
 Herpetology
 Molecular Ecology

EEB-04

Building A Large Phylogeny Of Archaea

Anthony Coleman (Oakland University)
Advisor: Fabia Battistuzzi (Oakland University)

Evolutionary histories are a powerful tool to reconstruct not only the early stages of life but also to understand the characteristics of Earth as a habitable planet. Of the three domains of life Archaea are among the most ancient ones holding information regarding the earliest steps of life’s evolution. Unfortunately, building stable archaeal phylogenies has proven to be an elusive task especially for poorly represented groups (e.g., Nanoarchaeota). This phylogenetic instability has often been attributed to taxon sampling or fast evolutionary rates among genes but little is known about the relative contribution of each of these conditions. We address this issue by using all of the available taxonomic samples to investigate the effect of evolutionary rates on a multi-gene dataset containing 135 species. Fifty individual trees were produced from fully represented orthologous group but did not result in a consensus phylogeny. We therefore proceeded to evaluate the effect of gene-specific evolutionary rates by creating subsets with slow and fast evolving concatenated genes. A comparison of these two phylogenies show a discrepancy in the location of the Thaumarchaeota, Nanoarchaeota and Korarchaeota suggesting an effect of evolutionary rates on their uncertain phylogenetic position. These unstable groups also negatively affect the overall accuracy of the trees in closely related clusters and also others that have traditionally been found to be phylogenetically stable. This analysis provides insights into the effect of evolutionary rates on deep phylogenies and suggest guidelines for future tree reconstructions.

Key Terms: Archaea
 Phylogeny
 Bioinformatics

STUDENT POSTER ABSTRACTS

EEB-05

The Buzz about Bee Behavior: Taking an Interdisciplinary Approach to Assess the Role of Pathogens in Bumblebee Declines

Melissa Mobley (Worcester Polytechnic Institute)
Advisor: Robert Gegear (Worcester Polytechnic Institute)

Bumblebees and other insect pollinators carry tremendous biological, social, and economic value due to the irreplaceable ecosystem service that they provide. These pollinators are essential for maintaining biodiversity and producing one third of our current diet. Over the past decade, critical worldwide pollinator populations, including several native North American bumblebee species, have declined significantly. Although the exact cause of these declines is currently unknown, one significant contributing factor is thought to be exposure to novel pathogens. However, there still remains a large gap in our knowledge of how pathogens negatively affect bumblebee health.

One way that pathogens might negatively impact bumblebee health is through sub-lethal effects on behavior (i.e. pathogens do not immediately kill bees, but alter behavior in a way that reduces survival and/or reproductive success). Here, we integrated immunological, psychological, and behavioral approaches to examine the effect of pathogens on the ability of bumblebee foragers to effectively switch between multiple floral resources; an ability directly related to reproductive output of the colony. Remarkably, we found artificial stimulation of the humoral pathway, similar to a bacterial or fungal infection, significantly impaired the ability of foragers to switch between floral resources by interfering with high-order brain functions. These results indicate pathogen exposure seriously threatens wild bumblebee health and may help explain current population declines. Our work will accelerate the development of conservation strategies and risk assessment techniques for bumblebees in North America and worldwide.

Key Terms: Native Pollinators
Cognitive Flexibility (Behavior)
Pathogens (Immunology)

EEB-06

The Clover and the Cross: The Long Term Adverse Effects of 19th Century Irish Immigration

Nicholas Malizia (College of Mount Saint Vincent),
Marielle Villanobos (College of Mount Saint Vincent)
Advisor: Ioanna Visviki (College of Mount Saint Vincent)

It has been hypothesized that susceptibility to epidemic and chronic diseases is shaped by fetal, childhood and adult experiences. In this study we examined how the early life experiences of Irish women that immigrated to the US during the 19th century contributed to their overall patterns of mortality. We compared the mortality of Irish immigrant women who joined the Catholic congregation of the Sisters of Charity of New York (S.C.N.Y.) to those of US born women of Irish descent that joined the same religious order. We obtained demographic data from the Archives of the S.C.N.Y. and for every entrant, demographic information such as secular and religious name, date of birth, birthplace, education, missions, and date of death were obtained. Our study population consisted of 1382 women that were born between 1820 and 1884 and entered the congregation between 1856 and 1902. Irish immigrants had lower survivorship even when their level of education was taken into account. They were more likely to die from pneumonia and exhibited earlier onset of heart disease. Our data offer support for the hypothesis of early life influences on adult health. The Irish born nuns spent most of their years in a religious order, sharing the same diet and environment as the US born nuns. However, they still experienced lower survivorship probably due to the adverse conditions they faced during their childhood in Ireland, as well as the hardships they encountered upon immigration to the US.

Key Terms: Epidemiology
Survivorship rates
Health

EEB-07**Genome Complexity in the Exportome of *Plasmodium falciparum***

Rita Kassab (Oakland University), Fabia Ursula Battistuzzi (Oakland University)

Advisor: Fabia Ursula Battistuzzi (Oakland University)

In 2012, the World Health Organization estimated that malaria caused 207 million clinical episodes, and 627,000 deaths. Malaria is well known from an epidemiological point of view but the evolutionary mechanisms at the base of the pathogenicity of its agents, e.g. *Plasmodium falciparum*, are mostly unknown. Our research uses bioinformatics tools to explore some of the genetic basis of *P. falciparum* with a focus on unique gene structures called low complexity regions (LCRs). These are repetitive protein sequences that are linked to high rates of evolutionary change. A subset of LCRs are homopolymeric repeats (HPRs), which are parts of the protein sequence that have a repeated single amino acid, and, because of their high frequency in Plasmodia's genomes, have been hypothesized to play a role in host-invasion mechanisms. In particular, we explore the quantitative difference of HPRs in exported proteins, which are proteins that interact with the host environment, versus non-exported proteins. Results show a significant difference in frequency of HPRs in exported vs. non-exported proteins (10.4% vs. 36.4%, respectively) and also in their amino acid composition. Because unique signatures within genomes of pathogens can act as candidates for future drug development, our in-depth analysis of HPRs in *P. falciparum* is a first step toward the identification of potentially new candidate genes that can be targeted by anti-malaria drugs.

Key Terms: *Plasmodium falciparum*
 Low complexity regions
 Evolutionary biology

EEB-08**Phenotypic Distribution Models Incorporate Ecotypic Variation Of The Dominant Prairie Grass *Andropogon gerardii* In Response To Climate Change In Midwest Grasslands**

Jacob Alsdurf (Kansas State University), Loretta Johnson (Kansas State University), Adam Smith (Missouri Botanical Garden) Nora Bello (Kansas State University), Mary Knapp (Kansas State University)
Advisor: Loretta Johnson (Kansas State University)

Andropogon gerardii is an ecologically dominant grass in the Midwest. With wide distribution across a precipitation gradient (40 -119cm/yr), we expect ecotypic variation in drought tolerance and local adaptation. Understanding ecotypic variation will help predict how a dominant prairie grass may respond to current and predicted future climate change and may inform sourcing of plant materials for restoration. Current practice uses species distribution modeling to predict an organism's response to climate change but fails to incorporate ecotypic variation within a species. Based on results from reciprocal gardens, we have shown evidence of local adaptation in big bluestem ecotypes as well as genetically-based adaptive divergence. Our study characterizes phenotypes of 37 geographically distributed populations across the Midwest to incorporate intraspecific variation into MAXENT models of current and predicted distribution under climate change. We grew plants from seed under greenhouse conditions and measured phenotypes; blade width, height, biomass, and chlorophyll absorbance. PCA analyses shows a phenotypic cline described by a longitude, mean annual precipitation, and vegetation type at the source collection site. We used PCA scores in a phenotypic distribution model to predict current and future phenotypes across the Midwest. Using climate projected for 2070, phenotypes from dry areas (short stature, low biomass, narrow leaves) are predicted to expand through the Midwest, eclipsing phenotypes from wet areas (robust, wide leaves), provided adequate migration. This novel phenotypic distribution model greatly refines current species distribution models that assume no ecotypic variation and may more accurately predict species' response to climate change.

Key Terms: Ecology
 Climate Change
 Restoration

STUDENT POSTER ABSTRACTS

EEB-09

De novo evolution of an Rnase E/RNA binding domain by expansion of tandemly repeated DNA sequences in the conserved protein phosphatase 2C (PP2C) gene in *Brassicaceae*

Anoumid Vaziri (Oakland University)
Advisor: Douglas Wendell (Oakland University)

Repetitive DNA are among the most variable types of DNA sequences, and are an established source of variation. Polymorphisms in these elements introduce functional variability in the corresponding protein, allowing them to adapt to changes in selective pressure. Studies have presented significant examples on how these highly mutable sequences have accelerated evolution of coding and regulatory regions, such as variation in skull morphology in domesticated dogs. In our study we focus on the evolution of an Rnase E/RNA binding domain by expansion of tandem repetitive DNA. Gene *Bra011448* has a predicted phosphatase domain in the plant *Brassica rapa*, upstream of this domain lies a predicted RNase E/RNA binding domain, which contains variable numbered tandemly repeated sequences (VNTR). The presence of homologs and functional analogs of this gene in a variety of prokaryotic and eukaryotic species suggests that its functions have been evolutionarily conserved, but little is known about the evolutionary history of the repeated region. To investigate this issue we acquired homologous mRNA sequences from species within the *Brassicaceae* and six other species outside of this family. Alignment and ancestor reconstructions indicate that the core sequences of the VNTRs were present in the oldest ancestor of all species analyzed. Ancestors leading towards the *Brassicaceae* all had the predicted Rne domain, yet, these sequences and the predicted Rne domain were lost in species outside the *Brassicales* order. Furthermore, units 3, 4 and 5 display higher conservation, and existence of these units correlate with the presence of the predicted Rne domain.

Key Terms: Genetics
Evolution
Molecular Biology

EEB-10

DNA Barcoding of The Great Salt Lake Invertebrates

Jonathan Clark (Weber University), Son Nguyen (Weber State University)
Advisor: Jonathan Clark (Weber State University)

Great Salt Lake (GSL), in northern Utah, is one of the largest lakes in the United States, with a total surface area of 4400 square kilometers. Arthropods constitute the most conspicuous and abundant animals inhabiting the waters of GSL. These include two principle species of brine flies (abundant in littoral areas); the corixid *Trichocorixa* (found in bays and along island margins); and the pelagic brine shrimp, *Artemia franciscana*. In addition, we have identified other invertebrates whose ecology and distribution have not been examined previously. The dynamic of interactions among these invertebrates is poorly studied and yet is an important influence in the community structure of this saline lake. DNA barcoding is the international recognized standard for species identification based on DNA. The results of this organized effort are freely available and are described at www.barcodinglife.org. A number of studies have shown that DNA barcodes are useful for species classification and are able to discriminate closely related species. This study uses the *cytochrome c oxidase* gene to establish DNA barcodes for several invertebrates associated with the GSL ecosystem. Data on intraspecific and interspecific sequence variation is considered for selected species and the utility of *cytochrome c oxidase* for examining phylogeny is discussed. These results provide genetic information that can be combined with traditional taxonomy to enhance our understanding of the biological diversity of this important ecosystem.

Key Terms: DNA
Barcoding
Invertebrates

EEB-11**Effects of Turbidity on Group Cohesion in Cyprinid Fishes of New Mexico**

Sabrina Michael (Eastern New Mexico University)
Advisor: Marv Lutnesky (Eastern New Mexico University)

Shoaling behavior in fishes is understudied and little is known about the different environmental factors that can change shoaling dynamics in fishes. For this research, we focused on ways that water turbidity can influence group cohesion in NM fishes. We hypothesized that group cohesion is sensitive to turbidity and predicted interfish distance would decrease (i.e. increase group cohesion) in turbid water, based on the selfish-herd hypothesis. Two common cyprinid fishes in NM were used, *Notropis stramineus* (Sand Shiner) and *Cyprinella lutrensis* (Red Shiner), in a repeated measures design with 25 groups of five fish each for both species. Groups were exposed to two turbidity treatments (0.34g/L, 0.68g/L) and a control (0g/L), in a randomly chosen order. A video camera connected to a PC utilized a software program, BioSense®, which automatically collected positions of fishes. We tested the influence of species (Red Shiners and Sand Shiners), and turbidity (two levels; 0g/L, 0.34g/L, 0.68g/L), and their interactions, on average inter-fish distances using a three-factor ANOVA with one factor being group identity due to the use of repeated measures. Red Shiners' and Sand Shiners' average interfish distances significantly increases ($p < .001$) in turbid water. However, we did not find significant differences between Sand Shiners and Red Shiners ($p > .05$) using this metric. More analyses are necessary, using other metrics (e.g. group polarity, velocity, etc.) before we can conclude that the species respond similarly to turbidity. Thus far, we can conclude that turbidity can influence group cohesion during shoaling in some cyprinid fishes of NM.

Key Terms: Behavioral Ecology
Fish Behavior
Shoaling Dynamics

EEB-12**Adaptive Trait Variation and Genetic Divergence of a Widespread Grass *Andropogon gerardii* across a Great Plains' Climate Gradient**

Matthew Galliard (Kansas State University), Paul St. Amand (Kansas State University), Jesse Poland (Kansas State University), Nora M. Bello (Kansas State University), Sofia Sabates (Kansas State University), Hannah Tetreault (Kansas State University), Mary Knapp (Kansas State University), Sara G. Baer (Southern Illinois University), David Gibson (Southern Illinois University), Laurel Wilson (Southern Illinois University), Brian R. Maricle (Fort Hays State University), Loretta Johnson (Kansas State University)
Advisor: Loretta Johnson (Kansas State University)

Local adaptation is fundamental to evolution, conservation, and climate change. Because of wide geographic distribution across a precipitation gradient (500-1200 mm/yr, western KS to IL), we expect variation in *Andropogon gerardii*, the ecologically dominant grass of the Great Plains. Objectives are to use reciprocal gardens to investigate ecotype differences in vegetative and reproductive traits and characterize genetic divergence among ecotypes. Ecotypes (central KS, eastern KS, and Illinois) were reciprocally planted in Colby, Hays, and Manhattan, KS, and Carbondale, IL. We evaluated ecotypic differences in vegetative and reproductive traits, predicting ecotypes would be locally adapted (perform best at "home"). Canopy area and height increased from west to east, with no evidence for ecotype differences in Colby and Hays. In Carbondale, IL ecotype showed local adaptation. In Carbondale and Manhattan, CKS ecotype flowered 20 days earlier than other ecotypes with greater probability of seed in western sites relative to other ecotypes. Morphology was primarily correlated with seasonal mean temperature. Genotyping-by-Sequencing was used to identify 4,641 SNPs and showed evidence for three genetic groups. IL ecotype existed as a distinct group. Outlier analysis identified 373 SNPs showing divergent selection. SNPs were primarily associated with seasonal diurnal temperature variation (20 SNPs) and seasonal precipitation (11 SNPs). SNPs were mapped to *Sorghum bicolor* genome, the closest relative of bluestem. Selected genes identified in genotype-to-phenotype association include: nitrogen content-glutamate synthase (nitrogen assimilation), height-GA1 (internode length), and emergence-WUSCHEL transcription factor (development). Results provide insight into candidate genes responsible for adaptive divergence and inform restoration in future climates.

Key Terms: Ecological Genomics
Trait Variation
Genetic Divergence

STUDENT POSTER ABSTRACTS

EEB-13

Reproductive Trait Variation In Big Bluestem (*Andropogon Gerardii*) Ecotypes Across The Great Plains: A Multi-Year Reciprocal Garden Study

Olivia Parrish (Kansas State University), Alexandria McChesney (Kansas State University), Matthew Gallart (Kansas State University), Sara Baer (Southern Illinois University), Nora Bello (Kansas State University), Keri Caudle (Fort Hays State University), Brian Maricle (Fort Hays State University), Evan McCrea (Southern Illinois University), Sofia Sabates (Kansas State University), David Gibson (Southern Illinois University), Laurel Wilson (Southern Illinois University) Loretta Johnson (Kansas State University)
Advisor: Loretta Johnson (Kansas State University)

Midwest grasslands are dominated by the C_4 grass big bluestem, *Andropogon gerardii*, which persists across a strong precipitation gradient (500 to 1200 mm/yr rainfall, western KS to IL). Knowledge of grasslands' responses to drought is critical for conservation and rangeland productivity. We used a reciprocal garden to investigate ecotype-specific seed production and phenology across a precipitation gradient. Three ecotypes (central KS, eastern KS, southern IL) were reciprocally planted in Colby, Hays, and Manhattan, KS, and Carbondale, IL. From 2012-2014, we recorded time to flowering and collected seed. We aim to determine annual variation in seed production and time to flowering in response to ecotype and precipitation. We predict ecotypes will have greatest seed production in their home environment. Presumably, drought-adapted CKS ecotype would show advanced flowering as an adaptation to drought. In 2012, the CKS ecotype flowered on average 20 days earlier than EKS and SIL ecotypes, independent of planting site. Moreover, when planted in Colby, the CKS ecotype was the only flowering ecotype. A less pronounced pattern of early flowering in CKS ecotype was evident in Kansas sites in 2013 and 2014 with no apparent difference in flowering time in Illinois site. Early flowering of the CKS ecotype in dry sites and years may be an adaptation to drought. CKS and SIL ecotypes both showed a home site advantage, having greater seed production in Hays and Carbondale. Results provide insight into adaptability of *A. gerardii* fitness in drier climates and will also help to identify best-suited ecotypes for restoration.

Key Terms: Ecotypes
Tall grass prairie, Big Bluestem
Intraspecific variation, Fitness

EEB-14

In the Canopy with Tardigrades and Wheelchairs: Engaging Mobility-Limited Students in Field Biology

Andrew Emanuels (Baker University), Samantha Zavertnik (Rockhurst University)

The objective of this undergraduate research project was to teach the process of field biology from hypothesis to publication and outreach by documenting the discovery and ecology of the phylum Tardigrada (water bears) in temperate forest canopies and demonstrate that ambulatory disabilities are not limitations to conducting field biology. During the program, 24 students, two in wheel chairs, climbed 350 trees at 11 different forest sites in northwest Kansas and northern Florida. More than 2,200 samples of tardigrade habitat (moss & lichen) were collected and examined. More than 20,000 tardigrades of 24 different species were captured and identified. Four species are new to science and being described. The project discovered significantly greater diversity and density of water bears higher in the trees than at the ground level where all sampling has been conducted for 250 years. The project also showed that mobility-limited students can ascend into the canopy, collect samples, use microscopes, identify new species, present posters, and write professional papers. Students learn to engage the public by conducting "Water Bear Hunts" at arboretums, university field stations, and natural history museums. This unique NSF funded REU program at Baker University puts students with or without a disability on the edge of knowledge with a little known phylum of animals in the understudied environment of the deciduous canopy and blends true exploration and discovery with a bit of adventure in the high frontier.

Key Terms: Tardigrades
Canopy
Wheelchairs

ENG-01

3D Printed Brain Model for Improved Preoperative Planning

Brittney Cotton (Clemson University), Madison Repp (Clemson University), Miriam Navarro (Clemson University), Aesha Desai (Clemson University)
Advisors: Jorge Rodriguez (Clemson University), Delphine Dean (Clemson University), Jane Joseph (Medical University of South Carolina)

Brain scans, such as MRIs and CTs, provide surgeons with preoperative imagining of a patient's brain. However, during surgery it becomes difficult to visualize the brain matter and structures of interest. Moreover, scanning while performing surgery can be inconvenient and time consuming. Fabrication of a 3D brain model using MRI scans shows potential to increase preoperative planning and practice for neurosurgeons. This project aims to develop a patient-specific, time- and cost-effective, 3D brain model using materials that resembles the physical properties of human brain tissue. This will aid surgeons in planning and predicting surgical outcomes with increased accuracy. For this study, our goal was to build a model of the core cerebral structures and a mold of the cerebral cortex. Based on MRIs provided by our collaborators at MUSC, we perform image segmentation using Mimics Research 17.0 software. Then, the segmented brain models are imported into 3-Matics Research 9.0 where virtual models were prepared for printing. A Cube 2 - 3D printer is used to fabricate the core structures and the mold for cerebral cortex using Acrylonitrile Butadiene Styrene (ABS). The molds are assembled and sealed with silicon. After the silicon has been allowed to set for 24 hours, two different materials (12% gelatin and 0.6% agarose) are poured in separate molds and stored at 4°C for 30 minutes. Two 3D brain models were fabricated resembling the physical properties of brain tissue. Our preliminary findings show that gelatin model had better integrity in comparison to the agarose model. Future work will involve searching for alternative materials for the model and evaluating model efficacy on preoperative planning in collaboration with neurosurgeons.

Key Terms: Biomedical Engineering
 Neuroscience
 3d Printing

ENG-02

Retrofit Distortion-Induced Fatigue Damaged Details in Skewed Girder to Cross-Frame Connections

Danqing Yu (University of Kansas)
Advisor: Caroline R. Bennett (University of Kansas)

Caused by secondary stresses induced by out-of-plane deformation, distortion-induced fatigue is a serious problem faced by many aging bridges. When live loads produce relative displacement between adjacent girders, fatigue moments generate and produce secondary stresses at connections. Usually, the secondary stresses are not large-magnitude, but for fatigue-sensitive details even small stress ranges may lead to cracking. Approximate 90% fatigue damages in steel bridges are caused by secondary stresses. A skewed connection is thought to be more sensitive to fatigue than a non-skewed connection since a cross-frame in a skewed bridge are connecting two different positions of a span. Developed at the University of Kansas, the angles-with-plates retrofit has shown its potential in repairing straight connections. The good performance of the retrofit is one of the motivations to apply it to skewed connections. This study mainly consists two physical tests on a 20deg skewed and a 40deg skewed girder to cross-frame connection subassemblies, and a series of computer models created by using commercially available finite element analysis software Abaqus V6.13. The study was aimed at evaluating the efficacy of the angles-with-plate retrofit in repairing fatigue damages in skewed girder to cross-frame connections, as well as better understanding the fatigue performance of the skewed girder to cross-frame connections.

Key Terms: Distortion-Induced Fatigue
 Skewed Girder to Cross-Frame
 Connection
 Angles-with-Plate Retrofit

ENG-03

Comprehensive Testbed for Integrated Secure and Reliable Vehicular Ad-Hoc Network Protocols

Kevin Lindenmayer (University of Mississippi)
Advisor: Matthew Morrison (University of Mississippi)

Automated vehicle-to-vehicle communication systems are being increasingly implemented to meet consumer demand for safety, fuel efficiency, and performance. These systems must quickly and securely establish and sever multiple connections based on proximity. Protocols for securing ad-hoc networks are already in use, and platforms currently test certain communication protocols by simulating real world traffic environments. Significant work has been done in the areas of simulating network congestion, maintaining node anonymity and efficiently processing passed messages. However, research of the effects of multiple security algorithms within vehicular ad-hoc networks (VANETs) have not been explored, nor have these protocols been implemented in simulating these networks under attack vectors over many nodes, in varying conditions, or when line-of-sight is not guaranteed. Effective wide-scale deployment of VANETs intended to provide increased safety will require reasonable assurance that all protocols in use are efficient and effective. Existing work focuses on the effectiveness of individual protocols and does not take into account an environment where multiple protocols are deployed across individual nodes, or the effects of geographical topology on network reliability and line-of-sight issues. We propose a comprehensive test-bed for design, simulation, and evaluation of anonymous authentication protocols for VANETs. Our developed infrastructure will permit rapid verification of proposed VANET protocols, and enable the development of a traffic environment simulator for verifying secure implementation and efficient response times for robust deployment hardware technologies of individual security VANET protocols.

Key Terms: VANET
Ad-Hoc Network
Security

ENG-04

Play-Action: Designing a Secure Wireless Protocol for Athletic Head Impact Detection Medical Sensors

George Humphrey (University Of Mississippi), Jason Ball (University Of Mississippi), Markis Barnes (University Of Mississippi) , Demba Komma (University Of Mississippi)
Advisor: Matthew Morrison (University of Mississippi)

Sports Brain Injuries resulting from Mild Traumatic Brain Injuries (mTBI) are a growing concern amongst professional, collegiate, and youth athletes, especially in football. Studies have revealed that many mTBIs go un-noticed. Inefficient monitoring of head impacts may result in a catastrophic condition known as Second Impact Syndrome (SIS), which is the rapid swelling of the brain, causing a second concussion before the earlier one subsided. X2 Biosystems, a Seattle-based company, has developed a medical sensor (xPatch) that monitors impacts to the head. Using a gyroscope and accelerometer developed by ST Microelectronics, the xPatch picks up rotational and translational forces on all axes. X2's new xPatch is outfitted with a radio transmitter that operates on the 915 MHz frequency band. The custom protocol for the RT is written in C programming language. Preliminary tests have yielded promising results.

As part of a Senior Design team at the University of Mississippi, under the Department of Electrical Engineering, we are collaborating with X2 Biosystems to test the xPatch development boards for power consumption, range, security, & reliability. We will modify their current of AES-128 using an AES-256 security protocol in order to reduce susceptibility to Man-in-the-Middle and side-channel attacks. Additionally, we will develop and make design choices to maximize optimization of power consumption, Tx/Rx tradeoffs, and reliability. Using equipment supplied by X2 Biosystems, a network platform will be created to install, debug, and test the wireless capabilities of the sensors and implement them as a wireless mesh access network in Vaught-Hemingway Stadium.

Key Terms: Electrical Engineering
Biomedical Engineering
Computer Science

STUDENT POSTER ABSTRACTS

ENG-05

Concussion in Women's Soccer: A Prescriptive Analysis of Force Loading during Heading

James Robinson (University of Mississippi)
Advisors: Matthew Morrison (University of Mississippi), Dwight Waddell (University of Mississippi)

Women's soccer has the highest incidence of concussions among female sports. However, relatively little research investigating the immediate and cumulative effects of soccer header on brain injury, especially at the youth levels, has been conducted. In an effort to better understand concussion in the often-under-served population of women's high school soccer players, we will investigate, both quantitatively and qualitatively the nature of force loading during heading of a soccer ball. The overall goal of the research is to provide prescriptive analysis and recommendation of form in relation to force loading of soccer headers with minimum training obtrusiveness and maximum player benefit.

Data will be collected using X2 Biosystem's xPatch, which measures force loading magnitude and direction with six degrees of linear and rotational freedom using a 3-axis gyroscope and a high-G 3-axis accelerometer. Analysis will include skill set differentiation, baseline assessment of heading skill, live-play data collection, and comparative analysis of player-by-player technique. Heading type--impact data will be analyzed to find if a correlation exists between the types of header (passing, shooting, clearing) and force loading. The distance, velocity, and angle of the incoming ball will be varied to examine how players may alter form in response to changes in these variables. In addition, form and force loading data will be contrasted for headers performed while stationary versus headers performed while moving. Player-by-player analysis will include differentiation of position (defender, midfielder, forward) to assess if correlations can be made regarding form/force loading and player position.

Key Terms: Engineering
 Neuroscience
 Concussion

ENV-01

The effects of Perchlorate exposure on growth and lipid metabolism in the model nematode *Caenorhabditis elegans*

Priscilla San Juan (University of California, Irvine)
Advisors: Stephen Sturzenbaum (King's College London), Sana Alsaleh (King's College London)

Perchlorate is a water soluble and environmentally persistent ion that is manufactured for propellant use. It is an endocrine disruptor in the human thyroid with effects so pronounced that auxiliary consequences are unknown. The model nematode *Caenorhabditis elegans*, an organism devoid of a thyroid, was used to address this shortfall. Growth was analyzed daily from the first larval stage (L1) to adult stage in two exposure conditions (1 ng/ml and 1 mg/ml perchlorate) in three temperatures (15°C, 20°C and 25°C). Results uncovered that at 15°C and high perchlorate concentration (1 mg/ml), worm development was impeded. On day 3 of exposure at 15°C, a divergence in worm size arose between doses, which was less evident at 25°C. This suggests that perchlorate induces phenotypic responses that are modulated by temperature dependent changes in metabolism. Lipid content within the lysosomal compartments of *C. elegans* was visualized using Nile Red in seven perchlorate exposure conditions (1 ng/ml to 3 mg/ml perchlorate) revealing that an increase in perchlorate exposure resulted in elevated fluorescence. A relationship was identified between lipid fluorescence and worm growth. Worms subjected to 1 ng/ml perchlorate were larger than control worms, yet exhibited weaker lipid fluorescence. Worms exposed to 1 mg/ml perchlorate were smaller than control worms but fluorescence was higher. Together this provides insight on the phenotypic effects of perchlorate exposure, aiding in the understanding of human toxicology.

Key Terms: Perchlorate
 C. elegans
 Toxicology

STUDENT POSTER ABSTRACTS

ENV-02

Investigation of the Prevalence of *Toxoplasma gondii* and *Giardia lamblia* in Oysters (*Crassostrea virginica*)

Steven Kowalyk (Manhattan College)
Advisor: Ghislaine Mayer (Manhattan College)

Bivalves, such as *Crassostrea virginica*, the Atlantic oyster, are excellent bio-indicators of marine environments. By filter feeding, these organisms often ingest various pollutants and parasites, providing an overall picture of the health of a marine habitat. *Toxoplasma gondii* is a common parasite of terrestrial animals. *G. lamblia* is a flagellated protozoan intestinal parasite that infects a wide variety of vertebrate hosts. Surprisingly, *T. gondii* and *G. lamblia* have been found recently in many marine organisms. Oysters are of economic importance as a food item and are often consumed raw. The goal of this study is to determine the prevalence of *T. gondii* and *G. lamblia* in *C. virginica*. As part of a larger study investigating protozoan parasites in bivalves, oyster samples were collected from Orchard Beach in New York on September 9, 2014 during low tide. Tissues were harvested from the oysters prior to DNA isolation. To determine whether the collected samples were infected with *T. gondii* and *G. lamblia*, polymerase chain reaction (PCR) was performed using primers specific to those parasites. We found that none of the tested samples, 0/10, were positive for *T. gondii*. However, 6/10 of the samples were positive for *G. lamblia*. It was determined that the *G. lamblia*-positive samples were of the assemblage A genotype. These data shows that Orchard Beach is likely to be contaminated with fecal matter. In addition, the results indicate that Atlantic oysters are excellent bio-indicators of human intestinal parasites. Future studies will aim at identifying the source of the contamination.

Key Terms: Microbiology
 Parasitology
 Water Quality

ENV-03

The effects of pollution and climate change on human health

Katie Baron (NYU College of Dentistry)
Advisor: Bapaniah Penugonda (NYU College of Dentistry)

Why do we pollute the air and water that we rely on for survival? There appears to be a disconnect: humans see themselves as distinct from their environment. This illusion is eliminated with evidence that environmental degradation impacts human health. Historically, we have had to learn quickly from our short term mistakes with largely felt outcomes. Heavy smog production by the industrial revolution and cholera epidemics led laws and regulations. These regulations acted to curve the anthropogenic impact on the environment while concurrently reducing the human health consequences. What makes some of today's human health issues unique is that we are exposing ourselves to low levels of pollutants over a longer time scale and the interactions between the environment and health are more complex. Climate change with its multiple levels of interaction with human health is especially challenging to quantify and study. More research is required to understand the true effects of these new environmental concerns. A link exists between: environmental degradation, human health, the importance of sustainability and the impact the environment has on health care professionals and their patients. This presentation will cover topics including: the effects of airborne pollutants on respiratory diseases such as asthma, the consequences of pharmaceuticals in fresh water systems as well as how climate change could influence the prevalence of disease. Considering the link between environmental issues and health, the union between providers and patients could be a novel way of working towards a healthier world.

Key Terms: Human health
 Environmental health
 Climate change

GSC-01

Interrogating a Paleothermometer: Understanding Alkenone Production by Algae as a Function of Light and Temperature

Imari Walker Karega (University of California, Berkeley)
Advisors: William D'Andrea (Columbia University), Andrew Juhl (Columbia University)

Alkenone paleothermometry (via the U_{37}^K and U_{37}^K indices) is widely used to reconstruct sea surface temperature and, more recently, lake water temperature. Genetic analyses indicate that there is a diversity of different alkenone-producing lacustrine haptophytes, and differences among U_{37}^K -temperature calibrations suggest that unique calibrations might be required to quantify past temperature variation from individual lakes. The only term needed to quantify U_{37}^K -inferred temperature relative to a reference period (e.g., modern temperature, or 20th Century mean temperature) is the slope of the calibration regression: U_{37}^K -temperature sensitivity (i.e., the change in U_{37}^K per °C temperature change). Here, we present new data developed by culturing four different species of alkenone-producing haptophyte algae across a range of temperatures (6-30 °C) and light levels (20-200 μ E). The simultaneous culture of four distinct species allows direct comparison of the absolute quantities of alkenones and alkenoates, as well as other lipids, produced by different species of haptophytes under identical environmental conditions. Our results indicate that algal growth rate, when controlled by light intensity, has no impact on U_{37}^K values. As expected, we find that growth temperature controls both the degree of alkenone unsaturation and the relative production of alkenones vs. alkenoates in all four species. Importantly, comparison of the four U_{37}^K -temperature calibrations resulting from our experiments with preexisting calibrations supports the hypothesis that U_{37}^K -temperature sensitivity is controlled by phylogeny. Therefore, even in the absence of a site-specific calibration, this term can be used to quantify past temperature variation from lake sediments if the genetic identity of the lake's alkenone-producer is known.

Key Terms: Paleothermometer
Geochemistry
Biology

GSC-02

Results of the 2015 field season's excavations on the first Uinta C, Eocene micro-mammal fossil locality from the Uinta Basin in northeastern Utah

Christopher Sanders (Lamar University), Melisa Guillot (Lamar University), Jeffery Westgate (Texas State University), James Westgate (Lamar University)
Advisor: James Westgate (Lamar University)

The WU-26 micro-mammal locality provides a unique glimpse into the mammal community which inhabited the Uinta Basin about 40 million years ago during middle Eocene time. WU-26 is the first micro-mammal community from the upper Uinta Formation. Stratigraphically WU-26 lies approximately 40m below the base of the Duchesne River Formation. Uinta Formation mammals define the Uintan North American Land Mammal age. Several mammal species thought to have gone extinct at the end of Uinta B time actually continued to inhabit the Uinta Basin throughout the deposition of the Uinta C Member. In the summer of 2015, our field crew collected bulk samples from WU-26 ("The Pond" locality) to increase the size and diversity of the known fauna. Our crew excavated about 3900 kg (4.3 tons) of bulk sample. After concentrating the samples by screen-washing in the Green River, we trucked the concentrate to the Lamar University Paleontology Lab. By soaking the concentrate in naphtha, and then water, and rescreen-washing, the sample was reduced to a few kilograms of bone and tooth-rich sample. It currently is being prepped for specimen discovery. Mammalian fossils are being identified to genus and or species. This fall we expect to increase the sample size of identifiable mammal specimens by up to 200 teeth. The sample size currently exceeds 600 mammal specimens. More common taxa are beginning to be represented by statistically significant sample sizes.

Key Terms: Uinta Basin
Mammal
Eocene

STUDENT POSTER ABSTRACTS

MCS-01

Empirical Investigation of Pair-wise Testing for Mixed Logical Expressions

Galen Pennell (East Carolina University)
Advisor: Sergiy Vilkomir (East Carolina University)

In software testing, when a specific approach is used, only one test set according to this approach is typically required. However, for the same testing approach, a test set can be selected in many different ways and some test values could be selected randomly (“don’t care” values). We investigate if the random selection of these values affects the quality of testing. Specifically, we analyze pair-wise testing, which requires tests to cover all possible pairs and is a great substitute for exhaustive testing.

The Automated Combinatorial Testing (ACTS) software tool was used to generate test sets with “don’t care” values, using three different algorithms. Then we randomly selected these values, repeating this process many times and creating different pair-wise test sets. We used these test sets for practice testing and compared the sets with each other. Thus, levels of the modified condition decision coverage (MC/DC) of the pair-wise test sets were compared, using the CodeCover tool. Each test set was measured against mixed logical expressions, ranging from size four to size eight, and the MC/DC coverage was recorded and analyzed. The overall average coverage ranged between 56 to 80 percent. However, the standard deviation was quite low with the range between 0.6 and 5.33 for all sizes. This shows that the “don’t care” values have an insignificant impact on the coverage and the test sets provided approximately the same quality of testing. Therefore, we can recommend pair-wise testing with a random selection of don’t care values as a reasonable practical approach.

Key Terms: Software Testing
 Pair-wise
 Modified Decision Condition
 Coverage (MC/DC)

MCS-02

Development of a Real-Time Object Tracking System for Studying Animal Behavior

Jon Patman (Eastern New Mexico University)
Advisors: Tom Brown (Eastern New Mexico University), Marv Lutnesky (Eastern New Mexico University)

Applications in the field of computer vision have been used extensively in numerous disciplines ranging from autonomous vehicle navigation to medical image analysis. A broad and potentially far-reaching sector for computer vision applications is in the field of animal behavior. Interesting, yet difficult to test hypotheses can now be tested by allowing researchers the opportunity to obtain large data sets that quantitatively represent the movement and interactions of various individuals in an environment. For example, the data can be used to extract complex information of interest such as group dynamics, movement patterns, and territorial properties of biological subjects.

The aim of this specific project was to propose a robust solution to the problem of collecting accurate and high resolution data for animals interacting in varying environments. The software was designed to be dynamic and insensitive to the type of individuals to be tracked in contrast to developing an over-specialized system that requires training sets for tracking specific animals. We also provide a performance analysis for evaluating the accuracy and reliability of the system’s various features for collecting experimental data. The exciting implications of offering a free, open-source data collection and analysis instrument to the scientific community is discussed as well as the current and ongoing research to further extend the system’s capabilities.

Key Terms: Computer Vision
 Data Collection
 Animal Behavior

STUDENT POSTER ABSTRACTS

MCS-03

Disease Detection in Social Networks: A Novel Application of NLP, Machine Learning and Big Data to Predicting Disease Spread

Manan Shah (The Harker School)
Advisor: Rok Susic (Stanford University)

We examine the use of information embedded in social network messages, such as Twitter tweets, to track public sentiment about their well-being, and track and measure actual disease activity. We hypothesize that Twitter may be used as a measure of public interest or concern about health-related events.

We isolated relevant hashtags reflecting potential disease or sickness, generated n -grams of tweets and isolated all disease-linked tweets from the Stanford Spinn3r database containing over 100 million tweets. We represented each hashtag group as a vectorized mini-corpus, which we used to ascertain relative similarity scores with other hashtag groups. We performed spam detection to reduce computational workload and improve network analysis. We chose the tweets via a combination of extensive linguistic marker regression and presence of medical term. We plotted the frequency of tweets as a function of the day of the year, resulting in a curve similar to the CDC influenza display with marked anomalies where outbreaks were encountered. The model graph's correlation coefficient with CDC graph was 0.76, indicating a strong relationship between the Twitter-centric graph and the empirical data. The correlation coefficient of the frequency graph produced by unprocessed data with CDC graph was near zero, indicating a vast improvement of our model over classical techniques.

Our approach can be easily deployed to the public health and informatics sector, is the first to readily discard and manage noise prevalent on large-scale social networks, and may provide an innovative scientific predictive tool to epidemiologists for better battling unknown infectious diseases.

Key Terms: Data Mining
 Social Networks
 Public Health

MCS-04

Smart System for Disaster Management

Junaid Zubairi (SUNY Fredonia), Anatoliy Biliciler (SUNY Fredonia)
Advisor: Junaid Zubairi (SUNY Fredonia)

This project involves extending the implementation of a system to automate the process of patient handling and processing in mass disasters involving scores of injured victims using location aware algorithms over wireless network. The MEDTOC system has been designed by Dr. Zubairi for management of patients in a mass disaster situation. The system consists of four computer programs in C and Matlab that work together for location aware placement of patients in hospitals near the disaster zone. This project involves a student at the undergraduate level in the integration of all the computer programs and setting up the hardware to enable the full functionality of the system. The student is working under the supervision of Dr. Zubairi to extend the MEDTOC for new experiments.

Key Terms: Disaster Management
 Location Aware Emergency
 Management
 Cellular and Wireless Networks

PHA-01

Testing Conditions for Optimal Performance of Tip Enhanced Raman Scattering Using Ntegra Spectra

Joseph Smolsky (University of Nebraska at Omaha, University of Nebraska Medical Center)
Advisors: Alexey Krasnoslobodtsev (University of Nebraska at Omaha, University of Nebraska Medical Center), Yuri Lyubchenko (University of Nebraska Medical Center)

Tip-enhanced Raman scattering (TERS) can be used for simultaneous structural and chemical characterization of materials with nanoscale resolution in ambient conditions, offering distinct advantages over other forms of imaging, especially for biomedical applications. The key to this is reliable TERS probes. After developing a reliable means for creating TERS active probes, the technique can be applied to imaging objects that require high spatial resolution in topography as well as structural characterization, for example fibrils and globular aggregates.

Our goal was to optimize the following conditions:

- 1) Making highly dispersed carbon nanotube (CNT) samples.
- 2) Preparation of TERS probes with various metal deposition techniques.
- 3) Testing the effects of light polarization and scanning modes on signal enhancement.

Multiple dispersing agents were tested for depositing CNT samples on glass slides: DMF, SDS, ethanol, and HCl. HCl was found to be the best dispersing agent. Enhancement factors were tested with graphene samples, comparing signals from unmodified probes with signals from probes with silver nanoparticles on the tips. Two different techniques for silver deposition were used: ion-beam sputtering and chemically grown nanoparticles. The highest signals came from the chemically modified probes. Combinations of linearly or radially polarized excitation light combined with contact or semi-contact scanning modes showed that semi-contact mode was sufficient and linear polarization generally was superior for enhancement factor tests on graphene. The study can be continued by varying deposition conditions and mapping CNT samples. This will reveal maximum possible enhancement factors and probe spatial resolutions.

Key Terms: Raman Scattering
Atomic Force Microscopy
Graphene

PHA-02

Effect of Disorder on the Structural, Magnetic, and Electron Transport Properties of $\text{CoFeCrAl}_{1-x}\text{Si}_x$ Spin Gapless Semiconductor

Simeon Gilbert (South Dakota State University), P. Kharel (South Dakota State University, University of Nebraska-Lincoln), W. Zhang (University of Nebraska-Lincoln), R. Skomski (University of Nebraska-Lincoln), S. Valloppilly (University of Nebraska-Lincoln), Y. Huh (South Dakota State University), R. Fuglsby (South Dakota State University) and D. J. Sellmyer (University of Nebraska-Lincoln)
Advisors: Parashu Kharel (South Dakota State University), Yung Huh (South Dakota State University)

Spin gapless semiconductors (SGS) are a special class of materials with novel properties combining the electronic band properties of a zero-gap semiconductor and a half-metallic magnet. These materials show high potential for spintronic applications due to their ability to conduct electrons with only one spin orientation. Several SGS compounds have been predicted theoretically, but the measured value of transport spin polarization is very low, mainly due to the structural disorder. We have synthesized and investigated the effect of disorder in one such SGS compound $\text{CoFeCrAl}_{1-x}\text{Si}_x$. CoFeCrAl and $\text{CoFeCrAl}_{0.5}\text{Si}_{0.5}$ ribbons were synthesized using arc melting and rapid quenching. X-ray diffraction patterns of the samples indicate a cubic Heschler structure with B2-type disorder, where the Cr and Al exchange positions within the unit cell. Rietveld analysis shows that 35% of Cr and Al exchanged their positions in the CoFeCrAl ribbons. This disorder was reduced to 20% in the Si doped samples. The samples show moderate magnetizations with saturation magnetizations (M_s) of about $2.0 \mu_B/\text{f.u.}$ and $2.5 \mu_B/\text{f.u.}$ for the CoFeCrAl and $\text{CoFeCrAl}_{0.5}\text{Si}_{0.5}$ ribbons, respectively, which are consistent with theoretical predictions. The Curie temperature for CoFeCrAl was 540 K which increased to 782 K after replacing half of the Al atoms with Si. The electrical resistivity of the CoFeCrAl shows a near linear decrease with increasing temperature at a rate of $-5 \times 10^{-7} \Omega\text{cmK}^{-1}$. This behavior is different from that of traditional semiconductors in which the resistivity decreases exponentially with temperature and is explained as a consequence of partial disorder.

Key Terms: Materials Science
Novel Magnetic Materials
Spintronics

PHA-03

Simulations of Strained Graphene Films on Triangular and Honeycomb Substrates

Marie Smirman (Oakland University)
Advisor: Ken Elder (Oakland University)

Graphene is an important new material with surprising mechanical and electrical properties. For most electronic applications, single crystal graphene sheets are required. Unfortunately it is very difficult to produce single crystal graphene with long range order and without defects, thus it is a critical issue to understand the growth and ordering of graphene sheets. In recent experimental research, graphene sheets have been observed to order at various misorientations with respect to the substrate that the films are grown on. Currently there is not a complete understanding of why these misorientations occur or how they will influence film properties. Thus it is an important issue to determine the most preferable film orientations. We are using a model which is an extension of the phase field crystal method (derived from density functional theory) that represents the densities of atoms by complex amplitudes. Numerical simulations of this model have been conducted to determine the free energy of the film/substrate system as a function of misorientation between the hexagonal graphene layer and a substrate of triangular symmetry. From these simulations we can predict the probability of a given misorientation as a function of misfit strain and film/substrate adhesion strength. Interestingly, the highest probability occurs at a small but finite misorientation, which may explain some of the new experimental results.

Key Terms: Graphene simulation
 Misorientation
 Condensed Matter Physics

PSI-01

Localization and Expression of Components of Energy Metabolism in Parkinson's Disease

Kimberly Veliz (University of California, Irvine)
Advisor: Richard Parsons (King's College London)

Nicotinamide *N*-methyltransferase (NNMT) is an important enzyme that metabolizes xenobiotic compounds as part of a protective effect against toxins. Although not yet known why, in patients with Parkinson's Disease there is an overexpression of NNMT, and studies have shown that an upregulation of NNMT is associated with an increase in Complex I activity and potentially, Complex IV and V. This ultimately leads to an increase in the production of ATP and an increase in reactive oxygen species, which then leads to the degeneration of dopaminergic neurons. In this study we have investigated the relationship between NNMT, tyrosine Hydroxylase (TH) as well as Complex I, Complex IV and Complex V and their potential expression on the outer cell membrane using two approaches. The first approach was to localize protein expression in the human midbrain using immunofluorescence histochemistry with confocal microscopy analysis, looking at protein expression on the extracellular membrane by the omission of the detergent IGEPAL, which permeabilizes membranes in tissue sections. With this approach we found that Complex I, IV and V staining in the absence of the detergent IGEPAL demonstrated punctate cellular staining similar to that observed in the presence of IGEPAL, which suggested that the fixation process for the tissues resulted in the permeabilization of cells and thus prevented the visualization of extracellular-only protein expression. The second approach investigated protein expression in the outer cell membrane using Western blotting, this analysis demonstrated the expression of Complex proteins in the outer membranes of cells.

Key Terms: Neurodegenerative Disease
 Immunohistochemistry
 Brain

PSI-02**Role of Cysteine-rich Domains of the vTNFR CrmB in the Immune Evasion Mechanism**

Hector Sanchez (University of California, Irvine)
Advisors: Antonio Alcami (Autonomous University of Madrid), Leyre Mestre (Autonomous University of Madrid)

During millions of years of interaction with their hosts, large DNA viruses like poxviruses have designed effective mechanisms to evade cellular immune response. One of these mechanisms is the production of viral TNF receptors (vTNFRs) characterized by mimicking the extracellular domain of TNF superfamily receptors (TNFSFRs) by binding and inhibiting the signalling induced by the host TNF superfamily ligands. Four different vTNFRs expressed by poxvirus have been described and named CrmB, CrmC, CrmD and CrmE.

The TNF-binding site of cellular TNFRs (N-term) and is characterized by three cysteine-rich domains (CRDs) named CRD1, CRD2, CRD3. While CRD1 is involved in receptor trimerization, CRD2 domain has been proved necessary for the TNF-vTNFR interaction. Nevertheless, the role of CDR3 is still unclear.

The purpose of the present work was to study the involvement of CRD3 domain in binding specificity of CrmB. In a baculovirus system three mutant proteins of CrmB were expressed exchanging the CRD3 domain of CrmC (LM24) or CrmE (LM25) or deleting the CRD3 domain of CrmB (LM26 recombinant protein) and analysed the ability of inhibiting the cytotoxic effect of TNF α or LT α . Our results show that while CRD3 domain of CrmB is not responsible for blocking cytotoxic effect induced by murine TNF α , it is necessary in case of hTNF α . The involvement of CRD3-CrmB in the inhibition of cytotoxicity induced by LT α is still unclear. This work contributes to the understanding of strategies used by viruses to evade the immune response which provide us a potent tool that could have therapeutic potential.

Key Terms: Immune evasion
Tumor necrosis factor
Viral pathogenesis

PSI-03**miR Overexpression can Induce Ectopic Proliferation in the Central Nervous System of *Drosophila melanogaster***

Orangel Gutierrez Fugon (University of California, Irvine), Chiara Pirillo, Rita Sousa Nunes (King's College London)
Advisor: Rita Sousa-Nunes (King's College London)

In *Drosophila melanogaster*, self-renewal and ending of neuroblast proliferation are crucial for the development and maintenance of the nervous system. If we understand the mechanisms involved in regulating neuroblast proliferation we may progress understanding of the pathology of some neural tumors. MicroRNAs regulate neuroblast development and their overexpression can lead to tumors. The objective is to test a UAS-miR library for the presence of ectopic proliferating cells in the adult *Drosophila* CNS, we can then investigate the microRNA's predicted targets, shortcutting *Drosophila* genome exploration. Detection of ectopic proliferation was performed by incorporation of EdU. The adult wild type brain does not have ectopic proliferation and is considered "blank" for EdU incorporation. *Drosophila* virgin females of the genotype *UAS-Dcr2; wor-Gal4, ase-Gal80/CyO; UAS-CD8::GFP* (type II neuroblast driver) were crossed with *UAS-miR* males potentially carrying also balancer chromosomes marked with Curly-O and/or Humeral dominant markers. The brains of selected progeny (overexpressing the miR in type II neuroblasts) were dissected, allowed to incorporate EdU for 2 hours, then fixed, stained and observed under the fluorescent microscope for the presence of ectopic proliferation. Larval brains and progeny of a cross to a *UAS-miR* line found in the lab to cause ectopic proliferation were used as positive controls. A total of 15 miR lines were analyzed and two (miR-314, miR-981) demonstrated ectopic proliferation. Study of the predicted target genes for these miR may provide insight into new regulatory events in neuroblast proliferation, which could be relevant to mammalian cancer research.

Key Terms: Neurobiology
Drosophila
MicroRNA

PSI-04

AII Amacrine Cells are Lost in a Mouse Model of Oxygen-induced Retinopathy

Joshua Hohlbein (Oakland University)
Advisor: Dao-Qi Zhang (Oakland University)

The retina is a patchwork of many different specialized neurons that all work together to pass visual stimuli to the brain for interpretation. Of all these neurons, this study focuses solely on the AII amacrine cell, an interneuron that transmits rod signals from the outer to the inner retina. Specifically it looked at how the cell reacts when subjected to the low-oxygen environment caused by oxygen-induced retinopathy, a condition similar to retinopathy of prematurity seen in humans. It was hypothesized that these cells exhibit substantial cell loss due to the hypoxic atmosphere surrounding them. To test the hypothesis, one week old pups were subjected to a high-oxygen environment for five days. This caused the vasculature in the retina to regress, leaving the inner portion with very little blood and oxygen supply. The mice were then sacrificed at either postnatal day 17 or 42, their eyes removed, and the retinas isolated. The retinas were then immunohistochemically stained to visualize the AII amacrine cells under a fluorescent microscope to test if there is cell loss present in the experimental group compared to the untreated control group. Once stained, the treated retinas exhibited AII amacrine cell loss in the central retina where most avascularization had occurred. The cell death was evident in the P17 models and remained consistent through P42, indicating that the cell loss is permanent. The data suggests that AII amacrine cell death may play a vital role in the loss of scotopic vision exhibited by patients with retinopathy of prematurity.

Key Terms: Oxygen-induced retinopathy
 AII amacrine cell
 Immunohistochemistry

PSI-05

Molecular Crosstalk Between Adipokines And Vascular Endothelial Cells Towards The Recruitment Of Immune Cells

Manindra Singh (Ohio University)
Advisor: Fabian Benencia (Ohio University)

Increasing evidence suggests that a chronic, low-grade state of inflammation is responsible for the exacerbation of metabolic responses and insulin sensitivity in obese subjects. Classically, adipose tissue (AT) was considered to be a compartment to store excess energy, but research in the past decade has confirmed its function as an active endocrine organ. AT secretes numerous bioactive signaling molecules called adipokines that target various tissues and control several biological responses. Studies involving obese human subjects and mice models indicate that the adipokine dysregulation is involved in the disruption of physiological homeostasis of the AT leading to insulin resistance and inflammation. The mechanism of recruitment of immune cells to AT is not clear, and the crosstalk between adipokines and vasculature may be involved. We hypothesized that adipokine signaling on vascular compartment plays a role to facilitate immune cell recruitment to AT. To test this hypothesis, human vascular endothelial cells (EC) were cultured in the presence or absence of adipokines: leptin, vaspin, and visfatin, in separate groups and resultant activation responses were measured. An antibody-based array was performed to detect over 40 cytokines released by EC in response to adipokine treatment. The cytokine secretion was further confirmed at both transcript and protein level using real-time polymerase chain reaction and enzyme-linked immunosorbant assay, respectively. We report for the first time, a cytokine profile secreted by EC in response to adipokine stimulation, and show the differential regulation of several cytokines that might be involved in the pathogenic recruitment of immune cells during obesity.

Key Terms: Inflammation
 Adipokines
 Endothelial cells

PSI-06

Computed Tomography Perfusion Imaging In Acute Ischemic Stroke: Do the Benefits Outweigh the Costs?

Brooke Willows (University of Arizona College of Medicine)
Advisor: John Karis (Barrow Neurological Institute)

Purpose: Computed tomography perfusion (CTP) studies are performed on patients with signs and symptoms of acute ischemic stroke with the supposed benefit of delineating the core infarct from salvageable penumbra. This information then helps determine the appropriateness and safety of tissue plasminogen activator (tPA) administration. The purpose of our study is to evaluate if CTP accurately identifies the infarct core in patients with acute ischemic stroke.

Population & Methods: This is a retrospective chart and imaging review of all patients who presented to the emergency department over a one-year period with the signs and symptoms of acute stroke, who underwent both CTP and magnetic resonance diffusion weighted imaging (MR-DWI), and who subsequently received tPA.

Results: CTP correctly identified the core infarct in 10% of patients and correctly identified the absence of a core infarct in 44% of patients. CTP was falsely positive in 1 patient and falsely negative in 44% of patients.

Conclusion: CTP only correctly identifies the presence or absence of a core infarct 54% of the time. This means the rest of the time, CT Perfusion may provide misinformation that could ultimately misguide treatment choices. Another imaging modality, such as rapid emergency department MR-DWI, may be the better technique to identify the infarct core.

Key Terms: Acute Ischemic Stroke
Ischemic Core
Computed Tomography Perfusion Imaging

PSI-07

Quantifying regeneration of sensory axons in the sciatic nerve following PTEN and PTEN/SOCS3 co-deletion in mouse dorsal root ganglia

Walter Guerrero (University of California, Irvine)
Advisors: Oswald Steward (University of California, Irvine) Zachary R. Gallaher (University of California, Irvine)

There are approximately 2 million peripheral nerve injuries as a result of trauma each year in the United States. The peripheral nervous system has some capacity for regeneration after injury, but full functional recovery is rare. Recent studies have shown that conditional deletion of two key signaling inhibitors—phosphatase and tensin homolog (PTEN) and suppressor of cytokine signaling-3 (SOCS3)—leads to regeneration of injured axons in the optic nerve and the corticospinal tract; however, PTEN and PTEN/SOCS3 co-deletion within the dorsal root ganglia (DRG)—the location of peripheral sensory neurons—has not been previously investigated. Therefore, we tested the hypothesis that PTEN and/or PTEN/SOCS3 co-deletion in the DRG will enhance regeneration of sensory axons following a sciatic nerve crush. Immunofluorescent staining of DRG sections determined the expression profile of PTEN and the active form of ribosomal protein S6, an indicator of PI3K signaling. Western blot analysis showed that the PI3K and Jack/Stat pathways were activated for a relatively brief period after sciatic nerve crush, both returning to baseline within seven days. We quantified regeneration in the sciatic nerve by staining for Stathmin-2, a marker of regenerating sensory axons. Our results indicate that PTEN/SOCS3 co-deletion may enhance regenerative branching beyond the injury site. The ultimate goal of this work is to guide therapeutic interventions in cases of peripheral nerve injury with the purpose of improving the lives of millions of individuals who suffer from these injuries each year.

Key Terms: Neurobiology
Anatomy
Biology

PSI-08

Respiratory Dysfunction in a Mouse Model of Rett Syndrome, an Autism Spectrum Disorder

Debolina Ghosh (Hathaway Brown School); Ian Adams (Case Western Reserve University School of Medicine); Najam Kazmi (Case Western Reserve University School of Medicine); David Katz (Case Western Reserve University)
Advisor: David Katz (Case Western Reserve University)

Rett syndrome (RTT) is a neurodevelopmental disorder caused almost exclusively by mutations in the *MECP2* gene. Because respiratory abnormalities (including apneas or pauses in breathing) are a prominent feature of this disorder, the present study investigated whether or not *Mecp2*^{tm1.1Jae} heterozygous (Het) female mice, a model of RTT, also exhibit breathing abnormalities. Nine wild-type (WT) mice were compared with eight Het mice. The mice were administered intraperitoneal injections of 0.9% NaCl (10 uL/g) (acting as controls for another experiment), placed in plethysmography chambers (EMMS) to measure breathing, and monitored by video recording. The same procedure was repeated after one week. Apneas/minute and apnea length were determined by observing each subject's breathing activity. Any pause in breathing greater than twice the average expiration time was defined as an apnea. The paired t-test was used to compare mean values of apneas/minute and apnea length in the WT versus Het mice. Fourteen observations were recorded in each group. Mean apneas/minute was 0.66 ± 0.06 in the WT mice and 1.47 ± 0.24 in the Het mice. The difference was statistically significant, $t = 3.23$ ($p = 0.003$). Mean apnea length was 1.19 ± 0.45 seconds in WT-mice and 2.01 ± 2.61 in Het-mice with no significant difference, $t = 1.15$ ($p = 0.25$). Therefore, there was significant increase in apneas/minute in the *Mecp2* Het mice compared to WT subjects, indicating that apneas/minute can be used as a reliable parameter to assess the therapeutic response to various experimental therapies in the RTT mouse model.

Key Terms: Neuroscience
Rett Syndrome
Apnea

PSI-09

Accuracy and Validity of a Novel Smartwatch Application for Shoulder and Elbow Range of Motion

David Zhu (Yale University School of Medicine), Stacey Gallacher (Yale University School of Medicine), Corinne Sommi (Yale University School of Medicine), Jason Young (Yale University School of Medicine)
Advisor: Theodore Blaine (Yale University School of Medicine)

Introduction: Measurement of joint range of motion (ROM) is an integral part of musculoskeletal examinations, and is essential for evaluating joint functionality, tracking surgical recovery, and assessing treatment efficacy. Given the prevalence of musculoskeletal injuries, having an efficient and accurate way to measure ROM is essential for healthcare providers. We built a novel smartwatch application to measure shoulder and elbow ROM, and investigate its accuracy and validity.

Methods: We developed a goniometer application for Pebble smartwatches, which uses the watch's accelerometer sensor to determine orientation when worn by the user. A smartwatch, connected via Bluetooth to a smartphone, was mounted on a custom rotating arm. The arm was rotated from 0 to 180 degrees, in 15 degree increments, and measurements from the application were recorded. Each measurement was repeated 3 times for each of the watch's three axes of rotation. Accuracy was evaluated using intraclass correlation coefficient [ICC(2,1)]. Validity was evaluated using Bland-Altman mean differences standard error of measurement (SEM)

Results: Measurements were accurate for all three axes, with ICC(2,1) values of 0.9991 (x), 0.9993 (y), and 0.9998 (z). SEM values were 0.04 (x), 0.03 (y), and 0.01 (z) degrees. Bland-Altman analysis showed no trends in measurement deviation.

Conclusion: The ROM measurements from the smartwatch goniometer application are accurate and valid. Clinical trials are in preparation. Considering the increasing popularity of smartwatches and the importance of measuring ROM, this application can be an important tool for clinicians.

Key Terms: Orthopaedics
Physical Therapy
Mobile software

PSI-10

Impact of Hydration on Mild Traumatic Brain Injury Susceptibility and Recovery

Lauren Woodard (The University of Mississippi)
Advisors: Melinda Valliant (The University of Mississippi), Matthew Morrison (The University of Mississippi)

The impact of dehydration on several key physiological functions that are critical for athletic performance is well studied. Impaired physical functions has been suggested as a limitation on proper hitting technique in contact sports. Recently, there has been suspicion that recurrent poor contact technique can lead to an increased risk of injury, particularly mild traumatic brain injury and Second Impact Syndrome. The purpose of this study is to investigate the correlation between biomarkers in sweat used to determine hydration and the head impact profiles that can be used as a preventative and proactive approach in reducing a collegiate athlete's susceptibility to mild traumatic brain injury. It is hypothesized that insufficient hydration levels will intensify head impact profiles of athletes, thus increasing an athlete's susceptibility to mild traumatic brain injury. Body mass, urine concentration, and wearable biomarker sweat sensors will be used to determine the hydration level of collegiate athletes. Real-time head impact data will be recorded and processed through X2 Biosystem's impact sensor "xPatch" during practices and games at Mississippi High Schools and University of Mississippi's Athletics teams. Following data collection, the relationship between individual hydration level and head impact severity will be further analyzed. Future research is essential to resolve the rising prevalence of sport related concussive impacts. Advancements in injury prevention strategies will decrease life threatening head impact exposure and potential long-term health consequences.

Key Terms: Nutrition
 Exercise Physiology
 Injury Prevention

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Coleman, Anthony J.	EEB-04	Pouriran, Khashayar	CBB-08
Cotton, Brittney	ENG-01	Repp, Madison	ENG-01
Dinsmore, Olivia	CBB-19	Robinson, James	ENG-05
Dominguez, Matthew	CBB-13	Salatto, Daniel	CBB-20
Emami, Michael	BSS-01	Saldana, David	CBB-01
Emanuel, Andrew	EEB-14	San Juan, Priscilla	ENV-01
Espinoza, Monica	CBB-06	Sanchez, Hector	PSI-02
Fugon, Orangel G.	PSI-03	Sanders, Christopher	GSC-02
Gallart, Matthew	EEB-12	Selvam, Eshaa	CHM-04
Ghosh, Debolina	PSI-08	Serafin, Sergio	CBB-16
Gilbert, Simeon	PHA-02	Shah, Manan	MSC-03
Grady, Jennica	See program update	Sharpe, Samantha	CBB-04
Guerrero, Walter	PSI-07	Shevagani, Rajkumar	CBB-14
Ham, James	CBB-22	Shifa, Feysel	CBB-21
Harvey, Cameron	CBB-05	Short, Kylee O.	ASNR-02
Harvey, Matthew	See program update	Singh, Manindra	PSI-05
Hildebrandt, Marisa C.	EEB-03	Smirman, Marie	PHA-03
Hohlbein, Joshua	PSI-04	Smolsky , Joseph	PHA-01
Humphrey, George	ENG-04	Tedford, Kinsey	EEB-01
Kabara, Megan	CBB-18	Thiebes, Joseph	CHM-03
Karega, Imari Walker	GSC-01	Tochtrop, Emily	BSS-02
Kassab, Rita	EEB-07	Vaziri, Anoumid	EEB-09
Khayyo, Shadi	CHM-02	Veliz , Kimberly	PSI-01
Kingston, Shanika	CBB-24	Wardia, Natalie	CBB-17
Kowalyk, Steven	ENV-02	Wells, Emily	CBB-19
Lindenmayer, Kevin	ENG-03	Willows, Brooke	PSI-06
Lynn, Annie	CBB-07	Wojcik, Christopher	CBB-10
Malizia, Nicholas	EEB-06	Woodard, Lauren	PSI-10
McDonald, Allison	See program update	Yu, Danqing	ENG-02
Michael, Sabrina	EEB-11	Zavertnik, Samantha	EEB-14
Mobley, Melissa	EEB-05	Zhu, David	PSI-09
Monahan, Ryan	CHM-01		