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UG-ANT-07

The Effect of Cage Size in Captivity on Physical Activity in *Propithecus coquereli*

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Advisor: Roshna Wunderlich (James Madison University)

The assessment of activity in captive environments is essential to animal health and husbandry decisions as well as the interpretation of experimental studies performed in these environments. The purpose of this experiment was to assess differences in locomotor activity and energy expenditure in sifakas (*Propithecus verreauxi*) in caged enclosures (CGEs) and natural habitat enclosures (NHEs) at the Duke Lemur Center (DLC). We hypothesized that sifakas in CGEs will demonstrate fewer leaps/hour, lower overall dynamic body acceleration (ODBA, a proxy for energy expenditure) and active time, and more rest time than those in NHEs since these animals are more restricted spatially. Using a datalogging inertial sensor attached to 7 sifakas, we collected three-dimensional acceleration for a total of 81 hours in CGEs (367.5– 843.5 ft^2 x 10 ft), and 170 hours in NHEs (1.5-14 acres) at the DLC. We used continuous focal animal sampling to ground-truth the data. We quantified number of leaps, ODBA, activity and rest time and compared each variable across enclosure type. Sifakas in CGEs did not differ in ODBA ($p=0.093$) but did leap more ($p=0.0008$), were more active ($p=0.02$), and rested less ($p=0.02$) than in NHEs. Our results suggest cage size alone does not determine activity levels in captive sifakas but that factors such as enrichment items may influence sifaka locomotion. We also demonstrate that inertial sensors provide a useful tool for quantifying locomotor behavior and energy expenditure in captive primates.

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Key Terms: Animal welfare
Captivity
Locomotion

GR-ANT-13

Creation of a Genomic Database using aDNA from New York African Burial Ground Soil Samples

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The New York African Burial Ground (NYABG) is a national historical site containing the remains of more than 15,000 free and enslaved Africans buried between 1640 and 1797. In 1991, the graves were excavated and the soil carefully retrieved and stored in a collection currently housed at Howard University. There are 59-cadaver associated grave soil samples available for study. It is of great importance to understand the presence of elements in these samples and the roles they may have played in relation to the inhabitants of the NYABG. Eight samples were selected for elemental analysis using a handheld x-ray fluorescence (XRF) spectrometer. This non-invasive, non-destructive technology was used to detect and identify metals in each sample. The XRF method quantitatively and qualitatively detects elements that can potentially be interpreted as indicators of human cadaver presence, contaminants, food debris, grave goods, and surrounding environmental factors. Frequently XRF is used in soil analyses to support archaeological finds or to track sources of contamination. This study, in addition to human and bacterial DNA analyses, is part of a multicomponent project aimed to reconstruct the lives of the NYABG inhabitants. Concentrations of elements such as iron, calcium and zinc were observed in all samples with evidence of lead in several samples. This investigation is the first of its kind to explore the elemental components in soil derived from human burials and to act as supporting information for human aDNA and bacterial DNA analyses. Our results also highlight the value of XRF technology and its uses in biological research.

Key Terms: Metagenomics
aDNA
Biological anthropology

HS-ASNR-01

The Effects of Soil Quality on Mimosa Strigillosa Tannin Contents and its Consequential Interaction with *Staphylococcus epidermidis*

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In the following study, the effect of soil quality was tested on *Mimosa strigillosa* tannin contents and therefore their effects on a population of *Staphylococcus epidermidis*. After a three-week exposure to low-quality (80% sand, 20% topsoil) or high-quality (100% topsoil) soil, root extracts were obtained from all plants and tested for tannin contents via the radial diffusion assay and absorbance testing. Results from both tests showed a consistent, significant increase in tannin concentrations from the plants exposed to high-quality soil (59% greater in absorbance testing and 75% greater in radial diffusion testing). Subsequently, these extracts were tested on a population of *Staphylococcus epidermidis* via the Kirby Bauer method and incubated at 37°C for a two-night (48 h) period with daily examination as to test the impact of these tannin dissimilarities in the extracts on such population. The data collected displayed, in correlation with results from previous tannin testing, that the plant group exposed to high-quality soil conditions had a more prohibiting effect on the growth of *Staphylococcus epidermidis*, given such plants' extracts created a zone of inhibition that was 68% larger than those resulting from the extracts of the plants exposed to low-quality soil. Moreover, the high-quality aspect of the soil was concluded to be of benefit when attempting to increase tannin production in plants with no secondary variables.

Key Terms: Soil quality
Tannins
Mimosa strigillosa

HS-ASNR-02

Identification of a New Algorithm Concerning the Impact of a Change in the Speed of Division of Nitrogen Fixing Bacteria on the Ecosystem of Soil with Reduced Organic Matter

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When the level of organic matter in soil changes through experimentation, the growth of the same soil bacteria changes. Soil bacteria naturally grow more slowly in soil containing inadequate organic matter than in richer soil. This phenomenon was also confirmed in the results of an experiment in which nitrogen-fixing soil bacteria were selectively cultured in the laboratory. Those bacteria were confirmed to not be a single type but diverse types as they showed at least five different growth patterns in their laboratory culture. We cultured them separately, mixed their culture products, cultured that mixed culture, and found that the nitrogen-fixing ability of nitrogen-fixing bacteria was affected. It was also confirmed that if culture products from nitrogen-fixing bacteria No. 1 are added to the other four types of nitrogen-fixing bacteria (of which growth has been suppressed due to exposure to stress), the four types of nitrogen-fixing bacteria recover their nitrogen-fixing ability despite slowing of their division.

Key Terms: Soil microbiology
Biochemistry
Environmental science

UG-ASNR-26

Neem *Azadirachta indica* Extracts Affect the Growth and Mortality of Insects - Oriental Leafworm

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The tropical neem tree, *Azadirachta indica*, has many medicinal and pesticidal properties. Research was conducted to determine if crude extracts of neem could control the Oriental leafworm, a significant pest worldwide. While synthetic chemical insecticides can provide effective control of this pest, they leave residues on the plant that may be objectionable for some producers, such as organic growers. Neem is a chemical pesticide. However, organic production often allows chemicals derived from plants to be used. Neem extracts, in contrast, are allowed in organic production systems and have the potential to be effective alternatives to synthetic insecticides. Virtually every part of the neem tree has been used by indigenous cultures for medicine or pest control for over 2,000 years. Neem extracts are used to treat various infections and to repel insects. It differs from synthetic compounds in that it is derived from a plant, rather than synthesized. But it is, nonetheless, a chemical. In this study, the efficacy of *A. indica* extracts was evaluated against different life stages of the armyworm *Spodoptera litura* (Oriental leafworm). We found that *A. indica* extracts killed 98.4% of eggs and 100% of larvae, pupae, and adult of *S. litura* exposed to extracts of neem leaves. Because *A. indica* extracts are not harmful to plants or humans, these chemicals can be used to control insects in gardens and around dwellings.

Key Terms: Azadirachtin
Pesticidal properties
Oriental leafworm

GR-ASNR-36

Elevation of Isoflavonoids and Phenolic Acid Conjugates in Response to Soybean Cyst Nematode in Wild Soybean (*Glycine soja*)

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Advisor: Bao-Hua Song (UNC Charlotte)

Plants produce a wide range of biologically active metabolites to protect themselves against attacking pests. Elucidating the key metabolites and associated pathways underlying defense responses is critical in understanding the molecular mechanisms of plant chemical defense. Non-targeted metabolomics analysis has emerged as a useful strategy to increase our understanding of the resistance-related (RR) metabolites and pathways in plant-pathogen interactions. In this study, we performed a non-targeted metabolomic analysis to determine and compare the roles of key metabolites and pathways in response to infection by the soybean cyst nematode (SCN, *Heterodera glycines*) in wild soybean (*Glycine soja*). SCN is the most devastating pest causing significant losses in soybean yield. A comparison of the metabolic profiles among SCN-resistant (S54) and susceptible (S67) genotypes showed clear differences, mirroring the effects of isoflavonoids (daidzein, daidzin, malonyl daidzin, formononetin, and iso-formononetin), as well as phenolic acids and phenolic acids-derived hydroxyl and methylated glucoside esters, in defense. To the best of our knowledge, these findings uncover the first metabolomics-based network for defending against SCN HG type 1.2.5.7. The results of the present research can facilitate the future metabolic engineering to develop novel and diverse soybean cultivars with enhanced SCN resistance and/or improved nutraceutical value.

Key Terms: Metabolomics
Resistance
Soybean cyst nematode (SCN)

HS-CBB-51

A Novel Method of Constructing Short Synthetic Gene Regulatory Elements

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Human Cytomegalovirus (HCMV) is a herpesvirus that can cause severe symptoms and be fatal for immunocompromised individuals. The HCMV gene is controlled by the CMV-IE (Human Cytomegalovirus Immediate-Early) promoter, which regulates expression activity. In previous studies, shorter promoters have been shown to increase gene expression efficiency and activity in Chinese Hamster Ovary (CHO) cells. Through the novel method constructed in this research, a new synthetic promoter was constructed derived from the GFAP (Glial Fibrillary Acidic Protein) gene regulatory sequence to increase transcriptional efficiency in CMV cells. The method included creating three different ratios of distinct GFAP primers, all three of which represented a different promoter sequence. A transcription factor binding site (TFBS) shuffled library was constructed with 2000 clones, which expressed different RNA barcodes. Each barcode was linked to a unique set of transcription factor binding sites, and thus each barcode served as a surrogate for a TFBS combination after transfection into 293 cells (Human Embryonic Kidney Cells). As a result, using RNA sequence analysis, the combination of TFBS that showed the greatest activity and the smallest length of base pairs was determined, and was used to create a compact promoter. The synthetic promoter libraries increases activity in HCMV and offers control over transcriptional recombinant activity. This technique can be applied to customize promoters for a variety of cell types and to design promoters with particular cellular constraints. Ultimately, this methodology can be used to target gene expression in other genetically-sourced diseases, including Huntington's disease, prostate cancer, and breast cancer.

Key Terms: Molecular genetics
Cellular biology
Gene regulation

HS-CBB-52

The Effect of Hyperglycemia on Gastrointestinal Development

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Maternal diabetes significantly increases the risk of birth defects in multiple organs, including those of the cardiovascular, nervous, skeletal and digestive systems. As the number of people with diabetes, and therefore the number of diabetic mothers, continues to rise, understanding the mechanisms that cause birth defects in diabetic pregnancy is of critical importance. Previous studies in animal models demonstrated that early embryonic exposure to high glucose levels can cause heart and neural tube defects, suggesting that the hyperglycemia of diabetes is the primary cause of malformations in diabetic pregnancies. However, the effect of elevated glucose on the development of the digestive organs is unknown. In the present study, we test the hypothesis that hyperglycemia causes defects in the gastrointestinal tract. *Xenopus laevis* frog embryos were exposed to varying concentrations of glucose at early stages of development (equivalent to first trimester), and then assessed at tadpole stages for the presence of malformations in the digestive organs. While control embryos developed a normal gastrointestinal tract, early exposure to levels of hyperglycemia comparable to human diabetes resulted in abnormal development and/or malrotation of the stomach, duodenum and intestine, organs that are also malformed in the infants of diabetic mothers. Ongoing experiments are focused on discovering the cellular changes in the developing gut that are caused by exposure to excess glucose. The results of this study suggest that hyperglycemic conditions can disrupt vertebrate gastrointestinal tract development, and may help explain the increased risk of digestive system birth defects in diabetic pregnancy.

Key Terms: Anatomy
Developmental biology
Toxicology

HS-CBB-53

The Effects of Dietary Supplements that Claim Nrf2 Activation in Humans on the Activation of SKN-1 in *C. elegans* and their Effects on Stress Resistance, Longevity, and Antioxidant and Enzyme Levels

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Advisor: Leya Joykutty (American Heritage School)

The purpose of this experiment was to determine if dietary supplements claiming to activate the Nrf2 pathway in humans can activate SKN-1 and affect stress resistance or longevity in three strains of *C. elegans*. The researcher hypothesized that dietary supplements activate and enhance the Nrf2 pathway, and are associated with increased longevity and enzyme production. In addition, if GFP *C. elegans* are exposed to the dietary supplements that activate the SKN-1 pathway, then the fluorescence levels will be higher in the worms with overexpressed levels of the SKN-1 pathway. Cayman Chemical assay kits and the spectrophotometer were used to determine which of the dietary supplements increased the levels of the enzymes Superoxide Dismutase, Catalase, and the levels of the antioxidant Glutathione (which are activated by the Nrf2 pathway) and fluorescence . To test for fluorescence, GFP *C. elegans* were exposed to the dietary supplements and then their fluorescence was read with a spectrophotometer. Synchronizing the *C. elegans* and then exposing them to the dietary supplements tested longevity. The first and second hypotheses were partially supported in that worms receiving the supplement Protandim had a longer observed lifespan than the worms in the control group and increased fluorescence levels, but the worms exposed to the other supplements had lower or similar results compared to those of the control group. This project can help determine which dietary supplement is better suited in preventing or delaying the onset of these diseases.

Key Terms: Skn-1 pathway
Dietary supplements
Enzymes/antioxidants

HS-CBB-55

In Vitro Biomineralization and Degradation of Mg-AZ31B Biodegradable Bone Implants from Laser-Induced Manipulations

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Because of their high biocompatibility, nontoxicity, and biodegradability, magnesium-based alloys are attractive candidates as a novel replacement for titanium (Ti-6%Al-4%V alloy) bone implants, which are responsible for a high surgical death rate due to the multiple surgeries necessary to maintain and remove it. However, Mg-alloy's rapid degradation and insufficient formation rate of Ca-minerals, most importantly hydroxyapatite (Ca10(PO4)6(OH)2), currently inhibit its implementation as a biodegradable bone implant. In this project, a unique and cutting-edge method of surface heat treatment— laser processing— was utilized to modify the Mg-AZ31B (Mg-3%Al-1%Zn) alloy to slow its rate of degradation, increase its rate of biomineralization (bone formation), and maximize the hydroxyapatite formed among other properties. Laser processing reduces the grain size, and thus increasing the β-Mg17Al12 phase, in order to improve its surface energy and resistance to degradation. To demonstrate the effectiveness of laser processing, in vitro immersions in simulated body fluid (SBF) that imitates blood plasma were used; additionally, a combination of degradation rate, biomineralization mass, and hydroxyapatite concentration was analyzed. It was concluded within experimental findings that laser-processed magnesium alloys successfully achieved balanced rates of degradation and biomineralization, as well as a 310% increase in hydroxyapatite that will lead to a healthy new bone. This not only satisfies the research goal for the implant behavior, but also establishes a significant foundation for the eventual implementation of the implant for medical use.

Key Terms: Laser processing
Magnesium AZ31B
Biomineralization

HS-CBB-56

Optimizing Goat Skin Fibroblast Culture Conditions For Cloning

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To maintain the nuclear integrity of somatic cells that provide the beneficial traits for cloning, tissue culture techniques are used to culture cells in vitro using a growth medium supplemented with serum. Scientists have commonly used growth medium containing 10% serum when growing cells. The aim of this project was to examine the effect of an increase in Fetal Bovine Serum (FBS) concentration from 0-70% added to growth medium on goat skin fibroblast proliferation. 20,000 fibroblast cells were added to 1.5 ml of DMEM growth medium supplemented with 0, 10, 20, 30, 40, 50, 60 or 70 percent FBS in each of the wells of a 24-well microtiter plate. Cells were grown for three days at 37 degrees Celsius in a CO_2 incubator. Results showed that addition of FBS to the medium increased the proliferation of fibroblast cells where maximal proliferation was observed at a concentration of 50% FBS. Further increase in FBS concentration to 60% and 70% led to a decline in fibroblast proliferation. The growth curve obtained using 10% FBS showed a decline in cell numbers after nine days. In contrast, cells grown in 50% FBS showed consistent growth until day twelve with a 15-fold increase in cell count as compared to cells grown in 10% FBS. In conclusion, to obtain an adequate number of cells for cloning, scientists can more efficiently grow fibroblast cells using 50% FBS which allows for a significant increase in cell proliferation as compared to the existing method of using 10% FBS.

Key Terms: Animal sciences
Cell biology
Cloning

UG-CBB-94

Determining the Role of UHRF1 and HELLS in Tumor Proliferation and Migration in Osteosarcoma

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Advisor: Claudia Benavente (University of California, Irvine)

Osteosarcoma is the most common type of primary bone cancer and typically arises in children and young adults. The current treatment of this cancer includes chemotherapy, but even then there is less than 50% 5-year survival rate. Current research interests in cancer studies focus on epigenetic regulation. Epigenetics refers to the changes in gene expression that allows genes to be turned "on" or "off" by mechanisms that do not involve alterations of the genetic code itself (e.g. chromatin remodeling through DNA methylation and histone modifications). Our lab is interested in studying the role of two chromatin remodelers, UHRF1 and HELLS. Ubiquitin-like with RING finger domain 1 (UHRF1) is a multifunctional protein that is involved in DNA methylation maintenance, histone methylation, acetylation and ubiquitination, while HELicase Lymphoid Specific (HELLS) is involved in *de novo* DNA methylation. Previous studies in our lab indicate that both of these genes and proteins are overexpressed in human osteosarcoma and are required for osteosarcoma survival and migration. Our goal is to determine the pathway(s)/mechanism(s) through which UHRF1 and HELLS aid tumor progression. While it has been shown that these genes are overexpressed in cancer, it has yet to be determined whether their overexpression affects differentiation of normal cells, particularly during bone development. We have generated an inducible lentiviral system that successfully overexpresses UHRF1 or HELLS in human mesenchymal stem cells (MSC). Our plan is to induce overexpression of UHRF1 or HELLS in MSC at different points of osteoblastic differentiation and assess whether this intervention alters their ability to differentiate into osteocytes. We will also analyze the effect of overexpressing these genes has on the cell's ability to migrate using a scratch-wound assay and will evaluate growth and survival potential using the CellTiter-Glo luminescent cell viability assay. Finally, we will also evaluate global DNA methylation changes caused by overexpression of these proteins.

Key Terms: Cancer
Overexpression
Cell migration

UG-CBB-95

Structural Insights into a DNA Polymerase with Non-Natural Reverse Transcriptase Activity

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Advisor: John Chaput (University of California, Irvine)

DNA polymerases, ubiquitous enzymes found in all kingdoms of life, replicate DNA using DNA templates. Recent studies demonstrate that *Geobacillus stearothermophilus* DNA polymerase I large fragment (Bst), also has the ability to reverse transcribe xenonucleic acids (XNAs). XNAs are synthetic genetic polymers containing non-natural sugar or nucleobase moieties. We postulate that structural characterization of Bst in complex with template/primer duplexes containing DNA and XNA templates will shed light into the mechanism of Bst promiscuity. We propose to use single-crystal X-ray crystallography to determine the three-dimensional structure of Bst in complex with different heteroduplexes. To that end, Bst was overexpressed in *E. coli* cells and purified using tandem liquid column chromatography. Purified Bst was incubated with a three-molar excess of the primer/template duplex and the resulting complex was used to set up approximately six hundred sparse-matrix crystallization conditions. Crystal growth was monitored periodically and layers of plate-like crystals were identified after three days from several conditions. Preliminary X-ray diffraction analyses of the crystals using an in-house X-ray source revealed weak diffraction (~6-8 Å). Further screening and optimization produced three dimensional, single crystals with 2 Å resolution. Data from these crystals is being analyzed and the resulting binary structures will be compared to previously solved binary structures of Bst with different templates in order to understand the mechanism and promiscuous activity of Bst DNA polymerase.

Key Terms: Synthetic biology
X-ray crystallography
Polymerase

UG-CBB-96

Longevity Outcomes and Genetic Regulation in Curly Wing *Drosophila*

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Caloric restriction (CR) is a systematic approach to eating that limits caloric intake without limiting essential macro and micronutrients. The purpose of this study is to observe if a calorically restricted feeding schedule leads to lifespan increases in experimental *Drosophila* along with the expression of longevity related genes via mRNA analysis. *Drosophila* were separated into calorie restricted groups CR1 (50) and non calorie restricted group NCR1 (50). In fly adulthood, the experimental (CR1) *drosophila* were fasted twice for 5 hours each week while the NCR1 drosophila were held at a constant. Two tailed T-tests will be used to evaluate the differences in mortality between CR1 and NCR1, and mRNA analysis will be conducted on 10 of longest surviving flies from CR1 and NCR1 for the potential explanations for time of death. The results are not yet evident as CR1 and NCR1 are alive, but we expect the preliminary results to suggest that CR1 flies under a 2 tailed T-test analysis will have statistically significant differences ($P \leq 0.05$) in longevity along with retarded disease processes within longest surviving flies of CR1 comparatively to NCR1.

Conclusion: The experiment is currently ongoing, but our future directions will include analyzing glucose regulation in calorie restricted flies for translational diabetic management and the introduction of glucosinolates (novel compounds in specific vegetables) to the *drosophila* diet as they are noted for their chemopreventative properties in mammals.

Key Terms: Calorie restriction
Drosophila
Longevity

UG-CBB-97

A Three-Dimensional Culture Method to Assess the Role of Stress Hormone in Osteoarthritic Degradation

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Osteoarthritis (OA) is the most common form of arthritis. OA results from the degenerative changes in the protective articular cartilage of the moveable joints. There has been an increase in the development and use of 3D culture models in the study of disease. 3D models can accurately mimic the in vivo environment when compared to 2D cell culture. We sought to create a 3D culture model to define the role of stress hormones in osteoarthritic degeneration. A model was established through the chondrogenic differentiation of mouse mesenchymal stem cells in a synthetic hyaluron matrix. We grew them in the matrix for 28 days with chondrogenic medium. Cultures were assessed for chondrogenic differentiation at 14, 21, and 28 days through qPCR analysis of chondrogenic markers; day 21 was established as the peak. Hyaluronidase was introduced at day 21 to induce cartilage matrix damage to mimic first step osteoarthritis degradation. The hyaluronidase treated chondrogenic pellets were then paraffin embedded, sectioned, and morphology examined after Masson's Trichrome staining. Chondrocyte lacunae and a mesenchymal perichondrium were apparent, and degradation to the outer perichondrium was evident. After establishing the damage model, we examined the role of stress hormones through exposure to dexamethasone for 7 days following damage. qPCR analysis of chondrogenic markers RUNX1, RUNX2, SOX9 indicate that stress hormones can have significant influence on damage induced cartilage degradation. Using our newly established damage model, we will continue to assess the role of stress hormones in osteoarthritis.

Key Terms: Chondrocytes
3-D culture
Hyaluronidase

UG-CBB-98

Using Chemical Genetics and Protein Localization to Understand Signaling Pathways in Eukaryotic Cells

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Advisor: James Moseley (Dartmouth College)

Schizosaccharomyces pombe is a model organism used to study cellular signaling pathways including the regulation of cell size and division. Many of the mechanisms for maintaining cell size in eukaryotic cells are unknown, while human diseases including cancer result from unregulated cell growth and division. *S. pombe*, like most eukaryotes, couple cell size regulation with cell cycle progression and enter mitosis upon reaching a critical cell size. In all eukaryotes, initiation of mitosis is regulated by a kinase which phosphorylates cyclin dependent kinase (Cdk1) and inhibits entry into mitosis. In *S. pombe* Wee1 kinase phosphorylates Cdk1 to inhibit mitosis. The kinase Cdr1 appears to phosphorylate and inhibit Wee1 kinase activity, allowing the initiation of mitosis. Cdr1 localizes to the cell cortex and associates with a related kinase Cdr2 and Wee1 forming node structures. We hypothesize that Cdr2 recruits Cdr1 to the cell cortex where Cdr1 phosphorylates Wee1 to inhibit its activity. We hypothesize that Wee1 phosphorylation by Cdr1 is dependent on Cdr1 localization to the cell cortex. To test this hypothesis, truncations were made in Cdr1 which resulted in the delocalization of Cdr1 from the cell cortex. This led to elongated cells due to delayed entry into mitosis. Truncations of Cdr1 will be tagged with Green Fluorescent Protein (GFP) while Cdr2 will be tagged with GFP-binding peptide to relocalize Cdr1 to the cell cortex. If Cdr1 kinase activity is dependent on localization to the cell cortex, kinase activity would be expected to be recovered.

Key Terms: Fission yeast
Mitosis
Protein localization

UG-CBB-99

Foxg1 Dosage in Establishment of Brain Excitatory/ Inhibitory Balance

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Advisor: Corinne Houart (King's College)

In the embryonic forebrain known as the telencephalon, the transcription factor *foxg1* is expressed throughout the structure in a gradient with a high ventral concentration and a lower dorsal concentration. This gradient of *foxg1* expression plays a major role in maintaining ventral and dorsal identities through the tight regulation of the Sonic Hedgehog signaling in the ventral side and Wnt signaling in the dorsal side. This transcription factor is conserved throughout vertebrates from zebrafish to mice and great apes. However, the mammalian *foxg1* contains an additional exon that is absent in zebrafish *foxg1*. The goal for my project is focused on determining the effects of telencephalic development in a *foxg1* dosage dependent manner. We will also identify the contribution(s) of the mammalian exon to telencephalon development. We will reach these objectives by modulating the expression of *foxg1* through injections of the mouse variant, *mfoxg1*, tagged with EGFP regulated under a UAS promoter into a zebrafish:GAL4 line. We will also inject a similar construct contain the zebrafish *foxg1*, *zfoxg1*, into a zebrafish:GAL4 line and from there make a comparison and association between morphological characteristics and expression levels for both *zfoxg1*and *mfoxg1*. To track expression levels, we will perform *in situ* hybridizations for ventral and dorsal specific genes and monitor any differences between *zfoxg1* injected, *mfoxg1* injected, and uninjected wildtype embryos. Further investigation would be needed to help garner support for telencephalic development being *foxg1* dosage dependent.

UG-CBB-100

Effect of Global Systems for Mobile Communication Radiation on Expression Levels of Heat Shock Protein 20 in *Pieris rapae*

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Advisor: Dr. Nancy Elwess (State University of New York at Plattsburgh)

Would you stop using your cell phone if you knew it had the potential to harm certain cells of your body? It is known that cellular devices operating on the Global Systems for Mobile communication or a GSM™ bandwidth have a phenotypical effect on *Paramecium* (Cammaerts, 2011). In order to measure possible harmful effects that cell phone emissions might cause to humans, studies must first be performed on lower class organisms. The organisms utilized in this study were *Pieris rapae* (cabbage white butterflies). Two groups (experimental and control) had separate and equal light sources and volumes of nourishment throughout experimentation. They were housed in the same lab, minimizing temperature changes. The only difference is that the experimental group was within close constant proximity of a cell signal repeater. A device that mimics GSM™ radiation at a constant power and dB output over a known area, this helps to control the randomness of radiation emission cell phones typically emit. Increased expression levels of HSP20 (heat shock protein 20) in experimental specimens would suggest a stressed environment and advocate that GSM™ radiation is harmful to the cellular function and entire organismal homeostasis.

Key Terms: GSM
Heat Shock Protein 20
Pieris rapae

UG-CBB-101

Analysis of the Binding of αA-crystallin (66-80) Peptide to Recombinant Human and Guinea Pig αA-crystallins *In Vitro*

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Advisor: Frank Giblin (Oakland University)

αA-crystallin, a major protein present in both the human and guinea pig lens, plays an important role in maintaining lens transparency. The protein exists as large multimers of 20 kDa subunits. Since there is no turnover of protein in the center of the lens, αA-crystallin can remain for many years, eventually degrading into fragments such as αA-(66-80) peptide. This peptide can bind to intact αA-crystallin to form "hydrophobic patches", resulting in formation of insoluble aggregates and nuclear cataract. The peptide has beta-amyloid characteristics and forms amyloid fibrils when incubated alone. Here, we investigated *in vitro* binding of αA-(66-80) peptide to recombinant human and guinea pig αA-crystallin, and subsequent aggregate formation, using transmission electron microscopy (TEM). Proteins (0.5 mg/ml) were incubated with peptide (0.1 mg/ml) for 24 hrs at 37° C, and analyzed by TEM. With human αA-crystallin, the peptide induced formation of large clusters of aggregates of αA-crystallin multimers. In contrast, for guinea pig αA-crystallin, long, linear amyloid fibrils containing multimers of αA-crystallin were formed. Here, it appeared that the peptide first formed long amyloid fibrils, followed by binding of αA-crystallin multimers to produce large aggregates. Sequences of human and guinea pig αA-crystallin differ by only 8 out of 173 amino acids. Studies are underway to determine the amino acid that is critical for formation of fibrils. Nuclear cataract and certain neurodegenerative diseases are known as "protein aggregation diseases". A better understanding of αA-crystallin amyloid fibril formation may lead to therapies for both nuclear cataract and neurodegenerative diseases.

Key Terms: Cell biology
Cataract
Microscopy

UG-CBB-102

Targeted Elimination of Chemoresistant Acute Myeloid Leukemia Cells Using Non Cell Cycle Dependent Mechanisms

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Advisor: Gerard Madlambayan (Oakland University)

Chemotherapy is used to treat acute myeloid leukemia (AML); however, with high relapse rates, AML continues to perplex the medical and scientific communities. In order to develop more effective therapies, a deeper understanding of the mechanisms governing AML growth and relapse is needed. We previously demonstrated a novel mechanism whereby AML-induced endothelial cell (EC) activation leads to subsequent leukemia cell adherence and quiescence. Since chemotherapy targets proliferative cells, the adherent population evades standard therapeutic approaches, identifying these cells as potential mediators of relapse. We hypothesized that targeting non-cell cycle dependent mechanisms may allow us to eliminate the adherent AML cell population. In these studies, we tested the ability of a drug combination comprising ABT-199 (Bcl-2 inhibitor) and CUDC-907 (dual HDAC/PI3K inhibitor) to kill adherent AML cells by targeting apoptosis-associated proteins. Using a co-culture system of AML and ECs, we found that the combination of ABT-199 and CUDC-907 was able to effectively induce apoptosis of adherent AML based on Annexin V staining. Initial studies using non-adherent AML cells has shown that enhanced apoptosis is due to an increase in free Bim mediated by the dissociation of Bim from Bcl-2 (ABT-199 effects) and stabilization of Mcl-1 (CUDC-907 effects) leading to activation of Bad and Bax, leading to apoptosis. Ongoing studies are now being performed to determine if the effect of ABT-199 and CUDC-907 combination treatment will kill adherent AML cells in co-cultures.

Key Terms: Cell biology
Apoptosis
Cell culture

UG-CBB-103

Decreased Glutamate Transporters in Retinas of Oxygen-induced Mice

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Advisor: Dao Zhang (Oakland University)

Glutamate is a primary excitatory neurotransmitter in the central nervous system as well as in the vertebrate retina. This neurotransmitter allows for the communication between cells of the retina. However, increased glutamate activity may lead to retinal cell death via a mechanism of excitotoxicity in degenerative eye disorders. The goal of this study is to determine whether retinal cell death in oxygen induced retinopathy (OIR) is a result of increased glutamate activity. The OIR mouse model was used to mimic vessel loss and vessel formation stages found in retinopathy of prematurity (ROP), a disease that affects low-birth-weight premature infants and can lead to blindness. An antibody against glutamate transporters was used to determine the expression of glutamate transporters throughout the retina in OIR and age-matched mice. We found that there was a decrease in glutamate transporter expression in the majority of the retinal layers quantified. Since the role of glutamate transporters is to translocate glutamate from the outside to the inside of a cell, the decreased expression of retinal glutamate transporters may increase the levels of extracellular glutamate which results in glutamate excitotoxicity of retinal cells. Our results indicate that dysfunction of glutamate transporters may play a crucial role in ischemic diseases such as ROP.

Key Terms: Cell biology
Glutamate transporter
Retina

UG-CBB-104

Casein Kinase II Opposes PP2A to Regulate Centrosome Duplication

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Advisor: Mi Hye Song (Oakland University)

Proper cell division is of great importance to maintain genomic integrity. During cell division in animal cells, centrosomes serve as the primary microtubule-organizing center and establish mitotic bipolar spindles that ensure the accurate segregation of chromosomes. Thus, tight control of centrosome number and function is critical for normal cell proliferation and development. It has been shown that deregulation of centrosome duplication leads to abnormal centrosome numbers and function, causing chromosome missegregation, aneuploidy and tumorigenesis. In our lab, we use the model, *Caenorhabitis elegans* to study the mechanisms of centrosome biogenesis. While it is clear that the kinase ZYG-1 is required for centrosome duplication in *C. elegans*, we still do not understand the precise mechanism by which ZYG-1 contributes to centrosome duplication. Recent studies suggest that phosphorylation of ZYG-1 influences ZYG-1 stability and activity. Protein Phosphatase 2A (PP2A) positively regulates ZYG-1 stability through the regulatory subunit SUR-6. Conversely, Casein Kinase II (CK2) negatively regulates ZYG-1 levels at the centrosome. Built on these findings, we set out to test the hypothesis that $PP2A^{SUR-6}$ and CK2 might counteract to regulate ZYG-1 activity and/or stability through their opposing biochemical roles as kinase/phosphatase. Our data show that inhibiting CK2 by RNAi restores embryonic viability and centrosome duplication to temperature sensitive *sur-6(or550)* mutants, suggesting that CK2 might antagonize $PP2A^{SUR-6}$ in centrosome assembly and embryonic development. To understand how $PP2A^{SUR-6}$ and CK2 coordinate their actions to regulate centrosome duplication, we are currently investigating how knocking down $PP2A^{SUR-6}$ and CK2 affect centrosomal levels of ZYG-1 and other centrosome duplication factors by using genetic and biochemical approach.

Key Terms: Cell biology
C. elegans
Cell division

UG-CBB-105

Effects of Prenatal Music Stimulation on Early Embryonic Development of *Gallus gallus*

Emma Strujo (SUNY Oswego)
Advisor: Poongodi Geetha-Loganathan (SUNY Oswego)

It is believed that listening to classical music such as Beethoven or Mozart will promote fetal brain development, although there has been no solid scientific evidence. Earlier studies on chick embryos and rat pups have shown increased size of brain cells when exposed to classical music such as Mozart, thus focused on the effect of music on growth phase during late embryonic development past the patterning and organogenesis. Here we investigate the effect of different genre music (classical/rock) on early embryonic development in chicken embryos as pregnant women are constantly exposed to music even during early pregnancy. Incubation of fertilized chicken eggs were carried out at 37°C and a relative humidity of 80. We tested two different types and decibel levels of classical and rock music on embryo development. To provide music impulse an iPod with a playlist connected to speaker was set inside the incubator and the music played for every 15 min with a 45 min of recorded silence in between. Control eggs were incubated at the same condition but received no sound impulse. Following incubation the embryos were fixed at two different stages, day 9 and 16, to analyze the phenotypes causes by sound exposure. Also the morphological parameter such as height, weight, forelimb/hind limb length, beak size, and eye diameter were measured. We found that high decibel music (HDM) irrespective of the genre increased the mortality rate in chicken embryos. Further HDM resulted in severe morphological defects due to delayed development. We presently investigate the effect of different levels of music on early embryo development.

Key Terms: Music stimulation
Chicken embryos
Developmental biology

UG-CBB-106

A Gradient of Shh Regulates SMOC1 Expression in Developing Limbs of the Chick

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Advisor: Clemens Kiecker (King's College)

The protein Sonic Hedgehog (Shh) is a morphogen responsible for polarizing the distal part of the limb. As limbs develop, digit identity is defined by a Shh concentration gradient, which raises the question: how are different structures produced by the same morphogen? Although we know that different concentrations of Shh protein induce different digit identities, the early transcriptional response underpinning changes in the identity of digit primordia have not been described. Our hypothesis is that a gradient of Shh regulates different combinations of genes dose-dependently in the early limb bud, and that these genetic markers define digit identity. Our objectives were (1) to find sets of genes regulated by different concentrations of Shh, and (2) describe the spatial expression of these genes with *in situ* hybridization. Insights from a previous transcriptome study predicted 80 genes that are expressed in response to different Shh concentrations in chick limbs, and we described their spatial expression during eight different stages of development spanning a critical phase of digit formation. One candidate marker, the Secreted Modular Calcium-binding protein 1 (SMOC1), had promising results having an expression pattern that appearss to mark digit 4 primordia in stages as early as HH21. The clinical relevance of this gene in digit formation was previously described as mutations in Smoc1 have been associated with Waardenburg anophthalmia syndrome, eye and limb anomalies. The expression of Smoc1 in response to a specific Shh concentration suggests a possible involvement in translating the Shh morphogen gradient into a specific digit identity.

Thank You

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UG-CBB-107

Identifying the Source of Infection in Snapping Turtle (*Cheleydra serpentine*) Eggs

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Advisor: Poongodi, Geetha-Loganathan (SUNY Oswego)

Microbial infections are one of the main causes for loss and extinction of animal wildlife posing a serious threat to ecosystem and biodiversity. It was observed that *Chelydra serpentina* (snapping turtle) eggs collected from Rice Creek Field Station (RCFS), SUNY Oswego, were infected with an unknown microbial contamination that lead to the death of 58% of clutches collected in last four years. We isolated and characterized the microbial colonization from the infected eggs and identified pathogenic fungal (Fusarium) and bacterial (Bacillus and Pseudomonas) species infecting *Chelydra serpentina* eggs inhibiting embryo development. Here, we continue to identify the source of fungal infection (soil or transmitted from parents or both) that is found to be a possible threat to significant loss in population sizes of snapping turtles. To collect swab samples from adult turtles, netted traps were set up around the RCFS during summer 2017 and swabbing method involved gentle scraping of the epithelium using sterile Q-tips. Soil samples were also collected from nesting and non-nesting areas and all the samples were stored at 4°C until analyzed. Cultures from samples collected were established on plates with Fusarium specific Rose Bengal medium. Morphological and molecular characterizations of cultures are performed to identify the infecting species.

Key Terms: Fungal infection
Turtle embryos
Developmental biology

UG-CBB-108

DNA Recognition by BRCA1 Protein Domains

Francesca Iacovo (Oakland University), Ann Fuelle (Oakland University), Colin Wu (Oakland University)
Advisor: Colin Wu (Oakland University)

The BRCA1 gene codes for a tumor suppressor protein that repairs double-stranded DNA breaks. Mutations in the BRCA1 gene are strongly linked to the onset of breast and ovarian cancers. The molecular mechanism by which the BRCA1 protein recognizes DNA damage remains unclear. In this work, we examined the DNA binding properties of three BRCA1 domains: DBD1, DBD2, and BRCT. Using Biolayer Interferometry (BLI) assays, the affinities of these individual BRCA1 protein domains to DNA structures that mimic repair intermediates were measured. The equilibrium constants determined from these binding experiments were used to rank the DNA binding preferences for these BRCA1 domains. These findings show that DBD1 preferentially binds to single stranded DNA and has a weaker affinity for double-stranded DNA and G-quadraplexes. DBD2, however, retains strong affinity for single-stranded DNA but does not interact with G-quadraplexes. Surprisingly, the BRCA1 BRCT domain, which has been shown to bind to phosphorylated proteins, displayed strong interactions with single-stranded DNA. The modular nature of these BRCA1-DNA interactions may allow recognitions of different damaged DNA structures. These DNA binding results will be supplemented with *in vivo* DNA repair studies to further dissect the tumor suppressive role of BRCA1 in human cells. Understanding of the BRCA1-DNA binding preferences can potentially lead to more precise cancer treatment in the future.

Key Terms: Biochemistry
DNA binding
BRCA1

UG-CBB-109

Repair of G-quadruplex DNA Facilitated by the FANCJ Helicase and the REV1 Polymerase

Mena Jirjees (Oakland University), Colin Wu (Oakland University)
Advisor: Colin Wu (Oakland University)

G-quadruplexes (G4s) are DNA structures formed by guanine rich nucleic acids. Damaged G4s can interfere with essential cellular processes such as DNA replication and RNA transcription. The mechanism by which damaged G4s are recognized and processed is not well-understood. The human FANCJ helicase facilitates DNA replication pass G4 forming regions and participates in DNA crosslink repair and homologous recombination. In a previous study, we have identified an AKKQ amino acid motif in FANCJ that allows this helicase to target G4 structures. In this work, we used fluorescence spectroscopy and biolayer interferometry (BLI) based binding assays to show that a FANCJ AKKQ peptide binds to G4 DNA with high affinity. Our BLI experiments also indicate that a separate FANCJ motif, known as the "PCNA Interacting Peptide" (PIP) can bind directly to the REV1 DNA repair polymerase. Taken together, these results are consistent with a model where FANCJ targets a stalled replication fork at a G4-containing DNA site, and then directly recruits REV1 to efficiently replicate DNA across from the unfolded quadruplex.

Key Terms: Biochemistry
Enzyme
G4s/ DNA

UG-CBB-110

Alpha A Crystallin (66-80) Peptide Enters Cultured Human Lens Epithelial Cells and Binds to Alpha A Crystallin

Annika Grupp (Oakland University), Frank Giblin (Oakland University)
Advisor: Frank Giblin (Oakland University)

Alpha A crystallin is a major protein in the lens that is vital for maintaining transparency of the tissue by performing a chaperone-like function to prevent protein precipitation in the lens center. With age, the protein degrades in the center of the human lens to form alpha A (66-80) crystallin peptides, which are believed to bind to alpha A crystallin causing aggregation of the crystallin and eventually nuclear cataract. The purpose of this study was to determine whether alpha A (66-80) peptide present in culture medium would be taken up by cultured human lens epithelial cells (LECs) and bind to alpha A crystallin within the cells to form aggregates. Cultured human SRA $_{01/04}$ LECs were exposed to fluorescently-labeled alpha A (66-80) peptide for one hour and then incubated normally for 24 hours. Immunocytochemistry, using a fluorescently-labeled alpha A crystallin antibody, was employed to stain the protein within the cells, and images were taken with a fluorescence microscope. Evidence of peptide binding was visualized through co-localization of the peptide and alpha A crystallin fluorescent stains. The results showed for the first time that alpha A (66-80) peptide can enter cultured human LECs and bind to alpha A crystallin to form aggregates. These data provide evidence for a possible role for this peptide in causing human nuclear cataract, and may help in developing therapies for preventing or delaying this type of lens opacity.

Key Terms: Cell biology
Protein
Alpha A crystallin

UG-CBB-111

Characterizing a Novel Genetically Engineered Mouse Model of Alveolar Rhabdomyosarcoma

Nina Kuprasertkul (Duke University)
Advisor: Corinne Linardic (Duke University)

Rhabdomyosarcoma is a rare pediatric cancer of mesenchymal origin comprising features of skeletal muscle. Of the two histological subtypes, alveolar rhabdomyosarcoma (aRMS) and embryonal rhabdomyosarcoma (eRMS), aRMS has the worse prognosis. High risk aRMS cases are hallmarked by the t(2;13) chromosomal translocation encoding for the oncogenic fusion protein PAX3-FOXO1. These tumors are frequently metastatic at diagnosis, for which the 5-year survival rate reduces to less than 10%. Previous investigations from our laboratory revealed that the Hippo (MST1/2) tumor suppressor pathway may play a role in aRMS. To further explore how this pathway contributes to sarcomagenesis, we developed a novel genetically engineered mouse model (GEMM) of aRMS showing that Pax3-Foxo1 fusion positive mice null for the MST1/2 kinases (Pax3P3F/P3F; Cdkn2aFl/Fl; MSTFl/Fl; Myf6ICN/+) develop significantly more tumors compared to wild-type MST controls ($p = 0.0009$). In the present study, we first confirm the recombination of alleles in our model using PCR. We also show by immunohistochemistry that GEMM derived tumor tissues have classic aRMS morphology and stain positively for the skeletal muscle markers used in standard clinical diagnosis: MyoD, Myogenin, and Myf5. Metastasis assays on GEMM derived cell lines demonstrate that compared to wild-type MST controls, MSTNull cells have increased invasion and motility. Overall, the results show that our mouse model encompasses the expected genetic changes and histopathology of aRMS, and presents promising avenues for modeling metastasis. Future studies will seek to utilize the MSTNull model to further characterize mechanisms for disease progression of aRMS; for example, by interrogating candidate genes for metastasis.

Key Terms: Oncology
Genetics
Molecular biology

UG-CBB-112

Monitoring ATP kinetics after DNA damage using FRET biosensor

Emmanuel Moncada (University of California, Irvine)
Advisor: Michael Berns (University of California, Irvine)

DNA damage can occur through UV light exposure, cellular metabolism, ionizing radiation and exposure to certain chemicals. In response to DNA damage, different damage-signaling enzymes become activated, such as ATM (ataxia-telangiectasia mutated), ATR (ataxia telangiectasia and Rad3-related protein), DNA-Pk (DNA-dependent protein kinase) and PARP (poly ADP ribose polymerase). ATP is an important energy source for cellular activities. However, detailed kinetics of ATP concentration changes following DNA damage induction, and its regulation are not well delineated. Here we use a fluorescence resonance energy transfer (FRET) sensor that allows measurements of intracellular ATP concentration in live cells at a single cell level. This FRET ATP sensor binds at a high affinity to ATP resulting in a fluorescence signal where intensity is proportional to ATP concentration. HeLa cells were transfected with each of three subcellular location-specific FRET ATP sensors (cytoplasm, mitochondria, or nucleus) to separately analyze changes of ATP levels in these subcellular compartments. DNA damage was induced using methyl methanesulfonate (MMS) or a 780nm laser. Changes in ATP concentration were observed over four hours following damage induction. DNA damage using both MMS and the 780nm laser caused a reduction of ATP in all three cellular compartments. Previous studies indicated that PARP activation results in ATP depletion. We found that addition of a PARP inhibitor, but not ATM/DNA-PK inhibitors, resulted in the reversal of damage-induced ATP depletion. These results indicate that PARP signaling is the primary regulator of the cellular ATP level during DNA damage response and repair.

Key Terms: PARP
ATR
DNA-Pk

HS-CHM-161

Biomineralization of Polyetheretherketone Through Surface Modification and Simple Chemistry

Aida Wen (American Heritage School)
Advisor: Iris Thompson (American Heritage School), Kevin Kang (Florida Atlantic University)

Polyetheretherketone (PEEK) has been widely used to make orthopedic and spinal devices; however, its ability to integrate with surrounding bone tissue has yet to be improved. This study investigated the effect of various surface modifications on biomimetic calcium phosphate formation on PEEK surface. Four different types of surface modifications include roughening by using sand paper, concentrated phosphoric acid (PA), sodium hydroxide (NaOH), and concentrated sulfuric acid (SA, sulfuration). Calcium phosphate mineralization was induced biomimetically by soaking PEEK disks in a modified supersaturated calcification solution (mSCS) buffered at pH 7.4 for 2 days at body temperature (37°C). An alternative mineralization method was also employed by incubating sulfuric acid treated disks with a beta tri-calcium phosphate (BTCP) slurry at room temperature. SA had much stronger reaction with PEEK surface than PA or NaOH. After the mSCS coating process, calcium phosphate mineral formation was consistently found on all the disks. Preliminary scanning electron microscopy and energy-dispersive X-ray microanalysis revealed discrete hemispherical deposits on most disks, consisting of fine calcium phosphate crystals. A thicker, continuous coating was observed on phosphoric acid treated disks. It appeared that delamination occurred more often on the disks with a thicker coating as compared to the disks with discrete deposits. The roughness of the disks did not seem to have an effect on coating formation. The BTCP method seems also promising for the SA treated disks. PEEK surface was successfully mineralized through surface modifications and simple chemistry. Future research is under way to improve coating evenness and adhesion.

Key Terms: Polyetheretherketone
Biomaterials
Supersaturated calcification solution

UG-CHM-171

Development of a Fluorescent Probe for Cancer Stem Cell Imaging

Sara Dibrell (University of Texas at San Antonio), Thomas Bearrood (University of Illinois at Urbana-Champaign)
Advisor: Jefferson Chan (University of Illinois at Urbana-Champaign)

Cancer Stem Cells (CSCs) are a small population of invasive tumor cells with stem cell-like properties that evade most chemo- and radiotherapies. After surviving anti-cancer treatment, CSCs differentiate and repopulate tumor cells. Thus the efficiency of tumor resection can be improved by targeting CSCs. CSC upregulation of a biomarker for stemness, aldehyde dehydrogenase (ALDH), allows for their identification and removal. ALDH catalyzes the oxidation of aldehydes, detoxifying cells and inducing differentiation via the retinoic acid pathway. We have developed a fluorescent probe that is specific for ALDH1A1, one of 19 human isoforms of ALDH, for use in live cell imaging. We have also made significant advancements in the development of a probe with pan-ALDH reactivity. Since it is not known which isoform is responsible for the ALDH activity of CSCs in different cancers, it is important to study the overall elevated activity of the ALDH family. Our modular probe can to be modified with fluorophores or anti-cancer drugs and allows for the fluorescent imaging, study, and clinical application of CSCs.

Key Terms: Chemical biology
Organic chemistry
Cancer

UG-CHM-172

Preparation of Recombinant Flavodoxin for Single Molecule Fluorescence Experiments

Edward Blocker (Clemson University)
Advisor: Hugo Sanabria (Clemson University)

The function of a protein is dependent upon its structure which in turn is determined by the unique sequence of amino acids the protein is made of. We describe a methodology to prepare a protein of interest for Förster resonance energy transfer (FRET) experiments at ensemble and single molecule conditions to gain insight into the mechanisms responsible for protein folding. We use Flavodoxin as a model system to study non-sequential folding pathways. Flavodoxin is a good candidate for study because computational theory predicts two folding pathways, each with a unique dependence on a specific amino acid. We employ two different site specific mutations (V33A and V88A) from the wild type sequence to directly monitor Flavodoxin's folding and unfolding pathways. For FRET experiments, we substitute two residues for cysteines in order to fluorescently tag them with a donor and acceptor fluorophores utilizing maleimide chemistry. We use these prepared samples to learn about the principles that lead to non-sequential folding and long-range amino acid interactions in protein folding and unfolding dynamics.

Key Terms: Phsyics
Biophsyics
Spectroscopy

UG-CHM-173

Computational Studies of a Donor-Acceptor1-Acceptor2 System for Solar Cell Application

Natasha VanTassell (Siena Heights University)
Advisor: Krishanthi C. Weerasinghe (Siena Heights University)

Most of today's energy comes from non-renewable sources like coal and fossil. Unless we give serious thought about renewable energy sources, the problem of energy crisis cannot be solved. Renewable energy sources can reduce our dependence on fossil fuels and also helps to reduce greenhouse gas emissions. Solar cells, if made more efficient, would be able to solve both problems. Solar cell uses sunlight to produce electricity in an efficient and cost effective way. In this particular research, a donor-accepter1-acceptor2 system is being studied by testing different electron donors and electron acceptors that showed to be a great potential candidate for solar cell application. Density Functional Theory (DFT) calculations were performed using the Gaussian16 software. HOMO- LUMO gaps, molecular orbital diagrams, and calculated absorption spectra showed how each part of the molecule in the system would be able to interact as a whole. It is expected that this will present a new and effective sensitizer to be used in solar cells as well as pave the way for future developments.

Key Terms: Chemistry
Solar energy
Computational chemistry

UG-CHM-174

An Electrochemical Investigation into the Unorthodox Redox Properties of Gadolinium and Europium Bridged Polyoxometalates

Imran Tariq (Quinnipiac University)
Advisor: James Kirby (Quinnipiac University)

Polyoxometalates are complex inorganic ions self-assembled from multiple metals and oxygen. Electrochemical analysis of single atom bridged monosubstituted ions in solution have demonstrated unusual redox properties. The investigation was to discern whether concentration would affect the redox potential, which was tested using cyclic voltammetry. The samples tested were prepared using the polyoxometalate $[P_2W_{17}O_{61}]^{10-}$ bridged by europium(III) and gadolinium(III). Previous testing has already demonstrated a shift in potential when the concentration of potassium ions has been varied, and research has been done verifying the importance of the pH of the solutions. This investigation demonstrated what effect the actual concentration of the ions has on this phenomenon.

Key Terms: Electrochemical
Redox properties
Chemistry

UG-CHM-175

Synthesis of Novel Schiff Base Ligands with Pendant Imidazole Rings: Evaluation of Metal Complexes Having Distinct Lewis Acid and Base Moieties

Brandon Knouse (Hampden-Sydney College)
Advisor: Paul Mueller (Hampden-Sydney College)

Four ligands were prepared from the reaction of 1-(3-aminopropyl)imidazole with various aldehydes. Three ligands were prepared as Schiff bases of the amine with substituted salicylaldehydes. Separately, another ligand, 2-{[3-(1H-imidazol-1-yl)propyl] amino}-5-nitrobenzaldehyde, was prepared by a nucleophilic aromatic substitution. The ligands were characterized by FT-IR, 13C NMR, and 1H NMR. The ligands were complexed with transition metal salts, and these coordination complexes were analyzed through Job's plots of the UV-Visible spectra and by Microwave Plasma – Atomic Emission Spectroscopy.

Key Terms: Organic chemistry
Schiff base ligand
Lewis acid catalysis

UG-CHM-176

Purification, Structure Determination and Characterization of the Coupling Reagent Ethyl 2- (tertbutoxycarbonyloxyimino)-2-cyanoacetate (Boc-Oxyma)

Carlos Vasquez (University of California, Irvine
Advisors: Gregory Weiss (University of California, Irvine), Mark Richardson (University of California, Irvine)

Coupling reagents directly convert carboxylic acids into activated esters, and provide a step-economic synthesis of esters and amides under mild conditions. Such reagents are required for the synthesis of peptides. A notable advance in the field of coupling chemistry was the development of phosphonium, aminium, and uronium salts which generate activated esters without additives, other than stoichiometric base. The most prominent of these coupling reagents are based on N-hydroxybenzotriazole (HOBt), which have been reclassified as UN0508, class 1.3C explosives. Less dangerous alternatives are therefore highly desirable. In 2013, a non-hazardous and plausible successor to HOBt was introduced. Ethyl 2-(tert-butoxycarbonyloxyimino)-2-cyanoacetate (Boc-Oxyma) was reported to generate activated esters without epimerization of the chiral α-carbon to yield esters, amides and thioesters. However, despite the obvious implications, the use of Boc-Oxyma as a coupling reagent has been non-existent. We hypothesized problems regarding the purity, characterization, and behavior of Boc-Oxyma, and set out to investigate the compound's identity and true potential as a coupling reagent. Here we provide the following: a convenient chromatography-free method for synthesis on multi-gram scales; a crystal structure determined by X-ray crystallography; and a full correction of physical properties. Furthermore, our results show that Boc-Oxyma effectively delivers activated esters via a decarboxylative pathway in the presence of only catalytic amounts of base, but is ineffective in amidation and thioesterification synthesis, which challenge what has been reported in literature. We hope this study not only convinces the wider chemical community of the identity of Boc-Oxyma, but also serves to establish the compound's use in coupling reactions.

Key Terms: Synthesis
Coupling reagents
Organic chemistry

UG-CHM-177

Comparative Anatomy and Physiology of the Electronic Cigarette: Coil Configuration Affects Toxic Chemical Emissions and E-liquid Consumption

Tetiana Korzun (Portland State University)
Advisors: Robert Strongin (Portland State University), Jorge Escobedo (Portland State University)

Considering the increasing population of e-cigarettes, especially among young tobacco-naïve users, there's a need for accurate quantification of toxicant levels for further toxicological assessment. There is currently interlaboratory variance in emission levels due to the rapid, ongoing emergence of a wide array of new device configurations and e-liquid flavors, and the lack of standardized analytical protocols. Attempts to configure an e-cigarette standard for research purposes led to the production of the Standardized Research E-Cigarette (SREC). However, most studies use devices based on their availability and popularity with vapers in order to better reflect real-world conditions. The relatively efficient wicking and air flow properties of newer devices afford higher evaporation rates while keeping device heating elements cooler. Herein, we show how specific configurations of the e-cigarette heating element and wicking materials account for wide variations in the evaporative dynamics occurring in different devices. We found that vertical heating coil configurations can afford relatively high wicking efficiency along with lower levels of the toxic byproducts of e-liquid degradation. The porous media of the wicking material can be envisioned as comprising an evaporative and a wet layer. Temperature probes placed within the wet layers of the cotton wick in different devices revealed that higher evaporative layer mobility corresponded to horizontal heating coil configurations. The rate of evaporative layer expansion and wet layer contraction was thus higher in horizontal coils compared to their vertical analogs.

Key Terms: Electronic cigarettes
Degradation products
Aerosol

UG-CHM-178

Nanofibers for Injectable Bone Scaffold

Mary Malloy (University of Arkansas), Parker Cole (University of Arkansas)
Advisor: Ryan Tian (University of Arkansas)

Disease, injury, and trauma defect the bone and present a complication to doctors and patients alike, as replacing the damaged bone is difficult and expensive. The ideal orthopedic implant has optimum surface area and roughness, strength, and biocompatibility. Titanium implants have been utilized for years in the orthopedic field with recent discoveries showing that oxide layers, comprised of TiO2, have led to enhanced osteointegration. Titanium dioxide nanomaterials offer durability, low toxicity, and strength that is comparable to native bone. Likewise, other heavy metals such as Zirconium, Niobium, and Tantalum are highly efficient for biomedical applications but can lead to steep costs. Herein, we are reporting the development of a novel, scalable synthesis mechanism to arrive at doped (Zr-, Nb-, or Ta-titania nanofibers for integration with an injectable hydrogel composite to serve as a dynamic bone tissue scaffold.

Key Terms: Nanofiber
Titanium dioxide
Injectable bone

UG-CHM-179

A Novel Organocatalytic Ring-Expanding Domino Process Towards the Total Synthesis of (+)-Ervatamine and Related Systems

Michelle Javier (University of California, Irvine)
Advisor: Andre Cobb (King's College)

Seven-membered rings fused with an indole, known as cyclohepta[b]indoles, are a common motif in a variety of natural and pharmaceutical products. The structure motif has received a lot of attention because of their association with biological activities such antimicrobial, antitumor, and anti-inflammatory activities. Due to these reasons, the development of an efficient and cost effective methodology to access cyclohepta[b]indoles is ideal. The project aims to synthesise cyclohepta[b]indoles via a novel organocatalytic domino reaction using bifunctional hydrogen-bonding catalysis. The organocatalytic cascade reaction will achieve increased molecular complexity and induce enantioselectivity in the product. The starting material that was synthesized bears a substituent that resembles a michael acceptor on 3-position of the indole.The synthesized compound has been tested against nitroolefin and also against acrolein. It was hypothesized that a six-member ring intermediate is formed via Friedel-Crafts alkylation followed by a Plancher rearrangement via 1,2-bond migration of the benzylic position to generate the 7-membered ring structure. To test the hypothesis, the reaction between the starting material and nitroolefin was carried out in different conditions using a variety of organocatalysts at room temperature. The starting material itself was also alternated by reducing the alpha-beta unsaturated ester to an aldehyde using diisobutylaluminium hydride. The work presented here shows the optimization of the reaction to access cyclohepta[b]indoles. Preliminary results have provided ways to improve the chemical pathway to achieve a organocatalytic cascade reaction. Future work includes adding a para-methoxide on the protecting group of the benzyl.

Key Terms: Natural product
Organic chemistry
Organocascade

GR-CHM-186

Synthesis of a Bifacially Binding Janus Nucleobase Oligomer on a Chiral Gamma-PNA Backbone

Daniel Evans (University of Pittsburgh), Gustavo Rama (University of Pittsburgh), Shivaji Thadke (University of Pittsburgh)
Advisor: Danith Ly (Carnegie Mellon University)

Synthetic oligonucleotides have been developed for the treatment of congenital, autoimmune, and infectious diseases since their discovery in the early 1990's. Two recent advances intended to improve their therapeutic potential are the development of a chiral "gamma" peptide-nucleic acid (γPNA) backbone, which confers greater intramolecular stability, and the synthesis of bifacial "Janus" nucleobase analogs that can form triplexes by simultaneously binding to two nucleotides by Watson-Crick base pairing. While both of these technologies have previously been shown to improve binding affinity, their ef ficacy in tandem had not yet been tested. We report the first successful synthesis of an oligonucleotide of Janus nucleobases on a chiral γPNA backbone, which can cooperatively bind to double-stranded DNA to form a stabilized triplex. Monomers were synthesized by fusion of (2,4-dioxo-1,2,3,4- tetrahydro-5-pyrimidinyl)acetic acid to a gamma-mini-PEG peptide backbone. A 1.82-kDa, 4-nucleobase oligomer was then constructed by solid-phase peptide synthesis (SPPS); its chirality was confirmed by circular dichroism (CD), and its bifacial binding to a DNA duplex was confirmed by ultraviolet (UV) melting assays and CD titration. This experiment confirmed our ability to construct short Janus nucleobase γPNA oligomers that stabilize nucleic acids by triplex base-pairing, thereby establishing their potential as oligonucleotide therapeutics. The comparatively small size and modularity of these oligomers, among other characteristics, may confer several advantages in therapeutic efficacy. We will further investigate the potential of this novel molecular platform to treat numerous diseases, including neurodegenerative trinucleotide repeat disorders and drug-resistant microbial infections.

Key Terms: Organic chemistry
Chemical biology
Nucleic acids

HS-EEB-201

A Wholistic Characterization of Rhizospheric Pathogenicity of Rice Blast Fungus *Magnaporthe oryzae* Using Spatial Science and Molecular Biology

Navami Jain (Myers Park High School)
Advisor: Chaula Jain (Mecklenburg County Government)

Magnaporthe oryzae, a model fungal pathogen, causes rice blast: a cereal infection responsible for 30% of annual global rice harvest loss. Although *M. oryzae* is characterized as a foliar pathogen, part I of this project studied root infection capabilities of the fungus. Results suggest the fungus receives cues from the root exudate to shift and align its pathogenic strategy with that of evolutionary close soilborne pathogens such as *Magnaporthe poae*. By adapting its developmental phases in the rhizosphere, the fungus can successfully penetrate the rice plant root. Failure to expand current crop protection strategies and combat this alternate infection strategy will sustain the global threat of rice blast. In part II, ArcGIS (Geographic Information Systems) regression known as OLS was performed to spatially correlate and characterize geological factors contributing to virulence of root pathogenesis. The identical alignment of *M. poae* and *M. oryzae* root pathogenic strategy indicated influences of *M. poae* pathogenesis, such as soil nitrogen availability, can be integrated in the OLS root rice blast model as potential factors. In addition, because rice paddies are grown in flooded fields, water flow was suggested to regulate rhizospheric spore dispersion. Thus, type and strength of the relationship between flow accumulation levels and rice blast intensity were analyzed. Conclusions from OLS regression have broad applications in computationally predicting a location's susceptibility to *M. oryzae* root pathogenesis, and can be an effective tool in constructing crop management strategies.

Key Terms: Pathogenicity
Ecological interactions
Evolutionary relationships

HS-EEB-202

Seasonal Time-budget Comparisons of Adult Songbird Behavior in Savannah, Georgia

Caroline Adkins (Islands High School), Jodis Hegg (Islands High School)
Advisor: Megan Heberle (Islands High School)

Avian species must carry out a number of behaviors successfully throughout the day to ensure survival. A time budget is a way to find out what percentage of the day a species will put towards a specific behavior or activity. These behaviors include alert behaviors, resting behaviors, parental behaviors, and foraging behaviors. For this study, we recorded seasonal time budgets to compare the differences in behaviors for each season throughout the year for three resident songbird species: Eastern Bluebirds (*Sialia sialis*), Brownheaded Nuthatches (*Sitta pusilla*), and Carolina Chickadees (*Poecile carolinensis*). The time budgets for the behaviors of these species vary between seasons. We used scan sampling for oneminute accumulated behavioral observations of our study species. Behaviors observed were grouped into three main categories: foraging, resting, and vigilance. Alert, resting, preening, chasing, and social behaviors changed significantly between seasons (ANOVA Single Factor, $F=2.92$, $p=0.033$; ANOVA Single Factor, $F=15.326$, $p<0.01$; ANOVA Single Factor, $F=2.933$, $p=0.032$; ANOVA Single Factor, $F=10.575$, $p<0.01$; ANOVA Single Factor, $F=18.773$, $p<0.01$). Time budgets differ between seasons as resource needs for survival fluctuate.

Key Terms: Bird behavior
Ethology
Ecology

HS-EEB-203

Songbird Nest Microclimate and Size Correlate with Nestling Development

Penelope Eltringham (Islands High School)
Advisor: Megan Heberle (Islands High School)

Nest temperature is a crucial factor to the survival of fledglings. Inner nest cup diameter is also an essential component to the number of nestlings successfully fledged. These factors impact the success of songbird nests and vary depending on the weather and placement of nest boxes. We recorded temperatures inside the nest cup of Eastern Bluebirds (*Sialia sialis*) using a thermocouple and data logger (Lascar EL-USB -TC). Temperature was recorded from when the eggs were laid to the day nestlings fledged. Older nestlings maintain a significantly warmer nest cup than younger nestlings during both day (Student's T-test, $p<0.0001$) and night (Student's T-test, $p<0.0001$). Nests with a cup diameter greater than 5.001 cm had significantly more chicks fledge than nests with cups smaller than 5.001 cm (Welch's T-test, $p=0.016$). A better understanding of nest microclimate and nestling development can be established with the knowledge this study provides. Future studies can use these results for further experimentation and gain additional knowledge on avian developmental.

Key Terms: Microclimate
Nest cup
Nestling development

UG-EEB-216

Responses of Male and Female Red Ruffed Lemurs (*Varecia rubra*) to a Novel Object

Haley Hollan (North Carolina State University)
Advisor: Lisa Paciulli (North Carolina State University)

Male and female animals differ in many ways including physiologically and behaviorally. Females spend more time feeding and less time resting in order to balance the high energetic costs of reproduction, while males spend less time feeding and more time resting in order to keep energy costs for mating low (Vasey 2005). Would sex differences also be seen in a novel object task? To test this, male and female red ruffed lemurs (*Varecia rubra*) at the Duke Lemur Center were studied. Individuals were separated from the group, and video-recorded responding to a novel object (a wireless speaker) and a control object (a paper plate). The latency to approach an object, and how many times it was approached were noted. The results showed that the overall, the mean latency to approach novel objects was shorter than for control objects. Also, males and females approached the novel object more than the control, with males approaching the novel object 2.2 times, and females, 1.5 times. Most females' latency to approach objects was about two times longer than males'. Individuals approached the novel object more quickly and more often likely because it was more interesting. Males approached objects faster and more often than females, which follows their more vigilant and anti-predator behavior. Future research should examine the differences between the sexes in the presence of a novel food to see if responses vary.

Key Terms: Biology
Animal behavior
Lemurs

UG-EEB-217

The Effect of Location on Novel Object Interactions of Mongoose Lemurs (*Eulemur mongoz*)

Hanna Rogers (North Carolina State University)
Advisor: Lisa Paciulli (North Carolina State University)

Location has a large effect on where species conduct various activities such as breeding, foraging, and sleeping. In order to test whether specific locations in mongoose lemurs' (*Eulemur mongoz*) enclosures affected their behavior with a novel object, a study was conducted at the Duke Lemur Center. The lemurs were observed for five minutes and the location they were in the most was recorded. Then, a randomly selected object (the control: paper plate or novel: "Nuby Octopus") was placed in a randomly selected location (neutral or frequented), and a randomly selected individual (1, 2, or 3) was let into the cage. This was repeated for all variations of conditions (object x location x individual). One session consisted of three trials, each 25 minutes long. Two trials were with one individual, and the third was with the two individuals together. The trials were video-recorded, and the videos were coded later for latency to approach and duration of interaction. It was found that the condition that yielded the shortest amount of time to approach was when individuals were together, and the item was the control object, in a frequented location. It seems that the lemurs used a 'a safety in numbers' approach and felt more comfortable approaching objects when with another individual. Location also seemed to play a factor, but the sample size was not large enough to garner a significant result (T-test, ns, p=0.12177). Future research should explore whether location and the type of object affects interactions with enrichment items and limits stress among the species.

Key Terms: Behavioral studies
Object interactions
Location preference

UG-EEB-218

Mongoose Lemur (*Eulemur mongoz*) Family Responses to Novel Objects

Kylie Litaker (North Carolina State University)
Advisor: Lisa Paciulli (North Carolina State University)

Closely related individuals may respond similarly to the same situation (Dingemanse et al. 2004). Some individuals are risk-prone, indicating a bold personality, which may be inherited in humans and other animals. In this study, mongoose lemur (*Eulemur mongoz*) behavior when alone or with family members was examined in response to objects to see if a pattern of boldness could be discerned. A total of eight subjects from the Duke Lemur Center were observed alone during five-minute trials alternating between a paper plate control and a rubber duck novel object. The procedure was then repeated with family members present. T-tests showed that significantly more time was spent touching the control object than the novel (P= .0026). Also, juveniles took less time to approach and touch objects, and spent more time touching and biting/licking them than adults. However, all individuals spent more time touching and biting/licking objects when they were in a group than when alone. These results indicate that item familiarity and a family setting make the lemurs feel safer to explore objects. In addition, the juveniles seemed bolder than adults, possibly because they are more curious and more likely to take risks due to a developing cognitive system and less experience. This study was limited by a small sample size and unexpected changes in family dynamics. Future research should examine risk taking and boldness in response to a threatening predator stimulus.

Key Terms: Animal behavior
Animal science
Zoology

UG-EEB-219

The Behavioral Responses of Coquerel's Sifakas (Propithecus coquereli) to a Mirror

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Advisors: Lisa Paciulli (North Carolina State University), Jennifer Verdolin (Duke University)

Mirror Self Recognition (MSR) is the ability of an individual to recognize themselves in a mirror. When individuals do not recognize their reflection, they usually act aggressive, thinking they are seeing a conspecific. Previous studies have found no evidence that prosimians have MSR. Thus, mirrors were used in a novel object study with four groups of Coquerel's sifakas (*Propithecus coquereli*) from April to May 2017, at the Duke Lemur Center. In one day, one group was exposed to three 25-minute rounds consisting of five 5-minute trials. One round included observing the group with the following conditions; First trial: no object, second trial: randomly selected item (mirror or cardboard paper towel roll), third trial: no object, fourth trial: second object, fifth trial: no object. A two-tailed paired t-test was run on latency to 1. approach, 2. hold, and 3. time spent staring and holding object. No significant differences were found for age and sex. Sifakas stared at the novel object significantly longer than the control ($p<.05$). They also approached the mirror quicker and spent more time with it than the paper towel roll. The sifakas likely favored the mirror because it was novel and exciting. These data demonstrate that even though prosimians do not recognize themselves in mirrors, mirrors can still be used for enrichment. Future studies should be conducted on a solitary species using the same research design, with improvements such as a larger sample size and a rock as the control.

Key Terms: Animal science
Animal behavior
Zoology

UG-EEB-220

Testing the Utility of Stable Isotope Analysis for Analyzing Bee Foraging Patterns Across Habitats

Robert Burkhart (The Ohio State University)
Advisor: Karen Goodell (The Ohio State University)

Concern about declining bee populations has stimulated interest in promoting habitat for bees and other pollinators, but a better understanding of habitat requirements of diverse bee species is needed. Traditional methods of studying bee foraging are labor intensive and limited spatially, temporally, and to certain bee genera. I tested the utility of stable isotope analysis, a new method for tracking the habitat origin of bee nutritional resources by comparing stable isotopes present in bee tissue to those in distinct foraging habitats. In a preliminary study, I showed that stable isotope analysis could distinguish bee habitat use over small spatial scales. I analyzed 21 native bee species collected in forests and old fields to determine if isotopic ratios of body tissue reflected that of flowers in their foraging habitat. Discriminate analysis assigned the bees to habitats with respect to δ15N and δ13C with 86% accuracy. Some of the variation in isotopic signature may come from species differences and the integration of larval and adult diet across years. In a second study, therefore, I investigated isotopic signatures of a single taxon, bumble bee workers, caught during two distinct seasons: spring and the mid-late summer, to determine what role time of capture and diet play in influencing isotopic signature. I collected 35 bumble bees and 75 flowers in 2016. Samples were identified, dried, pulverized, before being analyzed by an isotope ratio mass spectrometer. The results should help illuminate stable isotope effectiveness in tracking bee habitat use and as a tool in conservation ecology.

Key Terms: Stable isotopes
Bees
Foraging

UG-EEB-221

DNA Analysis of *Hadenoecus subterraneus* in Mammoth Cave National Park

Soyeon Kim (SUNY Plattsburgh)
Advisor: Nancy Elwess (SUNY Plattsburgh)

Hadenoecus subterraneus Cave Crickets are found in Mammoth Cave National Park (MCNP) in Kentucky. MCNP is known for the longest cave system in the world and more than four hundred miles of Green river passageways flow through. When a species is exposed to an extreme or an isolated environment for a long period of time, the environmental factor may cause mutations in the DNA or alteration of gene expressions; this phenomenon is called epigenetics. The Cytochrome C Oxidase Subunit 1 (CO1) within mitochondrial DNA has been a favored choice in DNA barcoding due to high mutation rate. We hypothesize that there will be a genetic diversity among groups of *H. subterraneus*, corresponding to given physical isolation and locations of caves. In this study, the phylogeny was analyzed within *H. subterraneus* using CO1, 28s RNA, and 16s rRNA. In order to clarify the phylogenetic relationships and genetic diversity between groups of *H. subterraneus*, a DNA analysis was performed using DNA isolation, amplification, and purification. Based on the phylogenetic relationships, more genetic differences were observed among groups that were from caves geographically apart. We concluded that the results supported our hypothesis and CO1 mitochondrial gene was more useful in determining the genetic diversity of *H. subterraneus* than using 28s RNA and 16s RNA.

Key Terms: Genetics
Genetic diversity
Cave crickets

UG-EEB-222

Evolutionary Analysis of Epitopes and Low Complexity Regions in Plasmodium

Sarah Medley (Oakland University), Alyssa Beaudet (Oakland University), Helen Piontkviska (Kent State University) , Fabia U. Battistuzzi (Oakland University)
Advisor: Fabia U. Battistuzzi (Oakland University)

Epitopes of the agent of malaria (*Plasmodium*) are of key interest due to their association with immunogenic responses in the host and their role as targets of antimalarial drugs and vaccines. The molecular sequence structure characteristic of epitopes contains similarities to another common feature of these genomes: low complexity regions (LCRs). It is therefore possible that LCRs may produce similar immunogenic functions to epitopes and could become new targets for drugs. To investigate their functional relationship, we have used an evolutionary approach that compares location and sequence conservation levels of LCRs and epitopes in multiple species with different hosts. We expect that epitopes and LCRs located in overlapping regions that show high conservation will have a greater likelihood of shared function and, therefore, will be candidates for future experimental studies. Based on pairwise species comparisons of 15 genes in 18 species (44 strains), we found that approximately 60% of LCRs and epitopes show conservation of amino acids. This is surprising given the known high evolutionary rate of these regions. We also found that nearly 40% of LCRs overlap with an epitope, and, of these overlapping regions, over 30% were conserved in both the epitope and the LCR. These results suggest that LCRs may be under selection and, thus, could play a functional role in pathogens similar to that of epitopes. Future analyses of different phylogenetic depth will allow us to identify if host preference and genome similarity determine the functions of LCRs.

Key Terms: Evolutionary biology
Malaria
Genome

UG-EEB-223

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

Nikaela Losievski (Michigan State University/Baker University), Mitchell DuBuc (University of Connecticut/Baker University)
Advisors: William Miller (Baker University), Margret Lowman (California Academy of Science)

A preliminary report on an undergraduate research project to quantify tardigrade (water bear) density, diversity, and distribution in temperate forest canopies conducted during the summers of 2013-2017. The objective was to teach undergraduates how to conduct field research with a co-objective to demonstrate that ambulatory disabilities are challenges but not limitations to becoming a field biology researcher. During the five years of this program, 30 students, four in wheel chairs, climbed 744 trees representing 34 different substrates (tree species) at 60 different forested sites in Kansas, Florida, Massachusetts and Oregon. 4,961 samples of tardigrade habitat (moss and lichen) were collected on vertical transects by ascending more than 30 meters above the ground. More than 40,000 water bears were captured of 32 different species, 27 are new distributional records to their state's biodiversity lists and six are new to science. The project documented inter-continental dispersal and proposed avian and mammalian vectors. This ecology project has revealed greater density and diversity of water bears in the canopy than at the ground level where sampling has been conducted for 200 years. The project has also demonstrated that mobility-limited students can participate fully in field-based research. This unique NSF funded Research Experiences for Undergraduates (REU) Program puts students on the edge of knowledge of the little understood ecology of the charismatic, space traveling phylum Tardigrada and fosters true exploration into the equally unexplored high frontier of the canopy.

Key Terms: Invertebrate ecology
Canopy ecology
Tardigrade

GR-EEB-241

Transmission of Parental Behavior in the California Mouse

Amanda Leithead (Saint Joseph's University), Elizabeth Becker (Saint Joseph's University)
Advisor: Elizabeth Becker (Saint Joseph's University)

Early interactions with parents play a significant role in the development of future parental behavior in offspring. In mother-daughter dyads, maternal behavior is transmitted via neuroendocrine modulation. Mechanisms of patrilineal transmission are largely untested because paternal care is rare among mammals. However, in the biparental California mouse (*Peromyscus californicus*), fathers frequently engage in retrievals (lifting and carrying pups by mouth) and grabs (grasping pups by mouth without carrying). Research shows that paternal retrievals influence future parental behavior and levels of arginine vasopressin (AVP) in male offspring. Few studies test opposite-sex interactions, yet in California mice, AVP expression in females is also modulated by paternal care. Since AVP is linked to parental behavior in males and females, we posit that paternal retrievals may also shape female offspring parental behavior. In the present study, we sought to establish a relationship between paternal care received and maternal behavior demonstrated by female offspring. To explore this aim, we used California mice reared in either high or low care conditions. In adulthood, the maternal behavior of females was observed for 7 consecutive days. Among all parental behaviors, paternal retrievals and grabs experienced in development were the only significant predictors of future maternal behavior. Further, higher rates of retrievals and grabs experienced were associated with higher rates of retrievals and grabs performed in adulthood. Therefore, paternal retrievals and grabs may serve as important indicators of parental behavior to female offspring, thereby informing future expression of maternal behavior in California mice.

Key Terms: Neuroscience
Parental behavior
Development

GR-EEB-242

Cold Tolerance Variation in Introduced Apple Snails (*Pomacea maculata*)

Marissa Granberry (Columbus State University)
Advisor: Clifton Ruehl (Columbus State University)

Island apple snails (*Pomacea maculata*) are invading wetlands, greatly reducing wetland vegetation, and negatively affecting species richness in the humid subtropical regions of the southeastern United States. *P. maculata* is much larger and more fecund than the native Florida apple snail, *Pomacea paludosa*, allowing the invasive apple snail to take over wetland environments very quickly. Besides having growing populations, *P. maculata* feeds on wetland vegetation, compared to native apple snails that feed on periphyton present in freshwater ecosystems. The destruction of natural habitats is a primary reason for the need for studies on their life history and physiological tolerances in order to develop predictions about the extent they will spread throughout North America. My research is focused on the survivorship and growth rate of *P. maculata* populations along a latitudinal gradient when raised at different temperatures in a common environment. I have collected egg masses from Miami, FL, Tampa, FL, and Albany, GA. Approximately 480 snails are currently being raised and will be exposed to low temperatures in the lab. I will determine the average growth rate of each group and measure the cold tolerance across all groups. This research will help determine if the invasive snails can continue to migrate north into the United States and how quickly they will grow when exposed to adverse conditions. This project will also help us understand how this introduced species might impact wetlands and aquatic ecosystems throughout the southeast. The presence of these non-native snails could reduce the species richness of the native *Pomacea* snails as well as negatively impact the vegetation that the native species feeds on. Greater knowledge of these invertebrates is necessary in order to prevent the spread of these potential pests.

Key Terms: Apple snails
Invasive species
Cold tolerance

GR-EEB-243

Bee Community Response to Urbanization and Floral Resource Availability.

Caleb Wilson (Oakland University), Mary Jamieson (Oakland University)
Advisor: Mary Jamieson (Oakland University)

Bees are the most effective and necessary pollinators of agricultural crops. However, bee population declines have been widely reported for many species. Recent research has found that land conversion and habitat removal are two major contributing factors to bee declines. As urban areas continue to grow in size at an increasing rate, they have dramatically changed the natural landscapes bee communities rely on. Our project examines how bee communities at urban farms and community gardens are influenced by environmental variables at different spatial scales. We collected local (bees, floral resources, temperature) and landscape scale (urbanization, land use, farm size) data at 15 farms in southeast Michigan across a gradient of urbanization. Preliminary analyses indicate that bee abundance is significantly correlated with floral resource availability, but unrelated to floral diversity or urbanization. We found a 4 fold increase in bee abundance coupled with a 17 fold increase in floral resource availability across our study sites. Our findings suggest that urban farms and community gardens could improve bee habitat by planting more flowering plants, regardless of how urban the surrounding landscape is. We are in the process of species identifications and further analyses will show how bee species diversity responds to environmental variables. Our research provides a better understanding of the key factors influencing bee diversity in urban areas to help support bee conservation. Such information is important for supporting pollination services in urban agriculture, an important ecosystem which provides a local source of healthy food while supporting community involvement.

Key Terms: Ecology
Bee conservation
Urban agriculture

HS-ENG-261

Dynamo Powered Refrigeration Method for Temperature Sensitive Medicines in Off-Grid Locations

Susanna Dorminy (Sola Fide Home School)
Advisor: Gustaf Mårtensson (Karolinska University)

Vaccine potency depends on maintaining the cold chain, a specific temperature range from manufacture to use. Polio, measles, and other vaccines, must be kept at temperatures of 2-8°C. Few options exist to deliver potent temperature sensitive vaccines to remote villages lacking electricity. The researcher created a reliable, lightweight system powered by a dynamo to maintain 2-8°C to protect temperature sensitive medicines in the last leg of transportation to remote villages inaccessible by motorized vehicles. The researcher programmed an Arduino Uno to maintain 2-8°C using thermoelectric coolers (TECs) and other electronic components for heat dispersal. The cooling chamber maintained those internal temperatures with external temperatures of approximately ~24°C to ~45°C. At 0°C externally, internal temperatures remained in range through the TECs limited ability to reverse heat movement. An independent temperature logger proved the unit's effectiveness. The wheel-based dynamo generator and its battery power the Arduino. Thermoelectric coolers (TECs), powered by stored energy or by wheel based dynamo, enabled use in off-grid locations. This active cooling system controls the temperature within, maintaining 2-8°C for temperature sensitive medicines. A metal plate within the cooling chamber transfers heat to a sink where airflow draws heat away. This TEC powered refrigeration device demonstrates an exciting advance in the technology of temperature control for sensitive medicines. Capturing the movement of a wheel to power the refrigeration capabilities of TECs is a novel pairing of old and new technologies to move world health forward, creating a positive effect on people in remote areas.

Key Terms: Electrical engineering
Vaccine cooler
Cold chain

HS-ENG-262

Creating A Cheap Distributed Landmine Sensing System Using GPS and GSM Technologies for Locating Undetonated Landmines in Developing Regions

Stefan Abi-Karam (American Heritage School)
Advisor: Leya Joykutty (American Heritage School)

Millions of undetonated landmines still exist in underdeveloped and developing countries as remnants from past military conflicts. There in an inability to detect and remove land mines safely using many modern methods because the resources to do so are too expensive, risky, unattainable, or impractical. The solution created in this project is to deploy many "modules" with each module contains an inductor coil/metal detector, GSM chip, GPS chip, and a standalone microcontroller and each module send data to a cloud application using GSM. The client side application receives location data and inductor sensor readings to create a heat map overlaid onto satellite imagery which is updated live. The design was successful at fulfilling it goal; the early prototypes for the module performed well and were practical to manufacture. The data from the coil test proved the efficacy of the metal detector circuit to provide accurate readings according to UN guidelines. The application of the project is groundbreaking for humanitarian groups and undeveloped countries extending beyond the scope of these users.

Key Terms: Landmine detection
Electrical engineering / computer science / distributed sensing
GPS / GSM / RF / Wireless

HS-ENG-263

Detecting *Salmonella* through DNA-Fingerprinting using Microfluidic Lab-on-Chip Pulsed-field Gel Electrophoresis

Eeshani Behara (American Heritage School)
Advisor: Iris Thompson (American Heritage School)

Salmonella is a foodborne pathogen and one of the leading causes of reported illnesses in the United States with over 19,000 hospitalizations and 380 reported deaths. Worldwide, 550 million people fall sick annually due to *Salmonella*, including 220 million children under age five. Improving diagnostic testing for Salmonella can help in early detection and treatment, and thereby prevent serious illness and even death. One of the current methods of detection of pathogens is to create a unique DNA band pattern or "fingerprint" to identify them using traditional gel electrophoresis methods. This approach is time consuming, complex, and expensive. Further, people in less developed countries may not have access to such complex diagnostic methods. Hence, the objective of this study is to design and test a fast and low-cost method using a microfluidic lab-on-chip to detect *Salmonella* by creating a DNA-fingerprint. The first research hypothesis of this study is that pulse-field gel electrophoresis can be implemented in a microfluidic environment of a lab-on-chip. For this, a microfluidic lab-on-chip was designed, fabricated, and tested successfully using nanoparticles, to demonstrate that pulse-field gel electrophoresis may be used for DNA fingerprinting in this environment. The second research hypothesis of this study is that this lab-on-chip design and method could then be used to detect *Salmonella*. The microfluidic lab-on-chip developed in this study successfully implemented pulse-field gel electrophoresis to create a *Salmonella* DNA-fingerprint within three minutes. This study shows that it is feasible to develop fast and low-cost microfluidic lab-on-chip solutions to detect foodborne pathogens.

Key Terms: Food pathogen
PFGE
Microfluidics

GR-ENG-286

NORM Air Sampling and Statistical Analysis for Radiological Emergency Response Applications

S. Joseph Cope (North Carolina State University)
Advisor: Robert Hayes (North Carolina State University)

In the nuclear nonproliferation, specifically radiological emergency response scenarios, atmospheric conditions may significantly influence transuranic activity evaluation through air sampling. Radon (222Rn) and thoron (220Rn) progeny (primarily bismuth and polonium), whose concentrations vary dynamically throughout the day, are known interferents when analyzing the alpha particle energy region of interest (3-5.5 MeV) for transuranic determination. This problem is magnified by the natural radon and thoron progeny concentrations often overwhelming the alpha spectra relative to any transuranic content, along with strong dependencies on temperature, humidity, and wind speed. Previous work has suggested a rapid, conservative transuranic activity estimation method for the temporal and regional consideration of the study. Novel implications will compare seasonal changes, including the effect on the radon and thoron concentrations, which may bias the transuranic activity estimate. A technical basis is sought to quantify the relative changes or to affirm statistically insignificant differences are seen in the transuranic estimator as a result of seasonal changes. Validation of this method across seasonal climatic variation could provide enhanced emergency response capability when the presence of transuranic activity is suspected.

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Key Terms: Air sampling
Radiological emergency response
Nonproliferation

HS-ENV-301

Carbon Capture Using Solid Sorbents. Amine-tethered polystyrene and polyacrylic polymers for CO_2 adsorption

Glenn Grimmett (American Heritage School)
Advisor: Iris Thompson (American Heritage School)

Efficient carbon dioxide (CO_2) separation from mixed gas streams is indispensable across multiple industries to include cleanup of industrial flue gas, fuel gas refining, and chemical production such as sulfur, ammonia, and hydrogen. Established liquid amine technology for CO_2 capture has the primary disadvantage of requiring high energy for regeneration due to water's heat capacity and covalent bonding of CO_2 to monoethanolamines. Solid sorbents represent a practical alternative due to their lower heat capacity and alternate sorption mechanisms. Using column breakthrough techniques, this study compared CO_2 adsorption performance across fifteen polystyrene and polyacrylic copolymers at typical flue gas CO_2 concentrations (11.4 – 11.8%). A110, a polystyrene polymer functionalized with primary amines, had high CO_2 adsorption capacity (Qe) and removed 1.138 mmol CO_2 g-1 ($p < 0.001$), which was consistent with chemisorption to form carbamate. Eight polystyrene copolymers functionalized with tertiary or quaternary amines performed poorly, with Qe values ranging between 0.009340 and 0.4038 mmol CO_2 g-1, due to steric hindrance or decreased amine density if hypercrosslinked. Polyacrylic copolymers A870, A830, and A847, functionalized with tertiary and/or quaternary amines, had high Qe values ranging between 0.9327 and 1.140 mmol CO_2 g-1 owing to favorable amine spatial arrangements for CO_2 adsorption, which is consistent with electrostatic attraction of bicarbonate to cationic amine moieties. Physisorption of CO_2 was trivial across differing polymer types. A847, A110, A830, and A870 show promise for CO_2 capture technologies. Further study should define CO_2 adsorption selectivity with appropriate contaminants, adsorption/desorption kinetics, regenerability, and operating limits (temperature, pressure, and humidity).

Key Terms: Carbon capture
Amine-tethered adsorbents
Global warming

HS-ENV-302

Contaminants of Emerging Concern: Effects of Common Wastewater Contaminants on Cellular Metabolic Function

Elizabeth Kinsey (North Carolina School of Science and Math)
Advisor: Jeff Overton (University of North Carolina Wilmington)

Approximately 83 trillion gallons of domestic wastewater are produced each year and these waters contain contaminants ranging from pathogenic microorganisms to micro-pollutants like medicines, personal care products, and cleaning agents. While many of these compounds are benign, some may pose a public health or ecological risk. These are called contaminants of emerging concern (CECs). Because CECs occur in very low concentrations, their organismal impact may not be immediately apparent even when harmful. Mitochondria, however, can act as "canaries in a coal mine" by providing an early warning sign of cellular stress. This project examined the potential effect of CECs on cellular function by asking the question "How does chronic exposure to compounds found in domestic wastewater effluent affect cell respiration?" To answer this question, I exposed myoblast cells to 3 contaminants and measured mitochondrial respiratory function. The contaminants were: triclosan (anti-bacterial agent), caffeine (non-pharmaceutical drug), and titanium oxide nanoparticles (found in cosmetics). I hypothesized that 24 hours of exposure to these compounds would decrease cell respiration. The results demonstrated that exposure to triclosan and caffeine significantly decreased respiration while nanoparticles had no effect. I also tested the hypothesis that charcoal or zeolite filters could be used to remove commonly occurring CECs. My research found that both filter materials effectively removed the majority of caffeine in a water sample. The results of this study indicate that the tested contaminants may have harmful effects on cellular respiration of aquatic organisms, and that charcoal/zeolite filters may be an effective means of treating effluent.

Key Terms: Contaminants
Mitochondria
Water quality

HS-ENV-303

Monitoring of Arsenic in Groundwater Sources using an Innovative IoT Sensor

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The EPA's Safe Drinking Water Act, governs the legal threshold of contaminants allowable in public water systems. The Maximum Contaminant Level (MCL) for arsenic, the #1 ranked toxin, was reduced from 50 ppb to 10 ppb, validating the severe health risks like cancers, blood toxicity, and keratosis, posed by arsenic exposure. Over 50 million people in the United States and over 1.8 billion people worldwide obtain water from ground-water and well-water sources. Unfortunately, the MCL goal does not govern these water sources, and humans are exposed to arsenic levels higher than 10 ppb on a regular basis. The engineering goal is to build an automated, portable, IoT-based sensor for arsenic using an original design. Although technologies for arsenic detection exist, they are expensive, time-consuming, or onerous to operate by a layperson. That is why a cost-effective sensor that digitally records the amount of arsenic in water sources over time and across locations and stores this data in the cloud is invaluable. The sensor prototype with >98.5% accuracy, programmed in Python and C, utilizes a colorimetric technique for arsenic detection where the input is a mercury bromide test strip, which is read inside a white box using LEDs. The sensor converts color values into arsenic concentrations in ppb. The data is collected and stored in the cloud for easy access as well as for ongoing comparative study of the arsenic levels. The components used include a Particle Electron cellular transmitter, an Intel Edison Arduino board, a camera, and LEDs, among others.

Key Terms: Arsenic sensor
Internet of things
Arduino microprocessor

HS-ENV-304

Use of Waste Carbon Dioxide as a Renewable Reagent to Catalytically Synthesize Commercially Useful Cyclic Carbonates

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Petroleum is heavily depended upon for energy production, the production of plastic, and the manufacturing of multiple important chemicals. Though petroleum is said to have broad areas of applications and the capacity to constantly produce a large amount of energy cheaply, it is also a nonrenewable resource that destroys our everyday environment. The extraction and burning of petroleum not only generates greenhouse gases which contribute to environmental pollution and leads to the increase of global warming, but when burned also releases toxic and carcinogenic (cancer causing) chemicals that are harmful both to us and the planet. As the population increase, the global demand for both energy and chemicals is gradually sky rocketing. Therefore, as a solution to this problem of utmost importance, the development of alternative and sustainable starting materials for chemical synthesis is necessary. The goal of this experiment was to utilize waste excess carbon dioxide readily available in the atmosphere as renewable reagent to develop and synthesize a commercially useful chemical – Cyclic carbonates. As cyclic carbonates are degradable and less toxic, they have a wide range of applications that include being used as polar aprotic solvents for paint and grease removal, to formulate certain pharmaceuticals and cosmetic products, precursors for polycarbonates, intermediates for small organic materials, and as an electrolyte medium for lithium ion batteries. The results suggested that cyclic carbonates could be produced in a one-pot reaction using commercially available synthetic alkenes such as styrene, octene, hexene, and cyclohexene. The carbonates synthesized were more economically and environmentally beneficial when compared to cyclic carbonates produced in recent literature.

Key Terms: Cyclic carbonates
Carbon dioxide
Amidomacrocyclic ligand

HS-ENV-305

A Comparative Analysis of Fluensulfone as a Nematicide on *Caenorhabditis elegans* SKN-1 Pathway Mutants and in vivo RNA interference Study as a Solution for Nematicidal Resistance

Emily Pallack (American Heritage School)
Advisor: Leya Joykutty (American Heritage School)

In the agricultural industry, nematicidal resistance is a looming problem that threatens a cost of billions of dollars in crop damages. The current solution to this resistance is fluensulfone, however, the possibility of a resistance being formed to fluensulfone is proposed by the SKN-1 pathway. This pathway controls detoxification and longevity, which has been previously not studied in *Caenorhabditis elegans*. The purpose of this study is to determine if the SKN-1 pathway in *C. elegans* causes resistance to fluensulfone and in addition, if RNA interference can overcome the problem of nematicide resistance. The researcher hypothesized that if SKN-1 mutant *C. elegans* are treated with fluensulfone then the overactive SKN-1 *C. elegans* will display a resistance to the fluensulfone because of the activation of the SKN-1 pathway, and therefore can be treated with RNAi to knock out the SKN-1 gene. To determine resistance, several assay including thrashing, paralysis, mortality, egg laying, and pharyngeal pumping, were conducted. The initial part of the study solidified the fact that overactive SKN-1 does create resistance to fluensulfone ($p<0.05$) through low thrashing rates, high paralysis rates, high mortality rates, low egg laying rates, and low pharyngeal pumping rates. The following part of the study utilized RNA interference to silence the SKN-1 gene and then the assays were repeated to compare the effectiveness of RNAi. The results of the RNAi study yielded significant results ($p<0.05$) that leads to the conclusion that RNAi can be applied to solve the problem of resistance to fluensulfone.

Key Terms: Nematicide
Nematicidal resistance
C. elegans

HS-HBS-366

***In Vitro* Comparison of the Resistance of the Suprachiasmatic Nucleus and Lateral Geniculate Nucleus of the Visual System Against Anterograde Neurodegeneration after Bilateral Optic Nerve Crush: Investigating Vision Restoration After Traumatic Injury**

Hemangi Rajpal (American Heritage School/University of Miami Miller School of Medicine, The Miami Project to Cure Paralysis)
Advisors: Kevin Park (University of Miami Miller School of Medicine, The Miami Project to Cure Paralysis), Leya Joykutty (American Heritage School)

The purpose of this study was to compare the ability of the suprachiasmatic nucleus (SCN) and the lateral geniculate nucleus (LGN), two visual targets of the brain, to resist anterograde neurodegeneration after bilateral optic nerve crush by assessing neuronal survival and apoptosis in mice. It was hypothesized that neuronal survival after injury would be greater in the SCN than in the LGN in one, three, and four (Bax gene deleted) months post crush mice, and apoptosis would occur in the dorsal LGN (dLGN) sixteen days after a bilateral optic nerve crush. The hypotheses were tested by cell imaging and counting using the Nikon Eclipse Ti fluorescent microscope and the ImageJ software, tissue sectioning using the cryostat, and the terminal deoxynucleotidyl transferase dNTP nick-end labeling assay on sectioned brain tissue. Although neither hypothesis was directly supported, the results showed that the SCN overall had higher cell densities than the LGN both before and after injury, which could be explained by the death resistant properties of neurons in the SCN. Results also indicated an overall increased cell density in the LGN (attributed to possible increased glial cell activation due to secondary neurodegeneration) after injury, decreased cell density in the SCN after injury, and no apoptotic activity in the dLGN at sixteen days post injury. Harnessing of the neurodegeneration-resistant properties of the SCN to the visual and nervous system can allow for vision restoration and effective treatments of neurodegenerative disorders and diseases.

Key Terms: Neuroscience
Ophthalmology
Neurobiology

HS-HBS-367

Increased Opioid-Related Overdose Deaths are Associated with Increased Illicit Use of Fentanyl in the U.S.

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Narcotic-like substances are agonists binding the opioid receptors of neurons in the human's nervous system. Recently, there has been a significantly increased use of fentanyl-like substances illegitimately, which poses serious health risks to the general public. To better understand the demographics of illicit use, the number of illicit uses of fentanyl-like substances and its correlation with opioid overdose deaths was reviewed and analyzed. The cohort datasets was collected from two major public health surveillance systems, including (1) The US' Center for Disease Control and Prevention (CDC)'s Morbidity and Mortality Weekly Report (MMWR) during the years from 2010 to 2016 and (2) the data published by the National Forensic Laboratory Information System (NFLIS), which systematically collects results from laboratories nationwide that monitor the illicit use and exhibit of psychoactive substances. The study results from both the CDC's MMWR and NFLIS demonstrated a substantial increase in the occurrence of opioid-related overdose deaths and the illegitimate use of fentanyl, respectively. Furthermore, this increase is drastic in several synthetic fentanyl-like substances with non-medical approval in the last three years. A correlation study shows that the increased illegitimate use and exhibit is positively correlated with the increase in overdose death rates in the US. The analytic result is statistically significant. The results offer substantial evidence that increased illegitimate use of fentanyl may positively contribute to increased death rate due to opioid overdose. Based on this preliminary study, a further regulatory assessment or legal enactment may help reduce the risk to public health.

Key Terms: Public health
Illicit fentanyl use
Opioid overdose related death

UG-HBS-376

The Effect of Text Messaging on Frontal Lobe Functioning

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Advisor: Paul Foster (Middle Tennessee State University)

There have been many targets of scrutiny regarding the negative effects cell phones can have on people, including: effect of radiation, effect on reading speed, effect on driving, effect on communication, and other similar topics. Not many researchers have looked at the effect the common use for cell phones has on the brain. The premise of this study is to establish that the right frontal lobe is not being used when cell phones are utilized for texting, and that this disuse is causing negative effects to right frontal lobe function. To assess the effect that this has on right frontal lobe function and to establish double dissociation, measures of right frontal lobe fluency (RUFF and Spatial Span) and left frontal lobe fluency (COWAT and Digit Span) were given. A Go-No-Go test was also given to test for response inhibition. The Beck Depression Inventory was administered to account for interference by individuals experiencing symptoms of depression. The individuals were also asked to count the number of text messages sent in the last seventy-two hours. The results indicated, consistent with the hypothesis, lower results on the tests of right frontal lobe functioning in individuals with higher rates of text messaging and no change in left frontal lobe functioning. This indicates that cell phone use causes decreased functionality and potential shrinkage of the right frontal lobes, leading to impairment and potential dysfunction in those who subject themselves to excessive amounts of text messaging.

Key Terms: Frontal lobe
Assessment
Psychology

HS-MMB-426

Utilization of Epigallocatechin gallate and Serine/Asparagine Compounds As a Natural Therapeutic for Glycosylation-Inhibited Breakdown of the Zika Virus Ectodomain

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Advisors: Pat Kite (Jasper High School), Shakheel Farooqui (Jasper High School)

Zika (ZIKV) poses unknown long-term-health threats to fetuses. Therefore, effective treatment that is safe for expectant mothers is needed. Epigallocatechin gallate (EGCg), a green-tea-polyphenol, has shown promise in inhibiting entry but is easily metabolized and too weak to pass the infection-clearance detection threshold. It was hypothesized that by inducing an inhibitory alkaline environment for viral protein maturation via Dolichol-cycle-glycosylation, effectivity of EGCg in reducing antigenic integrity would improve. ZIKV antigen samples were exposed to novelly synthesized Henderson-Hasselbalch-calculated alkaline N-linked-Asparagine/or O-linked-Serine glycosylation inhibitors of varying concentrations (serially-diluted)with EGCg noncovalently combined. A CLint test was done to scale in vivo bioavailability, and following incubation of the protein samples, an ELISA was done to analyze antigenic identity. All experimental groups of combination improved the control's efficacy in hiding epitopes by at least 71% as plotted through dosage-response-analysis, particularly the Serine/O-linked pathway at 89%. ANOVA/Tukey tests confirmed significant statistical difference between groups. Additionally, half-life of the composite proto-drugs increased by average 1.9 hours. These results support that the originally-synthesized, innovative two-front hemifusion-and-glycosylation inhibitor is an enhanced, organically-derived treatment that shows primacy in passing infection-clearance thresholds of 60% and could be developed into a formal drug to treat ZIKV infection in expectant mothers without danger to the fetus. The study also elucidated unknown novel biochemical assembly mechanisms of the virus, providing valuable insight into its virulence for the pharmacological and microbiological communities. Further drug development along this naturally-derived path could also sustainably protect the environment from pharmaceutical waste.

Key Terms: Virology
Glycobiology
Pharmaceutical biochemistry

HS-MMB-427

Quantitative Modeling of Zika Virus infection in the Developing Brain

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Advisor: Thomas Knudsen (Environmental Protection Agency)

The Zika Virus in 2016–17 caused a tragic number of birth defects, most notably microcephaly resulting from damage to the early fetal brain. Research on the pathways in which the virus infects cells have been done with *in-vivo* and *in vitro* models that determine the susceptibility of cells and the genes receptors responsible for infection. Computational models could be used to understand possible pathways and confirm or explain these results. I set out to model Zika infection of the developing brain to determine the number of cells infected in *in-vitro* models using mathematic formulas demining the relationship between AXL transporter, multiplicity of infection (MOI), and the infection rate of virions. CompuCell3D version 3.7.3 was used to model the number of cells infected. Data was gathered about Zika virus infection in *in-vitro* models, the number of infected cells at various times and MOI along with information about the expression of AXL in these cells. Equations were then fit to these points and transferred to code assuming that they are in a steady state scenario. The models were then run and data was collected. The models and functions were then confirmed by means of checking number of infected cells at various MOI's, AXL concentrations, and times. It was found the CompuCell3D modeling was able to predict the number of cells infected with an average uncertainty of 14.5%. The computational model, however had an average distribution of 7.6 compared to 1 from the data. Editing the way in which the cells are initially infected from being based in the Boolean variable of "infected" to creating virus particles could increase precision and will remain for future refinement of the infectivity model.

Key Terms: Computational
Environmental
Toxicology

HS-MMB-428

Effects of Acrylamide on the Development and Behavior of Wild type *C. elegans* and *wdr-23* Mutants

Ephraim Oyetunji (American Heritage School)
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Histones are eukaryotic proteins found around DNA. They allow for compaction of DNA into chromosomes and influence DNA replication and cell division. Acrylamide, a potential carcinogen, is a stressor that activates the worms' WDR-23/SKN-1 pathway. Nematode WDR-23, a regulatory protein for SKN-1 in C. elegans, is significant for cell cycle regulation, and its human counterpart, WDR23, is linked to maintaining histone levels. The purpose of this experiment was to see the effect exposure to acrylamide had on growth, parturition, and locomotion of *wdr-23* mutants and wild type worms. The researcher hypothesized that: "If *wdr-23* mutants and wild type worms are exposed to acrylamide, then the *wdr-23* mutants will be smaller, have fewer eggs, and fewer body bends per minute on average than the wild type worms and worms not exposed to acrylamide." The worms were grown in 90mm plates of nematode growth media with and without 2 mM acrylamide. The worms were fed *E. coli OP50*. Fifteen adult worms of each strain were transferred onto each plate. The number of eggs laid after one day of worm transfer as well as the size of three adult worms from each strain and the number of body bends per minute of one adult worm were noted and averaged. The results supported the hypothesis. On average, the *wdr-23* mutants exposed to acrylamide had fewer eggs, smaller lengths, and fewer body bends per minute than the other worms. This was likely due to the amplified stress of the acrylamide on worms lacking WDR-23.

Key Terms: *C. elegans*
Acrylamide
Histones

HS-MMB-429

Prospective Genomic Landscape of Advanced Cervical Cancer

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Advisors: Mark Donoghue (Memorial Sloan Kettering Cancer Center), Claire Friedman (Memorial Sloan Kettering Cancer Center)

Cervical cancer is the second leading cause of cancer-related death of women worldwide. In order to identify the molecular characteristics of advanced cervical cancer, 70 patients were prospectively sequenced using the MSK-IMPACT assay, a targeted tumor-sequencing test. Detailed analysis of the genomic and clinical data identified histologically driven differences from previous studies of primary cancers (The Cancer Genome Atlas). We identified novel loss-of-function (LOF) mutations in STK11 in our advanced disease cohort not present in early stage disease cohorts. Furthermore, cervical cancer was identified as the second most frequent cancer type to harbor STK11 LOF mutations, second only to non-small cell lung cancer. In contrast to KMT2D, KMT2C LOF mutations were identified as significantly enriched in metastatic disease compared to primary disease. Actionable mutations were found in ERBB2, BRCA2, KRAS, and PIK3CA. Sixty-four percent (7/11) patients matched to a trial through actionable mutations had durable responses (partial response or stable disease) in response to treatment. We highlight the tumor evolution in response to treatment for one patient on a matched therapy identifying a potential mechanism of resistance.

Key Terms: Bioinformatics
Cervical cancer
Genomics

HS-MMB-430

Utilizing Kefir Bacteria to Target NF-kB of the Bax Gene to Induce Apoptosis in Colorectal Adenocarcinoma Cells

Tushar Shenoy (American Heritage School)
Advisor: Iris Thompson (American Heritage School)

Kefir is fermented milk that is formulated with grains containing various bacteria and yeasts that coexist. In this study, the researcher has investigated the pro-apoptotic nature of kefir against a HT-29 human colorectal adenocarcinoma cell line. Studies have shown that transcription factor NF-kB can mediate up-regulation of the Bax pro-apoptotic gene. They have also indicated that kefir bacteria can stimulate apoptosis via the Bax gene. As a result, the researcher has investigated the mechanism in which kefir bacteria interfere with the Bax gene. He tested the cytotoxicity of kefir on colon cancer cells and three different Lactobacillus strains, as well as a yeast strain. Particular strains were chosen based on natural composition of kefir and strain percentages. The researcher hypothesized that kefir would be most cytotoxic to the HT-29 cells, and the cells would also contain the highest level of NF-kB. The researcher conducted a neutral red cell cytotoxicity assay as well as a NF-kB transcription factor assay to collect data. Ultimately, the researcher observed a significant cytotoxicity level of the kefir in comparison to other treatment groups. The disparity between kefir and other treatments remained consistent when the levels of NF-kB were measured. NF-kB was significantly higher in cancer cells treated with kefir when compared to the control or individual strains. The discovery of NF-kB as the mechanism for cancer cell apoptosis can impact the development of novel methods for cancer drug development and future research on the impact of kefir as alternative or adjunct therapy for colon cancer.

Key Terms: Colorectal adenocarcinoma
Apoptosis
Cytotoxicity

UG-MMB-436

Bacterial Viruses: A Promising Tool for Gut Microbiome Editing

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Bacteria that colonize the gastrointestinal tract play a significant role in maintaining the health of the human body by aiding in processes such as metabolism and immunity. However, some gut bacteria are opportunistic pathogens or can interfere with the metabolism of oral drugs; therefore, methods for precise removal of these bacteria would be useful. By harnessing the competitive relationship between bacterial viruses (or bacteriophages) and gut bacteria, we propose that bacteriophages may be used as a tool to modify the composition of the gut microbiome. The objective of this project was to identify and characterize bacteriophages capable of infecting specific gut bacteria, and to identify possible obstacles to this approach, such as bacteriophage resistance. To screen for species-specific bacteriophage, wastewater was filtered and cultured with 18 species of commonly found gut bacteria to enrich for bacteriophage present in the water. Bacteriophages were found for 4 of the 18 species of bacteria: *Bacteroides uniformis*, *Bacteroides fragilis*, *Clostridium asparagiforme*, and *Clostridium innocuum*. Plaque morphologies varied, but all had clear centers indicating lytic activity. Bacteriophage DNA was extracted for characterization. To confirm host susceptibility and bacteriophage specificity, cross-specificity assays were performed by testing obtained bacteriophages against all 4 species. The results confirmed that the bacteriophages can effectively infect the targeted species and do not infect other species. These results support the use of bacteriophages as an alternative therapy without disrupting the gut microbiome due to their bacterial specificity.

Key Terms: Bacteriophages
Gut microbiome
Molecular biology

UG-MMB-437

Molecular Cloning Involving the AAV-CXCL 12 Gene

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The American Cancer Society reports that this year there will be an estimated 600,920 deaths due to cancer in the United States. Current cancer research includes the use of biomarkers on the surface of cancer cells to distinguish the cancerous cells from normal body cells. Molecular cloning can enhance these biomarkers. Over the past thirty years, molecular cloning has progressed immensely. From digestion to plasmid insertion, the possibilities are endless. The AAV (Adeno Associated Virus) CXCL 12(C-X-C Motif Chemokine Ligand 12) is a Protein Coding gene that shows great promise with cloning and plasmid insertion. Our project aims to use this gene to bind tightly to biomarkers on the surface of cancer cells. However before this optimal binding can occur, it is essential to know more about the AAV CXCL 12 Gene itself. For this reason, our project includes multiple gel electrophoresis assays, plasmid insertion/digestion assays, and PCR purification. From the results of these assays, the efficacy of AAV CXCL 12 to bind to cancer biomarkers will become clear. In particular, the cloning assay for the AAV CXCL 12 gene holds great potential, as it is possible to clone extraneous DNA into a different host. If extraneous DNA can be cloned into a different host, then there is the possibility of that DNA binding to a biomarker on a cancer cell.

Key Terms: Cloning
Gene
Plasmid

UG-MMB-438

A Panoramic Dissection of RNA Polymerase-Associated Proteins

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Advisors: Padraig Deighan (Emmanuel College), Ann Hochschild (Harvard Medical School)

To support both cellular growth and prudent responses to changing environmental conditions, bacteria need to ensure that each of their genes is expressed at the appropriate level and at the appropriate time. The first step of gene expression, called transcription, is mediated by a molecular machine called RNA polymerase (RNAP). In *E. coli*, RNAP activity is modulated by a suite of approximately 250 associated proteins collectively named transcription factors. In this study, we have used a bacterial two-hybrid assay to discover and characterize the precise protein-protein interactions that occur between *E. coli* RNAP and its associated proteins. Specifically, we have assembled a library of 30+ surface-exposed and independently folded RNAP fragments, and tested these individually for interaction with 80 previously identified candidate RNAP-associated proteins. Using this methodical approach, we have uncovered the RNAP-binding determinants for several transcription factors. To further study selected transcription factors-RNAP domain interactions, we have mutagenized the DNA corresponding to the transcription factors or the RNAP domain of interest and used the bacterial two-hybrid assay to find amino acid substitutions that disrupt the protein-protein interaction. Finally, using purified components we will investigate if selected transcription factors alter the properties of RNAP during transcription *in vitro*.

Key Terms: Microbiology
Transcription
Genetic assay

UG-MMB-439

A Platform for the High-Throughput Discovery of RNA Polymerase-Associated Proteins

Tusneem Janoudi (Emmanuel College), Dionigi DiSaverio (Emmanuel College)
Advisor: Padraig Deighan (Emmanuel College)

Correct protein function often requires assembly of the protein into a multi-subunit complex or an interaction with partner proteins. To facilitate the study of protein-protein interactions in bacteria, we have modified a bacterial two-hybrid assay strain whereby a productive protein-protein interaction gives rise to green fluorescent protein (*gfp*) expression. We show the utility of GFP as a reporter of protein-protein interactions in an agar plate-based assay. Moreover, we have established working protocols that enable the use of fluorescence-activated cell sorting (FACS) to separate and substantially enrich for single cells of strain B2H-GFP harboring pairs of interacting proteins from a population of cells in which the majority harbors pairs of non-interacting proteins. We use these approaches to mine for *E. coli* proteins that interact with a panel of 30+ surface exposed regions of RNA polymerase.

Key Terms: Transcription
Protein-protein interaction
RNA polymerase

UG-MMB-440

Optimization of a Chromatin Immunoprecipitation Assay to Assess Target Genes of the FOXC2 Transcription Factor in Melanoma

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Advisor: Kriatian Hargadon (Hampden-Sydney College)

Increased expression of the transcription factor FOXC2 has been associated with more aggressive melanoma outgrowth and metastasis. We sought to optimize a chromatin immunoprecipitation assay to identify novel gene targets bound by FOXC2 in B16-F1 melanoma, specifically investigating genes regulating cell adhesion proteins and genes regulating tumor invasion and metastasis that we have been found to exhibit altered expression in wild-type B16-F1 versus a novel CRISPR-Cas9-engineered B16-F1ΔFOXC2 cell line with a homozygous disruption of the FOXC2 gene. Wild type B16-F1 chromatin was ChIPed using an anti-FOXC2 Ab, an anti-Histone H3 positive control Ab, and a normal goat IgG negative control Ab. Enrichment of known FOXC2 gene targets in the promotor regions of Itgb3 and PAI-1 was measured by qPCR for each condition. We demonstrated consistent enrichment of gene targets by anti-Histone H3 ChIP and anti-FOXC2 ChIP. We also reduced background from 14% of Input to 5.5% of Input by altering our protocol to accommodate a preclearing step and magnetic beads of a different protein-binding subtype. While background remains higher than our goal of 0.01% of Input, current work is focused on generating a novel CRISPR-Cas9-engineered variant of the wild-type B16-F1 melanoma with a homozygous disruption of the DNA-binding domain sequence of the FOXC2 gene for use as a strong negative control in further comparative ChIP-qPCR studies.

Key Terms: Chromatin immunopreciptation
Melanoma
Transcription factor

UG-MMB-441

The FOXC2 Transcription Factor is a Critical Regulator of Integrin Expression and Tumor Cell Adhesion in Melanoma

Corey Williams (Hampden-Sydney College), Coleman Johnson (Hampden-Sydney College), Kristian Hargadon (Hampden-Sydney College)
Advisor: Kristian Hargadon (Hampden-Sydney College)

Melanoma, a cancer derived from pigment-producing melanocytes of the skin, is a highly aggressive cancer that often progresses rapidly. Our previous studies have demonstrated a significant role for the FOXC2 transcription factor in promoting melanoma outgrowth and metastasis to regional lymph nodes. In order to better understand how FOXC2 regulates melanoma progression, we investigated the impact of FOXC2 gene disruption and FOXC2 overexpression in melanoma cells on tumor adhesion to extracellular matrix proteins and lymphatic endothelial cells. We show that melanoma-associated FOXC2 is a critical regulator of tumor cell adhesion to the ECM proteins fibrinogen and fibronectin as well as to lymphatic endothelial cells. This regulation of tumor cell adhesion correlates with FOXC2-mediated regulation of the integrins Itga5 and Itga9. Our data suggest that FOXC2 and proteins regulated by this transcription factor may serve as novel targets for therapies designed to limit melanoma invasion and metastasis.

Key Terms: Melanoma
Adhesion
Intern

UG-MMB-442

Identification of a Novel RNA Binding Protein in U12 Intron Splicing

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Advisor: Randal Westrick (Oakland University)

U12-introns constitute less than 0.5% of total introns in the genome. They are specifically spliced by the U12 (minor) spliceosome and are important in development. In maize a novel gene, called *rbm48* (RNA binding motif 48), has been shown to be involved in U12-intron splicing. Mutations in this gene resulted in uncontrolled cell-proliferation and cessation of cell differentiation. Since there is similarity in the phenotype between maize *rbm48* mutants and hematologic malignancies in humans, a chronic myeloid leukemia cell line was chosen to investigate whether human *RBM48* will have the same functional effects on U12-intron splicing as maize *rbm48*. In order to accomplish this, a CRISPR/Cas-9 mediated functional knockout of *RBM48* was created. Subsequently, this knockout enabled us to study the effect *RBM48* has on U12-intron splicing. After selecting a set of U12-intron-containing genes with orthologs in maize, it was found that all showed aberrant splicing of U12-introns. Current investigations include observation at the protein level through Western blot analysis to ensure that *RBM48* knockout has changed overall *RBM48* expression. Western blotting will also be done on U12-intron-containing genes to observe the effect *RBM48* knockout has on their protein expression. This provides a novel approach into investigation of uncharacterized genes and will also offer understanding of the role of the minor spliceosome in cell function and its impact on hematologic diseases.

Key Terms: Intron
CRISPR/Cas-9
rbm48

UG-MMB-443

Exploring the Role of CD55 as a Potential Receptor for *Plasmodium falciparum*

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Advisor: Elizabeth S. Egan (Stanford University)

Malaria is a mosquito-borne infectious disease caused by *Plasmodium* parasites that leads to enormous morbidity and mortality in the developing world. *Plasmodium falciparum* is the most virulent species and its tendency to develop resistance to available antimalarials is an ongoing challenge to public health. Since *Plasmodium spp.* are obligate intracellular parasites, understanding essential host-parasite interactions have the potential to inform the design of alternative therapeutic approaches to combat malaria. Recently, human CD55 was identified as a novel essential host factor important for *P. falciparum* invasion of erythrocytes, but its mechanistic function is unknown. Here, we explored whether CD55 could act as a receptor for *P. falciparum* merozoites, the erythrocyte-invasive form of the parasite. To enable studies aimed at understanding which domains of CD55 might be critical for binding of *P. falciparum* merozoites, we generated expression constructs lacking one or more specific domains of CD55 and introduced them into CHO-745 cells for ectopic expression. We confirmed expression of these variant forms of CD55 using flow cytometry and immunofluorescence analyses. In ongoing work, we are using the CHO-745 cells expressing full length or different variants of CD55 in parasite binding assays to determine 1) if CD55 is sufficient to mediate binding of *P. falciparum* and 2) if binding activity can be attributed to specific domains of the protein. Further studies using engineered red blood cells expressing different CD55 variants will help to further understand the role of this protein in *P. falciparum* invasion of erythrocytes.

Key Terms: CD55
Plasmodium falciparum
Parasite

UG-MMB-444

CRISPR/Cas9 Generation of Epitope-Tagged Thrombosis Suppressor Genes in Mouse Cell Lines

Linzi Hobbs (Oakland University), Amy Siebert (Oakland University), Randal Westrick (Oakland University)
Advisor: Randal Westrick (Oakland University)

Actin-related protein 2 (ARP2) encoded by the Actr2 gene, is an essential component of the evolutionarily conserved $Arp_{2/3}$ complex. The $Arp_{2/3}$ complex is responsible for generating branched actin networks in eukaryotic cells. Recently, our laboratory identified a novel, dominant p.R258G missense mutation in the Actr2 gene as a genetic suppressor of lethal thrombosis in mice. When studying the mechanism(s) of p.R258G thrombosis suppression, we observed increased liver expression of Protease Nexin-1 (PN-1) mRNA in the heterozygous mutant mice. PN-1 is an inhibitor of thrombin (a key thrombotic protein). Therefore, we aimed to investigate potential mechanisms by which mutant ARP2 regulates PN-1 expression in vitro. Mouse N2a cells containing mutant ARP2 or V5-tagged PN-1 were generated using CRISPR/Cas9. Genotyping by PCR and sequencing revealed homology directed repair (HDR)-mediated knock-in frequencies of 24.3% ($9/37$) for mutant ARP2 and 5.6% ($1/18$) for PN-1-V5. We then attempted to generate PN-1-V5 cells carrying mutant and/or Myc-tagged ARP2 ($GMyc^2$). Co-transfection of CRISPR components targeting the single Actr2 locus revealed HDR efficiencies of 4.4% ($2/45$) for mutant ARP2 and 26.7% ($12/45$) for ARP2-Myc. For the $GMyc^2$ lines, the HDR efficiency for double knock-in was 15.6% ($7/45$). Analysis of these cell lines revealed however, that indels were also present within both ARP2 and PN-1, indicating the generation of knockin/knockout cell lines. Taken together, our results demonstrate that HDR-mediated knock-in is highly efficient, while also illuminating the importance of carefully analyzing genome edited cell lines when developing model systems.

Key Terms: CRISPR
Genetics
Thrombosis

GR-MMB-451

Labeling of prokaryotic mRNA in live cells using fluorescent in situ hybridization of transcript-annealing molecular beacons (FISH-TAMB)

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Advisor: Tullis Onstott (Princeton University)

High-throughput sequencing and cellular imaging have expanded our knowledge of microbial diversity and expression of cellular activity. However, it remains challenging to characterize low-abundance, slow-growing microorganisms playing key roles in biogeochemical cycling. With the goal of isolating transcriptionally active cells of these microorganisms from environmental samples, we developed fluorescent *in situ* hybridization of transcript-annealing molecular beacons (FISH-TAMB) to label living prokaryotic cells. FISH-TAMB utilizes polyarginine cell-penetrating peptides to deliver molecular beacons across cell walls and membranes without affecting cell viability. Target cells are fluorescently labeled following hybridization between molecular beacons and messenger RNA of targeted functional genes. We describe FISH-TAMB's target specificity and deliverance into both bacterial and archaeal cells by labeling methyl-coenzyme M reductase A (*mcrA*) transcripts expressed within cells of *E. coli* $mcrA^+$, *M. barkeri*, and a methanogenic enrichment of deep continental fracture fluid. Growth curve analysis supports sustained cellular viability following FISH-TAMB treatment. FISH-TAMB-labeled single cells and single cells in aggregates with other unlabeled cells could be detected by flow cytometry and confocal microscopy. When coupled with a combination of single-cell sorting, imaging, and sequencing techniques, FISH-TAMB will enable characterization of key uncharacterized rare biosphere microorganisms and of the syntrophically activated metabolic pathways between physically associated microorganisms.

Key Terms: Biogeochemical cycling
Fluorescence *in situ* hybridization
Microbial ecology

UG-PHA-478

New Methods to Probe and Explore Magnetoelastic Properties of Amorphous Ferromagnetic Alloys

Lindsey Gray (Ramapo College of New Jersey), Alexander Clark (Ramapo College of New Jersey), Kamil Nowak (Ramapo College of New Jersey)
Advisors: Catalin Martin (Ramapo College of New Jersey), Philip Anderson (Ramapo College of New Jersey)

The strong magnetoelastic coupling in amorphous ferromagnetic alloys is currently guiding the development of various physical, chemical and biological sensors. The common procedure is to excite a strip of alloy with an AC-generated electromagnetic field, which produces mechanical vibrations via magnetoelastic coupling. These mechanical vibrations are sensitive to the medium in which the strip is placed, allowing the strip to detect changes in pressure, temperature, viscosity, density, or chemical composition of the medium. This research presents two relatively new approaches in probing and exploring the magnetoelastic effect in these strips. The first method involves mechanical, instead of magnetic, excitation of the strip. The second technique utilizes an RF-resonator for contactless measurements of magneto-impedance effects. Measuring this response is particularly important for potential use of amorphous magnetic alloys in the development of energy harvesting devices.

Key Terms: Physics
Magnetoelastic
Magnetism

UG-PHA-479

Collapse of Axion Stars and Collisions with Astrophysical Sources

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Advisor: Rohana Wijewardhana (University of Cincinnati)

Axions are elementary particles, which have zero spin and obey Bose statistics that have been postulated to solve the strong CP problem in quantum chromodynamics, the theory of strong interactions. At low temperatures bosons condense in the same energy state and form Bose-Einstein Condensates, due to their quantum mechanical properties. Further, these condensates, or "axion stars" are gravitationally bound. It has been proposed that axion stars could be contributing to dark matter. Previous studies have found axion stars have a dilute metastable state with a critical mass of ~1019 kg and a radius of ~200 km. By improving previous approximations of the configuration's energy, we determine a stable dense state exists at a radius of ~10 m. Furthermore, if the mass of the axion star is supercritical (including masses much greater than 1019 kg), the star will begin to collapse from its dilute state to the dense state. As it contracts, the star will decay and rapidly emit relativistic axions. We additionally analyze the probability of such a collapse being induced by a collision of an axion star with various astrophysical bodies.

Key Terms: Physics
Dark matter
Cosmology

UG-PHA-480

Phase Portraits of Non-minimally Coupled Inflaton Fields in the Early Universe

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Advisor: Gary Felder (Smith College)

The theory of inflation resolves some of the issues of the widely accepted Big Bang theory, namely the flatness problem and the horizon problem, by introducing a period of exponential expansion when the universe was 10^{-36} seconds old. What causes this period of inflation is a scalar field called the *inflaton* – a special type of a field with a large but slowly changing energy density. Although inflation is a widely accepted theory, the exact physics of this process are not yet known. Different models of inflation describe the relationship between the scalar field and local curvature of spacetime differently. In other words, the scalar field can be *non-minimally* or *minimally coupled* to the curvature of spacetime (i.e., gravity) – mutually dependent or not dependent on it, respectively. Non-minimal coupling arises from a term of the form $f(\varphi) * R$ in the Lagrangian, where R is the Ricci scalar. In our models, this coupling term is $\varphi^2/_{12} R$. The project we want to present aims to better understand the evolution of a non-minimally coupled scalar field by using three-dimensional phase portraits made in Mathematica. We have mapped regions in the 3D phase portrait where the equation of state enters the inflationary realm (i.e., it becomes less than -⅓), and that gave us insight into which initial conditions lead to inflation.

Key Terms: Inflationary cosmology
Scalar fields
Early universe

GR-PHA-490

H_2^+ Ion Source for IsoDAR Neutrino Experiment

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Advisors: Janet Conrad (MIT), Daniel Winklehner (MIT)

The 5 year IsoDAR cyclotron experiment at KamLAND will be: a definitive search for sterile neutrinos, a study of antineutrino-electron scattering, and sensitive to signals indicating physics beyond the standard model. The antineutrinos are produced by an accelerator driven Isotope-Decay-At Rest source, where protons impinge on a ^{9}Be target, producing neutrons that are captured in a surrounding ^{7}Li "sleeve". Experimental needs require 10 mA of 60 MeV protons to reach the target. We will achieve this by accelerating H_2^+ ions, instead of H^- which are more commonly used in cyclotrons. The ion source goal is 50 mA of H_2^+ to allow for 90% loss during acceleration and transport. Current research efforts are focused on the development of an ion source that can provide such a current. A systematic study of ion production and extraction is underway.

Key Terms: Particle physics
Neutrinos
Cyclotrons

HS-PSI-503

Effect of Diet on Diabetes and Body Composition in a Mouse Model

Frank Zhu (Brecksville-Broadview Heights High School)
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Diet is a well-known contributing factor to the development of metabolic syndrome. We investigated this relationship using a mouse model genetically predisposed to diabetes and obesity (FVB-diabetes). 18 mice in one of 5 diet groups were allowed to eat freely for 36 weeks. Five types of diet, including a 5% lard starch control diet, a 5% lard/60% fructose diet, a 10% lard/2% cholesterol starch diet, a 20% lard/30% fructose diet, and a 30% lard diet, were studied. Weight, waist circumference, fasting glucose level, and systolic blood pressure were measured every three weeks. Our results showed at 36 weeks that the 30% lard diet caused mice to gain on average 20% (94 g) more weight, and waist circumference increased by 11% (3 cm) compared to the control mice. Additionally, the 60% fructose diet caused the highest fasting glucose compared with the low fat control diet (118.3 vs. 101.9 mg/dl). Finally, all mice in all investigational diet groups had elevated systolic blood pressure compared to the control diet group, with increases ranging from 13-29 mmHg. These results show even in diabetically predisposed mice, a low fat and sugar diet is associated with a decrease in the likeliness of metabolic syndrome. This study has broad applications for future research to investigate the effect of other factors, such as different types of fat and sugars, exercise, and total caloric intake, on metabolic syndrome.

Key Terms: Diet
Diabetes
Nutrition

HS-PSI-504

Development of a Novel Monitoring System for Insulin-Producing Beta Cells Using Gaussia Luciferase Reporter Driven by the Synthetic Human Insulin Promoter

Anam Ahmed (American Heritage School)
Advisors: Dagmar Klein (University of Miami), Leya Joykutty (American Heritage School)

Type 1 diabetes (T1D) is an autoimmune disease with high rates of mortality and morbidity, in which the insulin producing beta cells in the pancreas are destroyed. There is no cure for T1D; patients need insulin administration as a temporary treatment. Beta islet transplantation is one possible cure, however, concerns include viability and maintaining a supply of donor cells. Scientists have established a method to reprogram a patient's own non-endocrine pancreatic tissue (hNEPT) into insulin-producing cells without genetic modification, using bone morphogenetic protein 7, but a method to monitor the conversion of these cells is lacking. This experiment develops such a monitoring system using the Gaussia Luciferase(GLuc) reporter driven by the Synthetic Human Insulin Promoter. Expression of the insulin gene is linked to GLuc production, which produces bioluminescence when exposed to the protein luciferin. The hypothesis was that a greater number insulin producing cells would correlate to a greater amount of bioluminescence than the bioluminescence in non-insulin producing cells. The GLuc reporter construct was transfected into mouse insulinoma and fibroblast cells and bioluminescence was monitored. With p-values <0.001, the results support the hypothesis, and prove to be extremely statistically significant. This project aims to provide a way to monitor beta cells in vitro but can also be applied in many research areas to monitor other biological processes. This experiment aims to mitigate the supply concern of beta islet transplantation, furthering research to establish a cure for T1D.

Key Terms: Diabetes
Cellular engineering
Biomedical science

HS-PSI-505

The Effects of Electrical Discharge Plasma Treatment on Cellular Growth and Wound Healing

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Advisor: Jeff Overton (University of North Carolina Wilmington)

Plasma is an ionized gas consisting of charged particles and UV photons. When plasma interacts with water, reactive oxygen species (ROS) are produced, and these compounds are recognized for their bactericidal properties. In previous experiments, I found that low doses of plasma led to larger muscle cell size in vitro and may enhance wound healing. The present study examined the effects of plasma on artificial wound healing in vitro using myoblast cells, and also wound healing in vivo using planarian flatworms. Myoblasts were grown to confluence, and a 1 cm artificial wound was produced on the culture plates. Both low and high doses of plasma led to significantly enhanced cell recruitment to the wound and higher rates of wound closure. Planarian worms, which can regenerate when cut into pieces, were then cut in half and subjected to control or plasma treated conditions. Both low and high plasma doses led to greater lengths of both the head and tail segment of the worm after 5 days of treatment. Further, the rate of wound closure in the cut region was greater in the plasma treated groups. In a separate experiment, I measured ROS production in the plasma treatment, and found that my plasma device significantly increased ROS in the media. Together, these results demonstrate that plasma enhances cell growth and wound healing both in vitro and in vivo, and that the effects of plasma are likely mediated by ROS production.

Key Terms: Electrical discharge plasma
Wound healing
Engineering

UG-PSI-513

***In Vitro* Interactions of Human Neural Stem Cells, Poly(Lactide-co-Glycolide), and the Innate Immune Response Following a Spinal Cord Injury**

Glenn Guardamondo (University of California, Irvine), Usha Nekanti (University of California, Irvine), Aileen Anderson (University of California, Irvine)
Advisor: Aileen Anderson (University of California, Irvine)

Spinal cord injuries leave people paralyzed below the level of injury. Currently, there is no treatment that can restore functionality after injury. The injury causes breakage of the blood spinal barrier causing immune cells to infiltrate into the lesion and the surrounding tissue. The principal innate immune cells present in the spinal cord injury environment are neutrophils and macrophages/microglia depending the time of injury. Neutrophils are dominant immediately after injury, and macrophages are dominant a week after injury, decline in number, then increase at two weeks post injury. Human neural stem cells (hNSC) represent a reparative approach that has been used because of the ability of these cells to differentiate into the three cell types of the central nervous system (CNS), astrocytes, oligodendrocytes, and neurons. Neutrophils and macrophages present after injury affect hNSC differentiation. Neutrophils promote astroglial differentiation, while macrophages promote neuronal differentiation. New oligodendrocytes can remyelinate spared or newly regenerated axons, supporting therapeutic use of hNSC. In parallel, another regenerative approach is the use of porous, biodegradable material— Poly(Lactide-co-Glycolide)—to enable a permissive environment to promote axon regrowth. Previous studies from our laboratory using a multichanneled PLG bridge demonstrated novel axonal regeneration through the impermeable environment of the SCI epicenter. We hypothesize that combination of these two approaches may yield both axonal regeneration and remyelination resulting in a synergistic outcome. In these experiments our objective is to understand the effect of interactions between innate immune cells, hNSC, and PLG material. Immune cell conditioned media (CM) will be generated by 72h culture of primary macrophages or neutrophils in the presence of PLG. The effect of CM on the fate of hNSC grown on PLG in vitro will be analyzed using quantification of immunocytochemical markers in IMARIS software. Preliminary data analyzing nuclear Olig2 expression using this paradigm suggests that that macrophage-derived CM enhances oligodendroglial fate.

Key Terms: Spinal cord injury inflammation
Human neural stem cells
Oligodendrocyte fate

UG-PSI-514

Interaction between Developmental Nicotine Exposure and a Genetic Risk for Nicotine Dependence across Multiple Generations

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Advisor: Jerry A. Stitzel (University of Colorado, Boulder)

In the U.S., approximately 8.4% of women smoke during pregnancy. Developmental nicotine exposure (DNE) through maternal smoking is associated with increased risks for attention deficit hyperactivity disorder (ADHD), nicotine dependence, and internalizing disorders such as anxiety. Furthermore, a genetic risk factor in the form of a single nucleotide polymorphism (SNP) of *CHRNA5* (rs16969968), which encodes the alpha-5 nicotinic acetylcholine receptor subunit, is associated with nicotine dependence. We hypothesize that the interaction between DNE and rs16969968, a non-synonymous amino acid substitution in *CHRNA5* (D398 is wild type, N398 is the risk allele), would alter responses in three measures: locomotor activity, intake of nicotine via drinking, and corticosterone levels. To model DNE, we exposed female D398 and N398 mice to nicotine (100 µg/mL in 0.2% saccharin) or saccharin alone in drinking water 30 days prior to mating with a nicotine-naïve male and continuing until weaning; resulting in four F1 offspring groups: D398 and N398 vehicle (D-Veh, N-Veh), D398 and N398 developmental nicotine exposed (D-Nic, N-Nic). F1 nicotine-exposed females were then mated with nicotine-naïve males to produce F2 generations (D-F2, N-F2). The four bottle choice test (FBCT) was administered to determine nicotine intake and data suggests a predisposition for increased nicotine consumption in F1s and F2s that differs based on genotype. Preliminary home cage locomotor activity data, collected during the FBCT, does not differ among groups. Pre-/post-nicotine open field testing indicates hyperactivity in D-F2 mice following nicotine consumption. Corticosterone data collection is ongoing. Future directions include studying interactions between mice heterozygous for rs16969968.

Key Terms: Behavioral genetics
Developmental nicotine exposure
CHRNA5 (rs16969968)

UG-PSI-515

The Role of Cell Adhesion Molecules CD106 and CD146 in mAo MSC-Induced Macrophage Phagocytosis

Anthony Morante (Molloy College), Anthony Ricigliano (Molloy College), Rachel Rex (Molloy College) , Jillian Weiss (Molloy College)
Advisor: Jodi Evans (Molloy College)

Mesenchymal progenitor cells have traditionally been studied for their regenerative properties, but more recently their immunoregulatory characteristics have been at the forefront. When interacting with immune cells they can be either suppressive or supportive and, therefore, represent an exciting new way to treat inflammatory diseases. In this study, we examined mesenchymal progenitor cell regulation of macrophage phagocytosis. Macrophage phagocytosis is an important part of the innate immune system response to infection and the mechanisms through which mesenchymal progenitors modulate this response are under active investigation. We hypothesized that mesenchymal progenitors regulate macrophage phagocytosis through both secreted factors and direct cell-cell contact and that direct contact regulation is dependent on mesenchymal progenitor cell expression of the vascular cell adhesion molecule 1 (Vcam1). To test this hypothesis, a mouse spleen-derived macrophage cell line (SpMΦ) was exposed to conditioned medium from mouse aorta-derived mesenchymal progenitors (mAo) and their phagocytosis of yeast zymosan particles was subsequently measured. SpMΦ were also cultured directly with aorta-derived progenitors with and without Vcam1 knockdown via siRNA. SpMΦ phagocytosis of zymosan was suppressed after exposure to mAo cell conditioned medium. In contrast, SpMΦ phagocytosis of zymosan was increased after direct contact with mouse mAo; alternately, deficiency of Vcam1 in mAo cells reverses this increase. Our study illuminates tools to amplify or suppress the innate immunity in infectious disease. Future studies are needed to identify the specific mediators of these responses to condition cells to have a predictable and effective clinical use in the treatment of inflammatory diseases.

Key Terms: Mesenchymal stem cells
Macrophage cells
Immunology

UG-PSI-516

Aggressive Behavior and Estrogen Levels of Pregnant Ruffed Lemurs (*Varecia rubra* and *V. variegata*) as Predictors of Neonatal Outcomes

Amaya Watters (North Carolina State University), Megha Ganatra (North Carolina State University), Mary Hawkins (North Carolina State University)
Advisor: Lisa Paciulli (North Carolina State University)

Hormones are the body's chemical messengers and are vital in regulating the body's natural functions. They can be used during pregnancy to predict changes in the mother's physiology. In addition, hormone levels influence behavior. A female's hormones and behavior are important in shaping the environment in which the fetus develops during pregnancy. This study was conducted to see if estrogen levels and agonistic behavior can be used to predict neonatal outcomes in non-human primates. Behavioral observations of one pregnant captive Duke Lemur Center ruffed lemur (*Varecia rubra*) and six non-pregnant lemurs (*Varecia rubra* and *V. variegata*) were made before, during, and after pregnancy. Female fecal samples were collected weekly for seven months. They will be analyzed using a competitive binding assay, and estrogen levels will be recorded. Results will be statistically analyzed longitudinally for changes in behavior and hormones over time. The data will be compared to neonatal outcomes. The results from this study will help document reproductive hormonal changes in adult female ruffed lemurs. These changes may be used to predict neonatal outcomes including miscarriages, preterm birth, low birth weight, and potential medical complications of the mother and/or infant. Future research should be conducted on more non-human primate species and include additional hormones to examine the relationship between pregnancy hormones and neonatal outcomes.

Key Terms: Estrogen
Maternal behavior
Neonatal outcomes

UG-PSI-517

Comparison Study of the Effects of Zerumbone and AG490 in Human Renal Cell Carcinoma on the Activation of the Janus Kinase Pathway and Cell Survival

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Advisor: Amy Banes-Berceli (Oakland University)

In the US, Renal Cell Carcinoma (RCC) accounts for 9 of 10 cases of kidney cancer. Development of new therapies is limited because the molecular mechanisms of RCC and the chemoresistance are poorly understood. However, we have have shown that alterations in the levels of the Janus Kinase (JAK2) and signal transducers of activators of transcription (STAT) pathway may be involved as it has been implicated in invasiveness and cell survival in RCC cell lines. We hypothesize that altered activation of the JAK/STAT/SHP-1 pathway contributes to the development of RCC and the chemoresistance observed. To test this hypothesis we used the RCC cell line (ATCC) and treated the cells for 24 hours with the JAK2 inhibitor AG490 and sunitinib (standard chemotherapy agent) alone and in combination. After 24 hours we found a 20% decrease in cell viability in the AG490 treated cells but not in the sunitinib treated cells. Combination treatment for 24 hours resulted in a 40% decrease in cell viability. At 24 hours we found significant decreases in JAK2 phosphorylation levels with both and almost undetectable levels by 48 hrs. We also treated cells with several inhibitors and measured cell viability for 24, 48, 72 and 96 hrs. We found an 80% reduction in cell viability at 96 hours of treatment with both the zerumbone and AG490. There data suggest that inhibition of JAK2 is a viable clinical target for future therapy as it enhanced the response to sunitinib as well as decreased cell viability on its own.

Key Terms: Physiology
Renal cancer
JAK/STAT

UG-PSI-518

Integrin Alpha-6 is Required for the Derivation of Human Induced Pluirpotent Stem Cells

Genna Wilber (Oakland University), G Bigoni (Oakland University), Suraj Timilsina (Oakland University), Luis Villa-Diaz (Oakland University)
Advisor: Luis Villa-Diaz (Oakland University)

Integrins function in cell attachment, gene expression, motility, polarity, shape, proliferation, and cell survival, which explains their wide expression across cell populations throughout the body. Integrin alpha-6 (ITGA6), an isoform of the integrin family, has been shown to play an integral role in pluripotent stem cell (PSC) self-renewal. We used the genetic reprogramming of somatic cells (human gingival fibroblasts) into induced pluripotent stem cells (hiPSCs), as an experimental model to determine the role of ITGA6 in the development of pluripotency. We knocked down ITGA6 in human gingival fibroblasts (hGF) utilizing CRISPR Cas9 single-guided (sg) RNAs targeting this gene. We used the following controls: wild-type (WT) hGFs and a sgRNA that targeted random nucleic acid sequences. These groups were infected with lentivirus encoding the reprogramming factors Oct4, Sox2, Klf4 and c-Myc. We confirmed that parental cells containing the vectors targeting ITGA6 expressed significantly lower levels of ITGA6 mRNA. By flow cytometry we verified that ITGA6 was not translated in the targeted hGFs after overexpression of c-Myc, a known up-regulator of ITGA6. hiPSC colonies developed in all groups, although a significantly lower rate was observed in the ITGA6 knockdown groups compared to the WT control. The resulting colonies in each group expressed ITGA6, indicating that the CRISPR Cas9 targeting of ITGA6 was not 100% effective. This suggests that ITGA6 is crucial for the development and maintenance of hiPSCs because no colony developed without the expression of this gene.

Key Terms: Immunology
Integrin
Stem cell

GR-PSI-523

Understanding the Link Between Vitamin D Deficiency and Obesity

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Vitamin D (1α, 25-dihydroxyvitamin D3) is a steroid hormone traditionally associated with mineral ion homeostasis; however, accumulating evidence suggests a wider biological role for VD and its importance in immune function, xenobiotic metabolism, cell differentiation, and neurodevelopment. Like other members of steroid hormones, the biological effects of VD are mediated through the binding of 1α, 25-dihydroxyvitamin D3 (ligand) to its hormone receptor, VDR. In recent years, the VD signaling axis has been implicated in metabolic control, where low systemic VD levels are associated with obesity and metabolic disorders. To investigate the role of VD/VDR in obesity, we established three dietary cohorts of zebrafish placed on engineered diets: a standard lab diet (1.4 iu/g) as a control, a VD null diet (0 iu), and a VD enriched diet (400,000 iu/g). We found that when zebrafish switch over from a standard lab diet to a VD null diet at 2 months of age, they develop grossly swollen abdomens by 6 months of age. This phenotype is attributed to significantly elevated levels of visceral and subcutaneous fat compared to controls. Concordantly, preliminary gene expression data shows an overall upregulation of adipogenic and lipogenic markers in VD deficient fish, and preliminary proteomics data demonstrates differential regulation of proteins specific to lipid metabolism. Currently we are utilizing RNA-Seq data to identify key obesogenic genes being regulated by VD and understand the molecular mechanisms associated with both VD deficiency and onset and progression of obesity and associated diseases such as diabetes.

Key Terms: Vitamin D
Obesity
Toxicology

GR-PSI-524

Magnetically Tissue Plasminogen Activator-loaded Fe3O4 Nanorods Improve Thrombolysis Rate After Ischemic Stroke

Jiangnan Hu (University of North Texas Health Science Center)
Advisor: Kunlin Jin (University of North Texas Health Science Center)

Stroke is the 5th leading cause of death in the US. The only FDA-approved treatment is the intravenous administration of tissue plasminogen activator (tPA). However, due to tPA's inability to lyse the clot fully, about 90% of these patients still live with speech or motor impediments. Moreover, the large dose of tPA administered increases the susceptibility to global tPA-mediated hemorrhage. Therefore, the purpose of the study was to increase tPA's thrombolysis rate and reduce total tPA administered using a novel nanomaterial, tPA-loaded Fe3O4 nanorods (tPA-NRs). We hypothesize that tPA-NRs will be more successful at thrombolysis and minimize the off-target effects of tPA. In vitro results demonstrated that tPA-NRs could achieve a mass loading ratio as high as 12.9% and the loaded tPA can be released when stimulated by an external rotating magnetic field. To examine the proposed approach in vivo, a FeCl3-induced distal middle cerebral artery occlusion (dMCAO) model was used. Our results unequivocally showed that: 1) intra-arterial injection of tPA-NRs could target the site of the clot under magnetic guidance; 2) the mechanical force generated by the spinning of the tPA-NRs under the external rotational magnetic field could significantly decrease dMCA blood flow recanalization time from 85 min with high dose tPA (10 mg/kg) to 25 min with low dose tPA-NRs (1 mg/kg) ($p < 0.001$). This work is significant in that it could revolutionize treatment for ischemic stroke and could be applied in the future to other deadly thrombotic diseases such as myocardial infarction and pulmonary embolism.

Key Terms: Neuroscience
Nanomaterial
Thrombolysis

GR-PSI-525

Potential Variation in the Effects of Known JAK Inhibitors on Primary Renal Clear Cell Carcinoma Cell Lines and Discovering Down-stream Targets of the JAK/STAT Pathway

Katie Hege (Oakland University), Amy Banes-Berceli (Oakland University)
Advisor: Amy Banes-Berceli (Oakland University)

Kidney cancer is among the top 10 most common cancers among middle aged men and women. The main challenge of RCC diagnosis is that most symptoms of kidney cancer only appear after it is advanced to metastasis, the most common subtype is clear cell renal carcinoma (ccRCC). At diagnosis, the cancer may have already gained resistance to the current treatments. Available drugs demonstrate different molecular and physical reactions by RCC cells such as those that effect the cancer promoting unregulated JAK/STAT pathway. Our in vitro analysis of the commercial ccRCC cell line, Caki-2, shows resistance and even viability increases to the chemotherapy drug, sunitinib, before reaching its effective EC50 value of 16.5 µM at 48 hours. The EC50 value decreased from 35 µM at 24 hour to 12 µM at 72 hour treatments. These changes were also observed for the JAK/STAT inhibitor, zerumbone with a 48 hour EC50 value of 33.6 µM. These values were significantly increased when the drugs were combined; the zerumbone EC50 value increased to 61 µM with the sunitinib EC50 concentration. These data suggest resistance to sunitinib and zerumbone exists in Caki-2 and co-treatment was detrimental to their ability to decrease cell viability. This may not be the case with primary RCC cell lines due to their physiological relationship to the intact RCC tumor. Direct analysis of the primary cell line from the tumor that has been surgically removed is essential to the patient's highest probability of survival with the most effective treatment.

Key Terms: Physiology
Renal cancer
JAK/STAT

GR-PSI-526

Gender Differences involving Serotonin (5-HT) Receptors in Type I Diabetic Rats

Tudor Moldovan (Oakland University), Marisa Cervantes (Oakland University), Jonathan Bucan (Oakland University) , Bernie LePage (Oakland University)
Advisor: Amy Banes-Berceli (Oakland University)

Diabetes mellitus affects millions of individuals and often leads to vascular and renal complications. Increased plasma levels of 5-HT exist in male diabetic rodent models and previous data in male Japanese diabetic patients demonstrated that inhibition of 5-HT_{2A} receptors reduced proteinuria, a marker for renal damage. Previous research employing rat models has failed to explore differences in 5-HT levels and function between males and females. We hypothesized that increased levels of 5-HT receptors may be the cause of the vascular damage observed in diabetics via increased vasoconstriction and that receptor levels would differ between males and females. To test this, we obtained male and female Sprague-Dawley rats (300-325g) and induced diabetes with the compound Streptozotocin (STZ). At 14 days and 28 days post-onset of diabetes we euthanized the animals and harvested tissues and blood vessels for Western blot, myograph analysis, and immunohistochemistry (IHC). Our findings revealed altered vascular contractions in major blood vessels between the male and female diabetic and control rats with female diabetic rats exhibiting increased sensitivity to 5-HT. Additionally, expression of the 5-HT_{2A} and 5-HT_{2B} receptor subtypes in both the vasculature and renal cortexes differed between the males and females at both 14 and 28 days. Our results support our hypothesis that 5-HT receptor levels are altered in a state of diabetes and also between the sexes. Our work aims to elucidate the role of serotonin in the development of diabetic complications in the hopes of generating targeted therapies to reduce these complications.

Key Terms: Physiology
Diabetes
Vascular

Program Update

Symposium on Atmospheric Chemistry, Climate, and Health

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November 11, 2017

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UG-CBB-113

Effects of Ether Lipid Metabolism on Platelet Aggregation

Ling Lin (University of North Carolina at Chapel Hill)
Advisor: Leslie Parise (University of North Carolina at Chapel Hill)

Human platelets are essential mediators of hemostasis and thrombosis. Platelets prevent blood loss by repairing damaged blood vessels to maintain homeostatic conditions, but also obstruct blood flow during thrombosis, which significantly increases the risk of heart attack and stroke. Although anticoagulants reduce this risk, bleeding is a major side effect. The development of novel antiplatelet therapeutics requires a better understanding of the underlying mechanisms of platelet activation. Our lab previously identified a lipid deacetylase, arylacetamide deacetylase-like 1 (AADACL1), as a regulator of human platelet activation. Inhibition of AADACL1 activity interferes with dense granule secretion by preventing the deacetylation of an ether lipid substrate found in platelets, hexadecyl acetyl glycerol (HAG), to 1-O-hexadecylglycerol (HG). We observed significant inhibition in platelet aggregation with HAG treatment. Interestingly, we did not observe the accumulation of HAG as a result of AADACL1 inhibition. Using LC-MS and tandem MS, we detected and identified a phosphorylated species of HAG, 1-O-hexadecyl-2-aceyl-sn-glycerol-3-phosphate (HAGP) in platelets under these conditions. Both HAG and HAGP impede protein kinase C α(PKC) activity by interacting at conserved C1 domains in PKC, which may causes downstream inhibition of dense granule secretion and consequently, platelet aggregation. Together, these data reveal the importance of AADACL1-mediated regulation of human platelet aggregation by ether lipid metabolization.

Key Terms: Platelets
AADACL1
HAG

UG-CBB-114

Understanding the Etiologies of Amyotrophic Lateral Sclerosis

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Advisor: Matt Begley (University of North Carolina at Chapel Hill)

Amyotrophic lateral sclerosis (ALS) is a devastating neurodegenerative disease that results in the destruction of the upper and lower motor neurons. A link has recently been found between a mutation in the isoenzyme, superoxide dismutase (SOD1), and ALS. This mutation results in the aggregation of the SOD1 protein. The exact mechanism of ALS is unknown, but it is known that protein aggregation is toxic to neuronal cells when exogenously added. The Dokholyan Lab is attempting to characterize the structure of these SOD1 aggregates, which will in turn help us to begin to study the mechanism of action for the toxicity. Characterization of this structure will be found through the use of molecular structural modeling and dynamic simulations, allowing study of structure and dynamics of biological molecules at time scales relevant to human biological systems. The study of the structure and its mechanisms will likely contribute to the understanding of the etiologies of ALS and help develop novel therapeutic strategies.

Key Terms: ALS
SOD1
Aggregate

UG-CBB-115

Studying Septins Using *C. elegans*

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Advisor: Amy Shaub Maddox (University of North Carolina at Chapel Hill)

Septins are GTP-binding proteins that form nonpolar rod subunits that assemble into filaments which scaffold regulatory and structural proteins to facilitate cell division and other processes. They interact interdependently and dynamically with other cytoskeletal filaments, including actin. In most species, septins are encoded in multiple genes, however, in *C. elegans*, septins are encoded by only two genes, *unc-59* and *unc-61*, which makes *C. elegans* an ideal model organism in which to study septin function. In a septin null mutant, worms are viable but have substantial morphological and developmental defects which lead to uncoordinated locomotion and reduced viability. The purpose of this research is to shed light on the role of septins during embryonic cytokinesis and germline morphogenesis by qualitatively examining the effects of mutating *unc-61*. I generated a strain of *C. elegans* expressing a red fluorescent probe for the actin cytoskeleton ("LifeAct") in combination with the septin loss of function allele. The embryos from this strain were imaged by live-cell microscopy during their first mitotic division. Then, the germline of each strain was imaged to study the morphogenic repercussions of the null mutation. We found that the architecture of the syncytial germline is distorted and actin is abnormally enriched. Additionally, in order to study the localization and stability of UNC-59 septin in the absence of UNC-61, I crossed a fluorescently tagged the *unc-59* allele with a null mutation of the *unc-61* allele. Based on the segregation of the tagged and null alleles, we suspect that *C. elegans* with both septin alleles altered simultaneously are not viable. These tools and methods will allow us to continue to study the function of septins during oogenesis and embryogenesis.

Key Terms: Septin localization
C. elegans embryo & germline
Embryonic cytokinesis

UG-CBB-116

Detection of Galectin-3 Binding Protein in Animal Cells

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Advisor: Sarah Adjei-Fremah (North Carolina Agricultural & Technical State University)

The objective of this study was to detect Galectin-3 binding protein in cow, sheep and goat serum. Galectin-3 binding protein (LGALS3BP) is secreted into serum and binds to galectin -3. By binding Galectin -3, LGALS3BP may regulate cell adhesion. Galectins are proteins that bind beta-galactoside sugars and mediate cell-cell and cell-matrix interactions. In this study blood serum collected from cows (N=3), Sheep (N=3) and goats (N=3) at NC A&T State University was used. Galectin-3 binding protein was detected in cow, sheep and goat serum using a commercial Human Galectin 3 binding protein Enzyme-linked immunosorbent assay (ELISA) kits have been used to detect secreted Human Galectin 3 binding protein. The concentration of Galectin binding protein 3 varied for each animal. The average concentration of galectin binding protein was highest in goat serum, followed by sheep and cow serum. These results show that LGALS3BP can be detected in serum from cows, sheep, and goats. Thus, this protein is present in the animal blood. Antibodies against human Galectin binding protein could be used to detect and quantify cow, sheep and goat galectin binding protein. Therefore, there is a similarity between human and animal galectin 3 binding protein. The concentration of Galectin binding protein varied among animal and animal species and its role in animal health and wellbeing needs further study.

Key Terms: Cell
Biology
Chemistry

UG-CBB-117

An Analysis of Conserved Intronic Repeat Elements in Back Splicing Leading to Circularization

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Advisor: Bill Marzluff (University of North Carolina at Chapel Hill)

The advent of next generation sequencing combined with careful analysis of chimeric reads has identified ubiquitous circular RNAs. Their function, purpose, and evolutionary origins however, remain largely unknown. One model for Circular RNA formation is back splicing, and it is generally believed that this requires the two introns to have complimentary base pairs, causing them to pair and facilitate back splicing. Interestingly, circular RNAs are found in every mammal's genome; one question is whether they co-evolved, which would suggest conserved function. Since there is so much that is unknown about circular RNAs, there is a need to create new methods to quickly parse data currently available data and make sense of it. We used BED files that contain data for specific coordinates in related mammalian genomes in to identify conserved regions in where complimentary repeat elements capable of base-pairing occur. We have developed computational tools and code that can take the data from these BED files and arrange them so that it shows how circular RNAs in the human and mouse genomes are related. The code will be developed using python, LINUX and the bedtools library.

GR-CBB-138

Ubisol Q-10 Protection Against Glutamate Toxicity Causing Mitochondrial Dysfunction on Neuronal Cells

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Advisors: Mary Zimmerman (North Carolina Central University), Andy Li (North Carolina Central University)

Mitochondrial dysfunction due to glutamate toxicity is one of the major events that accelerates neuronal cell death during acute brain injury. Coenzyme Q10 (CoQ10) has widely been used for the treatment of mitochondrial disorders and neurodegenerative diseases. The aims of the present study are to determine the neuroprotective effects of Ubisol-Q10 on glutamate-induced cell death and to explore its effect on mitochondrial biogenesis. HT22 neuronal cells were exposed to glutamate and were assayed to see which pathway is affected by the toxicity of the glutamate. We concluded that Ubisol-Q10 protects cells from glutamate toxicity by preserving the structure of mitochondrial structure and function. It was also shown that the protein expression in NRF2, TFAM and PGC1-alpha are being reduced and then restored. Therefore, adequate CoQ10 supplementation may be beneficial in preventing cerebral stroke and other disorders that involve mitochondrial dysfunction.

Key Terms: Neuroscience
Biochemistry
Physiology

GR-CBB-139

Investigation of UHRF1 as a Novel APC/C^{Cdh1} Chromatin Substrate

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Advisors: Rajarshi Choudhury (University of North Carolina at Chapel Hill), Michael J. Emanuele (University of North Carolina at Chapel Hill)

Ubiquitylation is a crucial post-translational modification that regulates multiple aspects of cell physiology including proliferation and repair. The anaphase-promoting complex (APC/C) is the preeminent E3 ubiquitin ligase that controls mitotic exit and S-phase entry of the cell cycle by orchestrating substrate-specific K11/K48-ubiqutin-mediated proteolysis. Highly evolutionarily conserved, the APC/C identifies substrates with the aid two co-receptors, Cdc20 and Cdh1. These substrate receptors bind conserved consensus sequences in target proteins called degrons, namely, KEN- and D-boxes. Beyond the crucial role in cell division, APC/C^{Cdh1} is integral to maintaining genome stability and Cdh1 is itself a haploinsufficient tumor suppressor. Moreover, many APC/C substrates are overexpressed and select APC/C core subunits are mutated in human cancers, demonstrating that APC/C dysfunction is associated with tumorigenesis. Thus, characterization of novel APC/C targets is critically important to further elucidate APC/C functions in both normal proliferative homeostasis and oncogenesis. Taking a bioinformatics approach, we identified Ubiquitin like with PHD and RING Finger Domains 1 (UHRF1) as a putative APC/C^{Cdh1} substrate. UHRF1 is an essential epigenetic regulator that maintains DNA methylation through successive cell divisions. As an oncogene overexpressed in many cancers, UHRF1 levels correlate with high tumor grade and poor prognosis, yet the downstream biological implications of UHRF1 to tumorigenesis remain unknown. Our preliminary data shows that UHRF1 protein levels oscillate throughout the cell cycle. Additionally, UHRF1 levels increase following genetic and pharmacological inhibition of APC/C^{Cdh1}, but diminish with Cdh1 overexpression. We demonstrate that UHRF1 and Cdh1 interact and alanine mutations of a conserved KEN box degron in UHRF1 impair this interaction with Cdh1. Moreover, this mutant UHRF1 protein has a longer half-life and resists Cdh1-mediated degradation compared to the wild-type UHRF1. These data support our hypothesis that UHRF1 is a novel APC/C^{Cdh1} target degraded in G1-phase of the cell cycle.

Key Terms: Ubiquitylation
Cell cycle
Epigenetics

UG-CHM-180

Selective Recognition of Asymmetric Dimethylarginine with a Synthetic DCC Receptor

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Advisor: Marcey Waters (University of North Carolina at Chapel Hill)

Methylation of histone lysine and arginine residues is an important regulator for gene expression; recognition of methylated peptides is most commonly performed using antibodies, but synthetic receptors are an emerging alternative tool. Currently, no receptor exists that selectively recognizes asymmetric dimethylarginine (Rme2a) over trimethyllysine (Kme3). A synthetic receptor for Rme2a was produced using dynamic combinatorial chemistry (DCC), which allows monomers to form various receptors, the concentrations of which are affected by interactions with guest compounds via Le Chatelier's Principle. Dynamic combinatorial libraries (DCLs) containing synthetic monomers G and N and different peptide guests were produced and allowed to equilibrate for 3 and 10 days, allowing the DCLs to undergo changes in equilibrium concentrations after introduction of guests. Using UV-vis HPLC, DCLs containing no peptide guest, RGGY, Rme2aGGY, and Kme3GGY were analyzed. A peak was significantly amplified solely for Rme2aGGY, indicating that the N_2G_2 DCL selectively recognized Rme2a over Kme3. nuclear Overhauser effect spectroscopy (NOESY) will indicate the conformation of N_2G_2 that best recognizes Rme2a, and this conformational analysis will guide the synthesis of a thioether-linked N_2G_2 receptor.

Key Terms: Selective molecular recognition
Dynamic combinatorial chemistry
Methylated Amino Acids

UG-CHM-181

Hydroquinone Oxidation Catalyzed by an Oxide-Bound Os Polypyridyl Catalyst and Base

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Advisors: Thomas Meyer (University of North Carolina at Chapel Hill), Prateek Dongare (University of North Carolina at Chapel Hill)

With near indefinite longevity and cost effective energy storage, redox flow batteries are considered to be the next breakthrough in renewable energy storage. The interconversion between hydroquinone and benzoquinone shows particular promise in redox flow batteries. This study aims to demonstrate the role of a basic solvent medium in the hydroquinone/benzoquinone (H2Q/Q) interconversion by taking advantage of Hydrogen-bonding between hydroquinone and the solvent medium buffer bases (phosphate, acetate, and citrate buffers) to influence the driving force of the overall proton-coupled electron transfer reaction. In this experiment, electrochemical measurements were performed using a potentiostat at room temperature. A surface bound $[Os(bpy)2((4,4'-PO3H2)2bpy)]^{3+}$ (bpy = bipyridine and 4,4'-(PO3H2)2 = 4,4'-phosphonato-2,2'-bipyridine) complex on a fluorine-doped tin oxide working electrode was used in a three electrode configuration to produce Cyclic Voltammograms (CVs). By varying the pH of the solvent medium from pH= 3.0 to pH= 5.0 a difference of approximately 122mV was observed. Furthermore, the rate constants were extracted and dramatically enhanced in the presence of a base. The results prove a pH dependence of the E^0 value for the Q/H2Q, 2 electron/2 proton couple; as well as implicates a Hydrogen bonding assisted catalysis.

Key Terms: Proton coupled electron transfer
Hydroquinone interconversion
Oxidation-reduction reactions

UG-EEB-224

Latching on to the Genetic Structure of the American Dog Tick (*Dermacentor variabilis*), a Disease-Vectoring Tick

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Advisor: Hans Klompenr (The Ohio State University)

The American Dog Tick (*Dermacentor variabilis*) is a vector for multiple diseases, including Rocky Mountain Spotted Fever, and poses risks to both humans and domestic animals. This species has a wide geographic distribution, mainly from the central United States to the Atlantic. Despite its large geographic range and risk to public health, there is little information about the tick population structure. Further studying and understanding vectors' genetic composition and population structure is useful in studying the diseases they transmit. A previous study evidenced some genetic variation between populations in Canada and parts of the U.S., finding ticks from central-eastern US more similar to Canadian samples than to specimens from the West Coast (Krakowetz, 2010). This study aimed to provide a preliminary analysis of the genetic variability across the American Dog Tick's geographic range and identify any genetic structure on the population level using next generation sequencing techniques (ddRADseq data). Preliminary results did not show evidence of significant population differentiation across large distances or geographic barriers, such as the Appalachian Mountains. Further, analyses varying the amount of 'missing data' included from the ddRAD sequencing gives evidence that useful genetic information is lost when all 'missing data' is excluded from analysis.

Key Terms: American Dog Tick
Population structure
ddRAD sequencing

HS-ENG-264

Matrix Assisted Pulsed Laser Evaporation of Antifungal Amphotericin B Coatings on Transdermal Drug Delivery Devices

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Advisor: Roger Narayan (North Carolina State University)

Matrix-assisted pulsed laser evaporation process is a physical vapor deposition process in which an excimer laser is used for ablation of a frozen target that contains a soft biomaterial (e.g., a pharmacologic agent) in a volatile solvent (e.g., dimethyl sulfoxide). The volatile solvent preferentially absorbs the laser energy and do not deposit on the substrate due to their low sticking coefficients. The pharmacologic agent molecules at the gas–matrix interface are ejected by the laser energy. The less volatile pharmacologic agent molecules deposit on a surface to form a coating. The matrix-assisted pulsed laser evaporation process allows the thickness of the coating that is deposited to be tightly controlled. Coatings made by Matrix-assisted pulsed laser evaporation show low roughness and high homogeneity. In addition, the pharmacologic agent is not heated during the matrix-assisted pulsed laser evaporation process. In this study, matrix-assisted pulsed laser evaporation was used to deposit the pharmacologic agent amphotericin B on the surfaces of polyglycolic acid microneedles. Amphotericin B is a commonly used pharmacological agent with activity against many types of fungi and protozoa, which is difficult to deliver to the body since it has poor solubility in aqueous solutions. The amphotericin B-loaded microneedles showed concentration-dependent activity against *Candida albicans* in a modified agar disk diffusion assay. Our results indicate that matrix-assisted pulsed laser evaporation was successful in depositing amphotericin B on microneedle surfaces; this approach may be useful for depositing pharmacologic agents with poor solubility in aqueous solutions on the surfaces of various medical devices.

Key Terms: Physical vapor deposition
Coating
Drug delivery

UG-ENG-271

Functional Utilization of Propulsive Capacity During Walking

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Advisor: Jason Franz (University of North Carolina at Chapel Hill)

The loss of independent mobility in older adults restricts community engagement; and compromises quality of life. A reduction in propulsive forces generated by the calf muscles during the push-off phase of walking decreases with old age and contributes to the loss of mobility. However, many older adults underutilize their capacity to generate these forces for reasons that remain unclear. We have developed a highly functional approach (i.e horizontal impeding forces) to quantify the utilization of propulsive capacity during walking toward opportunities to mitigate mobility impairment in old age. As an important first step, our purpose was to gain an improved joint-level understanding of the functional utilization of propulsive capacity during walking in young subjects, with a special emphasis on the propulsive plantarflexor muscles. First, we hypothesized that young adults retain a reserve propulsive capacity governed by the neuromechanical behavior of the ankle plantarflexor muscles. Second, we hypothesized that plantarflexor muscles reserve capacities during walking derived using our novel approach would be larger than those obtained using conventional strength testing. Our experimental data (n=12 young adults mean age: 24 years) fully supported both hypotheses. Moving forward, this project has incredible potential to improve the functional assessment of gait disability, and the tailored prescription of alternative therapies such as biofeedback.

Key Terms: Biomechanics
Aging
Walking

GR-ENG-287

Electromagnetic Scattering by 2-D Single Biological Cell Models

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The scattering of electromagnetic waves by dielectric particles is of interest in many applications ranging from remote sensing to radar meteorology, and biological sciences. The classification and detection of the biological cells have important applications in various fields, including life sciences, medical diagnosis, etc. Since biological structures are complex, it is generally difficult to study single scatterers. Still, for the red blood cell (RBC), also known as erythrocyte, a reasonable approximation can be made. RBC is important for tissue optics because it contains one of the strongest absorbers of visual light in the human body, hemoglobin. In addition, RBCs can easily be isolated and studied experimentally. Scattering patterns of a single cell provide essential information on the morphological properties of the cell. Although electromagnetic scattering problems involving a single cell have been investigated by employing various numerical solutions, such as Finite-Difference Time-Domain method, and Mie-series approximation; available solution methods mostly focused on the modeling of ordinary shapes, and less attention has been paid to deformed shapes of cells. In this paper, scattering cross section values for different cell shapes and orientations are obtained accurately and efficiently using Muller boundary integral equation method. The accuracy and smoothness of the solution are improved by applying Nystrom-type discretization. The numerical simulations show that the bistatic scattering pattern of the dumbbell-shaped cell is quite different from the values of the circular cell as compared with the elliptical cell. The amount of deviation can be used to detect the cell shape, orientation and phase of mitosis of the cell.

Key Terms: Bioengineering
Scattering
Computational modeling

UG-ENV-311

Quantifying Macrobioerosion within Two Coral Taxa and Across Three Reef Systems in the Western Caribbean Sea

Jared Richards (University of North Carolina at Chapel Hill)
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Macrobioerosion, the process by which organisms bore into coral reef substrate, weakens coral skeletons and degrades the quality of coral reef habitats. Prior studies show that macrobioerosion is enhanced by ocean acidification, nutrients, and other anthropogenic factors; however, little is known about the prevalence and distribution of this process across the wider Caribbean Sea. To address this shortcoming, we extracted 176 skeletal cores from two ubiquitous Caribbean reef-building corals (*Siderastrea siderea* and *Pseudodiploria strigosa*) in a hierarchical sampling design spanning inner (IR) and outer reef (OR) zones across three major reef systems: the Bocas del Toro Reef Complex (BTRC), the Belize Barrier Reef System (BBRS), and the Florida Keys Reef Tract (FKRT). We hypothesized that IR corals would be more severely impacted by macrobioerosion due to their proximity to human activity, and that species would differ in their susceptibility due to differences in skeletal architecture. The program CoralCT was used to determine the percent volume of *S. siderea* cores that has been bioeroded, and the number of bivalve borings on cores of both species was quantified. The macrobioerosion calculated by volume is greater in IR corals on the BTRC and the BBRS, suggesting that the factors differentiating IR and OR zones are less significant on the FKRT. Moreover, bivalve borings are more common in *S. siderea*, providing evidence for a host preference amongst bivalve bioeroders. Understanding these patterns of macrobioerosion provides a foundation for further investigation and may help us combat the impact of climate change on coral reefs.

Key Terms: Caribbean
Coral
Macrobioerosion

UG-ENV-312

The Impact of Bioinspired Prototypes on Pollution Management in an Aquatic Environment

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Advisors: Michael Wolyniak (Hampden-Sydney College), David Schmale (Virginia Polytechnic Institute and State University)

The pollution of natural waterways by manmade garbage is a global pandemic. This is especially true in rivers. Trash in rivers is a threat to all organisms in the immediate environment and environments beyond. The most common form of pollution found in waterways is plastic bottles. A majority of litter ends up in a river, as it either gets washed down the watershed through rainfall or ends up in a sewer that filters to a river. From there the trash not only pollutes the river, but the river also carries that trash to beaches, oceans, lakes, bays, etc. which in turn ruins multiple different ecosystems. Rivers are the primary source of transportation of litter and waste; therefore, the best way to limit aquatic pollution damage is to stop it at the source. This project tests new, innovated, 3D printed, bioinspired prototypes that will be used to collect common manmade waste found in rivers and other water ways. The prototypes are bioinspired, meaning that their design is drawn from already existing biological organisms. The three designs being tested are: a spider-web inspired design, a whale baleen inspired design, and a mangrove root inspired design. These products will undergo three trials in tanks with common minnow, 3D printed, scaled trash, and a current to simulate that of a river current. The prototypes will be observed and judged based on their effectiveness collecting the trash and their impact on the health of the minnows.

Key Terms: Environmental management
Bio-inspired prototypes
Environmental interactions

UG-ENV-313

Physiological Changes of Phytoplankton in a Simulated Upwelling Environment

Gustavo Hernandez (University of North Carolina at Chapel Hill)
Advisor: Adrian Marchetti (University of North Carolina at Chapel Hill)

Coastal upwelling regions are among the most biologically productive areas in the ocean. As nutrient rich water is frequently brought to the surface, large phytoplankton, usually diatoms, bloom. In these highly dynamic ecosystems, phytoplankton communities must respond and be resilient to regular changes in the availability of light and nutrients. Additionally, the micronutrient iron is anticipated to become more limiting as a result of climate change. Examining the physiological response of phytoplankton to upwelling throughout these light and nutrient scenarios will help to understand current and future primary production. Upwelling was simulated in the laboratory with the diatom, *Chaetoceros decipiens*, and a common haptophyte, *Emiliania huxleyi* while tracking cell abundance, chlorophyll, and photosynthetic efficiency under high and low iron conditions. In *Chaetoceros*, iron-limitation resulted in slower growth rates. The photosynthetic efficiency of the iron-replete samples was variable but remained consistently low throughout iron-limitation which was matched by chlorophyll content. For *E. huxleyi*, the cells retained a consistently low chlorophyll content but had variable photosynthetic efficiently similar to the high iron *Chaetoceros* samples. The response time upon return to light was faster for *Chaetoceros* compared to *E. huxleyi* and unaffected by iron limitation. We have provided preliminary insights into the physiology of these organisms during upwelling. Future work will include examining physiological changes in relation to nitrogen as well as examining changes in gene expression to understand how they respond on a molecular level.

UG-HBS-377

Temporal Trends in Maternal Phthalate Exposure and Associations with Preterm Birth

Cherrel Manley (University of North Carolina at Chapel Hill)
Advisor: Stephanie Engel (University of North Carolina at Chapel Hill)

Phthalates are man-made, plasticizer chemicals commonly used in consumer goods such as plastics, cosmetics, and cleaning products. As known endocrine disrupters, there is increasing evidence of correlation between preterm birth and phthalate exposure. Preterm birth is associated with substantial risks for neurodevelopmental disability and is the principal driver of infant mortality, particularly in minority communities. In this research, we described temporal changes and trends in levels of phthalate metabolites within the Norwegian Mother and Child Cohort. We examined predictors of phthalate metabolite concentrations measured in urine spot samples collected from a sample of pregnant Norwegian women enrolled between 2003 and 2007. Fluctuations in concentrations over time were compared to trends in the U.S. population over the same time period. We also considered associations between phthalate exposure and preterm births and compared them to results from similar studies in different populations. We hypothesized that increased regulation of phthalate classes would be associated with decreased concentrations of those phthalates in our population; that decreasing levels of banned phthalates would correlate with increasing levels of substitute phthalate concentrations; that fluctuations in exposure in Norwegian populations would be similar to those in the U.S. following regulatory change; and that elevated urinary concentrations of phthalate metabolites would correlate with higher odds of preterm births. Establishing an association between maternal phthalate exposure and subsequent preterm birth could inform policy changes and improve research to better understand and combat the causes of preterm birth.

Key Terms: Phthalate
Preterm birth
Temporal trends

UG-HBS-378

Writing Diabetes: An Interdisciplinary Collaboration Examining the Significance of Illness Essays

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Advisor: Jordynn Jack (University of North Carolina at Chapel Hill)

The Writing Diabetes Study was developed to explore connections between writing and health using a multi-disciplinary approach. Unlike most biomedical research, which tend to focus on the biological components of a disease rather than the impacts of the humanities, the Writing Diabetes Study seeks to combine quantitative and qualitative methods from across the disciplines by asking: How can crafting stories about their experience help patients with chronic illness? Participants underwent an initial baseline visit at the UNC Diabetes Care Center where they completed surveys and a blood glucose test, followed by a weekly workshop for three months. The curriculum emphasized writing techniques based on the five canons of rhetoric: invention, arrangement, style, memory, and delivery. After the workshop ended, participants completed a follow-up visit at the UNC Diabetes Care Center where they repeated a series of surveys and the blood glucose test. Ultimately, eleven participants completed the baseline/follow-up visits and at least half of the workshop sessions (i.e., four or more weeks). After the data collection phase, we began processing and analyzing our findings by examining correlations among the following factors: HbA1c (blood glucose levels), responses to diabetes surveys, trends in discourse, and the narrative, rhetorical and linguistic aspects of participants' writings. Preliminary results suggest that individuals recently diagnosed (<5 years) with type-2 diabetes may benefit significantly from a narrative-type intervention. The archive of participant writing offers a rich resource into the patient experience of diabetes that we will continue to study.

Key Terms: Medical humanities
Diabetes
Interdisciplinary

UG-HBS-379

The Impacts of Stress on Adolescent Working Memory Capacity

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Adolescence is a critical period in development when heightened cortical maturation occurs in the frontal and limbic circuitry of the brain. These regions of the brain provide the structural capabilities necessary for an individual to reach the capacity of higher order cognitive and emotional processing. This research study looks at the effects of stress in adolescent participants ages nine to sixteen. Through the use of EEG analysis, such as event related potentials, we are able to view performance before and after stress and identify the effect of stress on working memory. EEG measurements show changes in neuronal activation in various brain regions, which are measured using a series of electrodes and electrolyte gel. In conjunction with the use of working memory and stress tasks, we are able to measure the impacts of stress on working memory performance. We hypothesize that experiencing significant stress disrupts the function of frontal and limbic regions associated with stress regulation and working memory.

Key Terms: EEG
Stress
Working memory capacity

HS-MCS-396

Alzheimer's Disease Prediction In At-Risk Patients: Statistically Predicting Disease Onset

Saloni Shah (The Harker School)
Advisor: Mike Pistacchi (The Harker School)

The number of people worldwide living with Alzheimer's Disease (AD) is growing rapidly. In 2017, an estimated 5.5 million Americans have AD, an estimated 5.3 million are age 65 and older, and approximately 200,000 individuals are under age 65 and have younger-onset of Alzheimer's. We aim to identify which individuals within an age group at-risk of AD will start to show symptoms in the short to medium term. We hypothesize that progression of AD is predictable in at-risk individuals by utilizing historical measurements and statistically predictive models to forecast future measurements. We focused on individuals in the Alzheimer's Disease Neuroimaging Initiative (ADNI) study. ADNI individuals have provided data within earlier ADNI studies and have agreed to provide follow-up data. For each individual, we forecasted three attributes which are common or likely outcome measure for clinical trials – Cognitively Normal (CN), Mild Cognitive Impairment (MCI) or Probable Alzheimer's Disease (AD). We also predicted the ADAS-Cog 13 score, which is used as the primary outcome measure in clinical trials, as well as the ventricles volume. We utilized three data sets from ADNI which provide multimodal set of measurements from various kinds of imaging including MRI and PET and take CSF samples to measure protein levels providing useful biomarkers for AD. They also provide some genetic profiling information and a report of number of demographic and lifestyle factors important for AD. We concluded that it is possible to predict, with statistical significance, which individuals in the at-risk category would show symptoms of AD.

Key Terms: Alzheimer
Disease progression
Statistical prediction

UG-MCS-406

Controlling Protein Activity with Conformational Switches

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Controlling protein activity with external stimuli can be effective method to study its function inside the cell. Artificially designed regulatory domains are powerful tools for achieving this goal as they are easily insertable within protein structures and undergo conformational change upon being affected by external stimuli (such as light- and drug-sensitivity), which in turn also alters the dynamics of the host protein. Engineered allostery, which is the binding transmission that allows for control of activity within a cell, can further improve the design of protein switches as it allows for the insertion of switches in distant regions of the proteins, which are allosterically coupled to the active site and do not interfere with normal protein function. Here, we computationally design (in silico) a ligand-sensitive conformational switch for the chemotaxis-signaling protein CheY. We insert the ligand-sensitive UniRapR protein domain into a loop of CheY that is involved with allosteric communication between the active and allosteric sites of the protein. In order to determine the effectiveness of the switch, we use discrete molecular dynamics (DMD) simulations to compare the dynamics of the UniRapR-CheY complex, with and without the drug, to the native CheY dynamics. Results of this work, which include data and figures that interpret the efficacy of the switch, will be used in the future in regards to an in vitro design of the complex.

UG-MCS-407

Exploring a Flexible Computational Method for Comparing Massive Interaction Data from Science Visualizations

Sweta Karlekar (University of North Carolina at Chapel Hill), Emily Toutkoushian (University of North Carolina at Chapel Hill)
Advisor: Kelly Ryoo (University of North Carolina at Chapel Hill

Interactive visualization technologies, such as simulations, can automatically collect massive data on how students interact with tools while learning science. Grouping and comparing such data can identify students' interaction patterns which can be used to create more personalized learning environments. Existing methods for analyzing and comparing interaction data are often inflexible and hard to incorporate in newly developed visualizations. The purpose of this study is to explore the effects of a new computational method that uses numerical encoding and Levenshtein edit distance, developed to be simple and flexible for encoding and comparing student interaction data. The study involved linguistically diverse 8th-grade students from a low-income middle school. Students engaged in predict-observe-reflect activities using interactive simulations to explore chemistry concepts. All students' interactions with the simulations were automatically logged, including the order of various button clicks. Reflection questions were scored based on a rubric evaluating content, claim, and evidence provided by the student. Students were grouped based on reflection score and, upon processing the interaction data with the proposed method, statistically significant differences were found between mean edit distances of each score group. The results suggest that this new method shows promise for comparing interaction data as differences in learning patterns were found between the score groups

Key Terms: Human behavioral & social science
Math & Computer science

UG-MCS-408

NIM on a Network

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The game of NIM is a strategy game played by two players. Historically, it involves a specific number of objects being removed from distinct piles. In this project, I look at how the game would be played on a network made up of nodes and edges. The rules are as follows: given any finite graph, players take turns removing either an edge or a node with all attached edges; the last player to remove a node wins the game. The purpose of my project is to determine which player will win the game given only what the network looks like, and who goes first. Using a divide and conquer strategy along with information about the original game, I found a way to determine the winner for almost all networks. My results show that if the method used for winning smaller portions of the larger network is known, the winner of the total game can be found with four steps of algebra.

UG-MMB-445

Regulated Induction of Neuronal Injury Responses to Promote Axon Regeneration: Tunable Expression of the Dual Leucine-Zipper Kinase (OLK) Pathway

Ashleigh Rawls (Hampton University), Trent Watkins (Baylor College of Medicine)
Advisor: Trent Watkins (Baylor College of Medicine)

Injured axons of the central nervous system (CNS) fail to regenerate, resulting in irreversible damage. Conversely, peripheralaxon regenerationis enabled by intrinsic neuronal injury signaling controlled by the Dual Leucine-zipper Kinase (OLK). Stimulating this pro-regenerative OLK response may therefore be vital for successful CNS regeneration strategies. Yet OLK signaling is also pro-apoptotic; specifically, OLK is responsible for extensive neurodegeneration in glaucoma models. The factors that determine neuronal death are poorly understood but may relate to persistently high OLK activity within the inhibitory growth context of the CNS. We hypothesize that controlled, intermittent stimulation of OLK activation will support regenerative signaling with minimal neuronal loss. Our strategy to induce OLK activity in a regulated manner involves fusing an active portion of OLK to an engineered destabilizing domain derived from E.coli dihydrofolate reductase (OHFR). The antibiotic trimethoprim (TMP) stabilizes this construct and activates OLK. In preparation for studies in the mouse retina and optic nerve, my experiments aim to evaluate and optimize the properties of OLK-OHFR fusions in 293T cells in vitro. Pharmacodynamic assessments of TMP-regulated OLK include dose-response of protein stabilization, time course of activation and resolution, and dynamics of the downstream transcription factors ATF3, ATF4, and Jun, as well as correlation with apoptosis measured by activated Caspase-3. Preliminary results reveal that TMP in combination with DHFR is a viable tool for the tunable expression of OLK. These efforts will provide essential insights into the dynamic relationship between OLK signaling and neurodegeneration to enable its manipulation for CNS repair.

Key Terms: Neuroscience
Neurobiology
Protein regulation

UG-MMB-446

Creation of a Cell Line for the Study of SIV Viral Entry Phenotypes

Sam Raines (University of North Carolina at Chapel Hill)
Advisor: Ron Swanstrom (University of North Carolina at Chapel Hill)

This project is attempting to create a cell line for the determination of the entry phenotypes of various SIV lineages. For HIV research, currently phenotypic studies on viral entry are conducted on affinophile cells by varying co-receptor amounts/density and then examining viral entry rates. Though affinophile cells can be used with SIV, many complications arise and the assay is generally less reliable. For this reason, the project looks to create a cell line that more easily mimics the cells that SIV virions enter in vivo. Currently, I am in the process of cloning various envelope segments into plasmids from varying SIV samples. Upon the creation of a representative sample size from previously acquired SIV samples, these envelopes will be placed into a backbone. After growing up these viruses, and the creation of this cell line, a far more accurate and realistic method will exist for determining SIV viral entry phenotypes. This will greatly facilitate research attempting to learn about SIV and HIV.

Key Terms: SIV
Cell-Line-Development
Viral-Entry

HS-PSI-506

Analyzing Resulting Outcomes from XLIF Spinal Surgeries and Disproving Limitations of Retractor Time

Phillip Glascock (Phoenix Country Day School)
Advisor: Randall Porter (Phoenix Country Day School)

Since 2001, neurosurgeons and spinal surgeons have utilized the Extreme Lateral Interbody Fusion surgery, or XLIF, to treat their patients for a variety of spinal issues. This lateral approach to the lumbar and thoracic spine has become a very common method to obtain spinal fusion. The XLIF procedure has been typically used to help treat patients with lumbar degenerative disc disease, spondylolisthesis, scoliosis, lower back disc herniations, and certain types of lumbar stenosis. Many neurosurgeons and neurosurgical data analysts have noted several advantages to this surgical technique, such as reduced tissue dissection, minimally invasive incisions, reduced blood loss, shortened pain post-op, and, most importantly, reduced operative time. The general belief amongst various neurosurgeons is that the time during XLIF surgeries should not surpass 20 minutes in length. However, the research conducted at Barrow Neurological Institute under Neurosurgeon Dr. Randall Porter suggests otherwise. The hypothesis of this project is whether retractor time during XLIF surgeries makes a large difference in neurological outcomes and deficits post-op. After organizing patient information, the software program Centricity was used to access specific patient information, both pre-op and post-op, and organized the data into a large Excel spread sheet. The analytical categories included a variety of pertinent questions, the prominent ones being the retractor time, pre-op/post-op leg weakness, thigh numbness, and leg pain. This data and research is the first of its kind and will reveal several unknown factors surrounding the time limitations during XLIF surgeries and the overall techniques used in minimally invasive spinal surgeries.

Key Terms: Neurology
Surgical studies
Spinal procedures

HS-PSI-507

Inhibition of MDA-MB-231 and PC-3 to Bone Metastasis by the Extracellular Adherence Protein of *Staphylococcus aureus*

Trishala Kumar (American Heritage School)
Advisor: Leya Joykutty (American Heritage School)

The purpose of this project was twofold. First, to look at the effect of Staphylococcus Protein A, the Extracellular Adherence Protein of the bacteria, on bone metastatic processes of MDA-MB-231, breast cancer, and PC-3 prostate cancer cells. Second to see if there was a difference in the effect of the protein on the two cell types. Specifically, migration, invasion and adhesion of the cells to OPN, a component of the extracellular matrix of the bone, were looked at. To look at the effect of the protein on migration invasion and adhesion of PC-3 and MDA-MB-231 cells, a Boyden Chamber Assay was performed. In both the migration and invasion assay, 80,000 cells were seeded in the upper well of the Transwell insert and migration to the lower well, which contained OPN was quantified. In the migration assay, only migration was observed, while in the invasion assay, the ability of the cells to migrate through the Matrigel layer (on the insert) towards OPN was observed. In both, total migrating/invading cells and the number of cells adhering to the membrane were looked at. It was found that overall S. aureus Protein A had an effect on the metastasis of both MDA-MB-231 and PC-3 cells to bone especially at the highest concentration (20 µg/ml). While there were not differences in the reactions of the MDA-M-231 and PC-3 cells at all concentrations, it was found that the protein was generally more effective in MDA-MB-231 cells, and the difference in the inhibition of bone metastatic processes between the two cells was more apparent at lower concentrations.

UG-PSI-519

Fusionetics Mobile Device Application: A Clinical Device for Detecting Biomechanical Errors that May Increase Risk of Lower Extremity Injury

Lauren Gullett (University of North Carolina at Chapel Hill)
Advisors: Darin Padua (University of North Carolina at Chapel Hill), Barnett Frank (University of North Carolina at Chapel Hill)

Context: Noncontact mechanisms account for a majority of lower extremity joint and soft tissue injuries. Currently, there is not a clinically efficient method to objectively evaluate biomechanics. The Fusionetics mobile device application (FSSapp) was created to close this gap between accurate and accessible risk assessments. Objective: Determine the reliability of the FSSapp to accurately identify clinical movement patterns associated with muscle imbalance and injury. Participants: 39 healthy (N=39) college students (male = 13, female = 26; height= 168.3 ± 11.1 cm, weight = 68.1 ± 15.0 kg) volunteered to participate in this study. Methods: Participants were recorded performing overhead double-leg squats (DLS) and single-leg squats (SLS). Images were captured when the participants were at the bottom point of the squat tasks. Virtual markers were placed on body landmarks, which would allow the FSSapp to evaluate movement patterns. Movement patterns were identified by both the FSS app and by an expert rater; agreement was evaluated and analyzed using kappa, adjusted kappa, and ICC statistics.
Results: Most variables demonstrated slight to fair agreement (kappa values: $0.01 \leq \kappa \leq 0.40$). When adjusted for prevalence and bias (PABAK), some variables demonstrated fair to substantial agreement (kappa values: $0.21 \leq \kappa \leq 0.80$). Conclusion: The DLS and SLS exhibit slight to moderate inter-rater reliability. The findings suggest that the agreement between the app and by the expert could likely be due to chance. This indicates that future work should focus on tuning the FSSapp algorithm to improve agreement with expert raters prior to clinical deployment.

UG-PSI-520

Growing Up with Genetic Testing: Grouping Testing into Age-Based Panels

Falecia Metcalf (University of North Carolina at Chapel Hill)
Advisor: Jonathan Berg (University of North Carolina at Chapel Hill)

Introduction: Newborn screening (NBS) is important for the detection of rare and severe conditions sometimes before a child even presents with symptoms. Next-generation sequencing (NGS) techniques has the potential to greatly increase the number of diseases identified for presymptomatic intervention. However, overall genetic complexity and ethical issues dealing with returning results of whole exome sequencing must be carefully addressed. Thus, we have decided to group testing into age-based panels to allow the most relevant information to be relayed to parents.
Methods: Gene-condition pairs were curated and given overall scores based on severity and likelihood of symptoms, efficacy and acceptability of treatment, and the knowledge about the gene-condition association. These scores and age of onset were used to place the gene-disease pairs into four different panels. I took genes in the upper left quadrant that had variable age of onset and curated them for the earliest presentation in order to place them into an age-based panel. Results: 6 gene-disease pairs were placed into the 1st neonatal age-based panel, 2 placed into the 2nd neonatal panel, 1 placed into the 1st infant panel, 4 placed into the 2nd infant panel, and the remaining 4 require further investigation to determine which panel they should be placed in. Specifically, the average age of onset must be determined.
Discussion and Conclusion: The many nuances that accompany age-based panel placement make the task difficult. By segmenting information provided to parents, they are able to make decisions relevant to their child's age without being overwhelmed with information all at once.

Institutions Represented by Student Presenters in this Program Update

American Heritage School

Bilkent University

Hampden-Sydney College

Hampton University

Harvard Medical School

North Carolina Central University

Phoenix Country Day School

The Harker School

University of North Carolina at Chapel Hill

Wake Early College of Health and Sciences

Cancellations

Cinthia Garcia, UG-MMB-438

Tusneem Janoudi, UG-MMB-439

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