

UG-ASNR-007

A Non-destructive Method of Artificial Inoculating Mature Onion Bulbs for Selection Against Fusarium Basal Rot

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Advisor: Christopher Cramer (New Mexico State University)

Fusarium basal rot (FBR) of onion (*Allium cepa* L.), caused by *Fusarium oxysporum* f. sp. *cepae* (FOC), results in severe crop damage in all onion producing regions of the world. Using resistant cultivars is the best alternative to controlling this disease. FBR-resistant cultivars have yet to be developed and effective screening methods are needed. The primary objective of the present project was to compare the FBR development efficiencies of a non-destructive method of inoculum delivery with the current destructive method. Additionally, we wanted to compare different inoculum concentrations for their effect on FBR incidence and severity using each spore delivery method. In spring 2016, mature bulbs of 'Mayan Sweets' were inoculated with PDA containing suspended FOC spores of virulent isolate 'CSC-515'. Three spore concentrations of 3.0, 0.30 and 0.03 $\times 10^5$ spores mL^{-1} were used to inoculate bulbs with transversely-cut and intact basal plates. Bulbs with an undisturbed basal plate exhibited less disease incidence and severity than bulbs with cut basal plates. An increase in spore concentration also increased FBR incidence and severity for cut bulbs, but had no effect on uncut bulbs. Spore concentrations of 0.3 $\times 10^5$ or less may not produce enough disease regardless of the processing of the basal plate. Results will be presented from a second trial in which the same procedures were used on five autumn-sown, Grano type hybrid breeding lines from the NMSU program and a susceptible check.

Key Terms: *Allium cepa* L.
Fusarium basal rot
Inoculum delivery

GR-ASNR-013

Varying Tolerance of Mature Loblolly Pine (*Pinus taeda* L.) Families to Root Infecting Fungi

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Advisor: Lori Eckhardt (Auburn University)

Pine decline is an emerging problem in the southern United States. Root feeding bark beetles and their fungal associates *Leptographium terebrantis* (native) and *Grosmannia huntii* (non-native) are the biotic factors involved in decline. This study was conducted to understand the susceptibility of mature loblolly pine (*Pinus taeda* L.) families to these fungi and correlate results with the same pre-screened seedling families. Two mature families which were susceptible and two families which were tolerant in the previous seedling screening study were included. In the study, two primary lateral roots were excavated from each tree. Each of the roots was artificially inoculated with either *L. terebrantis* or *G. huntii* along with a control. Eight weeks following inoculation, host responses was recorded as the lesion and vascular occlusion. Both of the fungi caused lesions and occlusions upward and downward radiating from the point of initial inoculation. Families screened showed different levels of susceptibility to the fungal species tested, as indicated by their average lesion length. The pattern of susceptibility and tolerance in the large mature tree families and seedling families was similar. In summary, the same level of family difference exists in mature as well as in premature stages of loblolly pine families.

Key Terms: Pine decline
Loblolly pine
Inoculation

STUDENT POSTER ABSTRACTS

GR-ASNR-014

Effect of Growth Rate on *Amylostereum* spp. Fungus by Terpenes

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Advisor: Lori Eckhardt (Auburn University)

Sirex noctilio is a species of woodwasp native to Europe that has been identified as invasive in Australia, South Africa, and the Northeastern United States, but has not yet been identified in the southeast. This pest has caused significant economic and ecological damage, and in some cases mortality of previously healthy trees. Females cause damage to *Pinus* spp. by drilling into the xylem to oviposit eggs, venom, and a mutualistic fungus, causing trees to begin to die within days of inoculation. Certain chemicals emitted by stressed pines have been observed to serve as chemical attractants to the wasps. As a means of exploring pine resistance to *Sirex* associated fungi, the effect of these mentioned host plant secondary metabolites on the growth of these fungi were tested. Eighteen isolates of *Amylostereum* spp. collected worldwide were grown in saturated atmospheres or in direct contact with pure monoterpenes for 7 days. Fungal growth in the saturated atmosphere was measured on day 7 while the tactile experiment was measured at 3, 5, and 7 days. These experiments showed that certain metabolites such as 4AA, α -Phellandrene, (+) Camphene, and (-) Limonene were shown to significantly reduce growth of isolates compared to control treatments. Conversely, α -Pinene and β -Pinene treatments tended to increase growth rates of the fungal isolates. A difference in growth rates between isolates from the northern hemisphere and southern hemisphere was also observed. The treatments (+) α -Pinene and β -Myrcene resulted in the highest percentage of fungal growth for all isolates tested when comparing fungal growth as a percent area relative to the controls.

Key Terms: Forestry
 Mycology
 Entomology

GR-ASNR-015

Bermudagrass Stem Maggot: Devastating New Pest in Southern Hay Production

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Advisors: William Hudson (University of Georgia), William Anderson (USDA)

Bermudagrass stem maggot (BSM) or *Atherigona reversura* is a new invasive species that has invaded the Southeastern United States and is crippling the hay production. This species of *Atherigona* is native to Japan, Indonesia, India, and Hawaii. Bermudagrass stem maggot was first noticed in Georgia in 2010. The damage from this insect occurs at the last node of the stem where the leaf emerges. The larva or maggot burrows into the shoot and feeds, and the leaves above the feeding area die. This feeding usually occurs on the top node. The discoloration of the upper leaves causes the field to look like there has been a light frost. If left uncontrolled, up to 80 percent of the tillers in the field can be affected, resulting in significant yield reduction. As of right now, there are very few options for controlling this pest other than the foliar application of pesticides, mainly pyrethroids. Greenhouse studies indicated that fine stem cultivars are more susceptible to BSM. A field study compared spray controlled plots to unsprayed plots in Tifton in 2015 and 2016. For clippings in mid to late summer, BSM reduced yield of Alicia and Russell over 60%. Tifton 85 and Coastcross II also had some yield reduction but not as severe.

Key Terms: Entomology
 Agricultural
 Invasive species

STUDENT POSTER ABSTRACTS

HS-BSS-026

Effect of Measurement Burden on Patient Participation: A Case Study

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Advisor: Peter Kaufmann (NHLBI/NIH)

In a large clinical study, patients often have to fill out numerous medical forms and surveys at each visit. In this presentation, we investigate how such measurement burden affects patient participation and responses to self-reported outcomes. Using real clinical trial data, we demonstrate that measurement burden has a significant negative impact on participation, and there is an interaction between disease severity and measurement burden. Using statistical models, we identify factors that also contribute to patient participation. Our study indicates that the measurement burden may influence the dropout rate so it should be considered at the design stage, especially when the clinical trial involves gravely ill patients.

Key Terms: Measurement burden
 Patient participation
 Clinical trial

UG-BSS-032

An Experimental Approach to Evaluating Bone Tools from the Early Hominin Site of Swartkrans, South Africa

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Advisor: Frank Williams (Georgia State University)

Swartkrans, a lower Paleolithic South African cave has yielded the remains of *Australopithecus robustus* and rudimentary bone tools. Previous functional assessments of these bone tools include extraction of underground storage organs (USOs) of plants and the exploitation of termite mounds. To address artifact function, three sets of experimental bone tools were utilized to extract (1) USOs, (2) termites and (3) both resources each for a total of 120 minutes, and casts of the tools were observed. Stereomicroscopy and maneuverable light sources were employed to classify scratches as either superficial or destructive, and digital measurements recorded their angles relative to the midline of the tool, calculated using a reference grid to bisect and align the microscope lens and tools. Observation of striations were taken at the midline and approximately five millimeters towards the right and left margins. A Kruskal-Wallis Analysis of Variance yielded non-significant differences ($p = 0.378$) between striation angles at the midline and the two margins. However, a Kruskal-Wallis test shows that significantly higher angles ($p = 0.001$) characterize bone tool casts used to exploit USOs and both resources, with lower angles for termite tools. A Kolmogorov-Smirnov Test revealed no difference in angle for destructive or superficial striations. However, destructive scratches at higher angles were absent from bone tools used for termites. These results indicate greater angulation oblique to the main axis of the tool was needed to exploit USOs. Therefore, bone tools from Swartkrans may have been utilized to exploit USOs or both resources, but not termites alone.

Key Terms: Anthropology
 Experimental archaeology
 Paleoanthropology

UG-BSS-033

The Development of Standard Operating Procedure for Patient and Public Involvement to Improve Safe Injection Process

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Approximately 16 billion injections are given each year in developing countries; sometimes injections that are intended to promote health act in the opposite way. This issue occurs when injections are given in an unsafe way. Therefore, the World Health Organization (WHO) is launching a new policy on safe injection to assist countries tackle the pervasive issue of unsafe injections. The nobility of this scientific study was finding strategies to improve safe injection. To efficiently target patient's safety, Chen's theory-driven evaluation as a framework was employed. We carried out a systemic search by using different electronic databases including: Medline, Embase, Cochrane, Google Scholar, Elsevier, and Web of Science. The entire publication until 2015 in Iran and internationally were reviewed. The search was in the areas of patient and public involvement in Safe Injection. Primary structural and process determinants of SOP were developed by using material obtained from literature review and experts analysis; furthermore, a questionnaire was designed. The structural components and related process were placed in the framework of our Chen's theory-driven evaluation model. Indeed, a standard operating procedure was defined for safe injection in three steps: the first step was program infrastructure, the second step was process dimension, and the third step was different indicators for evaluation of the structure and safe injection programs. It is clear that this guidance could be used for patient and public involvement in Safe Injection and making deliberate efforts to engage those who are at high risk of unsafe injection.

Key Terms: World Health Organization
Patients and public involvement
Safe injection

HS-CBB-051

Potential Role of BTK-52 in Aggressive Breast Cancer

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Advisor: Douglas Conklin (University at Albany)

Breast cancer is the most common form of cancer in women worldwide, and new ways to fight the disease are needed. Tyrosine kinases are enzymes that normally transduce signals that promote cell proliferation and survival. Bruton's Tyrosine Kinase (BTK) and an altered form of Abelson Tyrosine Kinase (BCR-ABL1) enzymes have been identified in aggressive breast cancer. In another cancer, pre-B cell leukemia, BCR-ABL1 has been shown to promote leukemia by inducing the expression of BTK-52, a splice variant of BTK. The proteins BCR-ABL1, BTK-52 and BTK form a cell-signaling complex which promotes resistance to apoptosis. This research investigates if BTK-52 expression is present in breast cancer, suggesting that a similar BCR-ABL1, BTK-52 and BTK cell-signaling complex may be formed. This is important because anti-BCR-ABL1 drugs exist and anti-BTK drugs are being developed to treat leukemia. Perhaps they could treat breast cancer too. The objective of this work is to determine if BTK-52 plays a similar role in breast cancer as in pre-B cell leukemia. This poster presents work to identify the presence or absence of BTK-52 expression in breast cancer cell lines. Results from computer assisted analysis to determine the amino acid sequence BTK and BTK-52 expressed proteins and to design polymerase chain reaction (PCR) primers for BTK and BTK-52 complimentary DNA (cDNA) are shown. Results of experiments to analyze pre-B cell leukemia cells (as a positive control) and breast cancer cells for the presence of BTK and BTK-52 through PCR of cDNA are also shown.

Key Terms: Cancer
Cell biology
Molecular biology

HS-CBB-052

Extracellular Vesicle-Mediated Phenotype Switching in Malignant and Non-malignant Colon Cells

Elise Mochizuki (Jericho High School), Devasis Chatterjee (Warren Alpert Medical School of Brown University), Peter Quesenberry (Warren Alpert Medical School of Brown University)

Extracellular vesicles (EV) play a role in tumorigenesis, and are composed of microvesicles (MV) and exosomes secreted by a variety of cell types. Higher levels of EVs in advanced stages of cancer not only transport proteins and nucleic acids, but may also facilitate the horizontal transfer of information in tumorigenesis by the activation of signaling pathways and the transfer of cellular phenotype. This study examined if EVs derived from malignant human patient tissue or cancer line would affect the phenotype of recipient cells. Human colon tissue samples, human adenocarcinoma HCT116, and normal colon fibroblast 1459 cells were cultured. Soft agar colony formation assay, mass spectrometry, NK- κ B luciferase reporter assay, and small interfering ribonucleic acid (siRNA) against the 14-3-3 zeta/delta protein were performed on co-cultures of cells and isolated EVs. Malignancy was measured by increased anchorage independent growth, increased transcription of NK- κ B, and expression of 14-3-3 zeta/delta. EV derived from normal patient tissue as well as from non-malignant cell lines reversed the malignant phenotype of HCT116 cells. An inhibitor of NK- κ B showed decreased transcription of NK- κ B, and the knock down of 14-3-3 zeta/delta showed decreased anchorage independent growth of HCT116 cells as well as 1459 cells co-cultured with HCT116 derived EVs. Because a malignant phenotype was induced as well as reversed, these results suggest EV-mediated phenotype switching in both malignant and non-malignant colon cells. 14-3-3 zeta/delta may be a potential target in the treatment of colorectal cancer, where the upregulation of this protein in malignant cells might be prevented.

Key Terms: Hematology/oncology
Colorectal cancer
Extracellular vesicles

HS-CBB-053

Targeting Alzheimer's Disease Neuro-Metabolic Dysfunction with a Small Molecule Nuclear Receptor Agonist (T3D-959) Reverses Disease Pathologies

Elise Mochizuki (Jericho High School), Suzanne de la Monte (Warren Alpert Medical School of Brown University)

Glucose is the sole energy source for the brain. Brain insulin resistance contributes to cognitive impairment and Alzheimer's Disease (AD). Because of the abundant expression of insulin receptors, the cerebellum is a major target of brain insulin resistance and of neurodegeneration in AD. Peroxisome proliferator-activated receptors (PPARs) are nuclear hormone receptors which function as transcription factors and regulate gene expression. PPAR- β/δ is more highly expressed in the brain, while PPAR- γ is more highly expressed in the rest of the body. Agonists of both treat the intracerebral (i.c.) streptozotocin (STZ) animal model of brain diabetes which mimics many aspects of sporadic AD. A former diabetes drug candidate now being repositioned as an AD-modifying therapy, T3D-959 is a dual nuclear receptor agonist with PPAR- δ as the primary target and PPAR- γ as the secondary target. Our null hypothesis was that T3D-959 would not effect motor function or reverse cerebellar neurodegeneration in the STZ animal model of sporadic AD. Long Evan rats were dosed orally with saline or T3D-959 from 1 day or 7 days after the i.c. STZ treatment, for a total of 21 or 28 days. Rotarod tests assessed motor function and long term effects of STZ. Histological and image analysis studies assessed cerebellar atrophy. Both rotarod data and cerebellar histopathology showed a greater reversal of neurodegeneration with T3D-959 treatment starting 7 days after i.c. STZ. Because therapeutic effects occurred even after a delay in treatment, these results suggest that individuals diagnosed late with mild or moderate AD would benefit from T3D-959.

Key Terms: Neurosurgery
Alzheimer
PPAR agonist

STUDENT POSTER ABSTRACTS

HS-CBB-054

Contagious Cancer: Horizontal Transmission of Clonal Cancer Cells Causes Leukemia in Soft-Shell Clams

Elise Mochizuki (Jericho High School), Stephen Goff (Columbia University Medical Center)

Disseminated, or hemic, neoplasia is a leukemia-like cancer causing significant loss in the marine bivalve population, and the origin of the cancer cells was unknown. The retrotransposon *Steamer* is amplified in neoplastic cells of soft-shell clams (*Mya arenaria*). Hemocytes present in the hemolymph of *Mya arenaria* collected from four different locations in New York, Maine, and Canada were examined by phase-contrast microscopy, and DNA extracted from the hemocytes was examined. Inverse PCR identified integration sites of the new *Steamer* elements in the neoplastic cells, and integration site-specific PCR scored for the presence of particular integrations. Both mitochondrial and nuclear DNAs were examined by sequence analysis to provide genotyping of the tumor and host. Twelve new 12 *Steamer* integration sites were identified that were not present in healthy animals, where 7 of the sites were found in neoplastic cells from all geographic locations. Four sites were found in New York and Maine neoplasms, but not in Canada neoplasms. A particular single nucleotide polymorphism (SNP), C785T, was found in the neoplastic hemocyte DNA of all leukemic animals, and G649A was found in all of the leukemic animals from Canada although in none from New York and Maine. The genotypes based on microsatellite DNA lengths in the neoplastic hemocytes were distinct from those in the host tissue, and additionally were the same in all leukemic animals. The results suggest that a clonal transmissible cell derived from a single original clam was likely to be responsible for the cancer spreading between these marine animals.

Key Terms: Contagious cancer
Steamer
Mya arenaria

HS-CBB-055

Stabilization of Morphine Tolerance with Long-Term Dosing: Association with Selective Upregulation of Mu-opioid Receptor Splice Variant mRNAs

Elise Mochizuki (Jericho High School), Gavril Pasternak (Memorial Sloan-Kettering Cancer Center/Weill Medical School of Cornell University)

There has been a disconnect between preclinical observations of dose-dependent morphine tolerance which increases over time, and clinical observations that patients could be maintained on fixed opioid doses for extended periods of time without dose escalation, implying no further development of tolerance. Many prior studies didn't examine the mRNA or protein levels of multiple clones of the mu-opioid receptor (MOR) for an extended duration of treatment. The objective of this study was to see if tolerance would increase in the short term and then reach a steady state, reconciling the preclinical and clinical literature. The median effective dose (ED50) values were measured over 6 weeks in mice subcutaneously injected with different doses of morphine. mRNA levels of MOR splice variants were determined by qPCR assays in three independent determinations on pooled (n=3-4) prefrontal cortex, striatum, thalamus, hypothalamus, hippocampus, periaqueductal gray, brainstem, cerebellum, spinal cord samples, and whole brain samples. After continued administration of various fixed morphine doses well beyond the one week dosing typically used in preclinical studies, selective upregulation causing increases in variant mRNA levels of up to 300-fold were seen in the striatum, hypothalamus, and hippocampus. Consistent with such short term animal studies, a linear increase in tolerance as measured by ED50 was seen over the first 3 weeks of dosing. Long term morphine administration up to 6 weeks demonstrated a stabilization of the degree of tolerance, where the ED50 values remained constant or leveled off. This is consistent and reconciles with clinical experience.

Key Terms: Analgesia
MOR-1
Splice variant

HS-CBB-056

Interferon γ -induced Intratumoral Expression of CXCL9 Alters the Local Distribution of T Cells Following Immunotherapy with *Listeria monocytogenes*

Elise Mochizuki (Jericho High School), Yvonne Pater-son (Perelman School of Medicine at the University of Pennsylvania)

Listeria monocytogenes-based vaccines induce the secretion of cytokines and the production of interferon γ (IFN γ) as well as induce the expansion of antigen-specific CD4⁺ and CD8⁺ T cells. The null hypothesis was that vaccination with immunotherapeutic *L. monocytogenes* (Lm-LLO-E7) would not induce the IFN γ -dependent production of chemokines which regulate migration and optimal infiltration of tumors by CD8⁺ T cells. Chemokine (C-X-C motif) ligand 9 (CXCL9) expressing or controlling knock down type 16 human papillomavirus (HPV-16)-immortalized murine tumor (TC-1) cells were implanted in the flanks of female C57BL/6 mice, and tumor plugs allowed to form. The mice were sacrificed after one or two immunizations of live Lm-LLO-E7, and qPCR chemokine arrays, individual primer assays, enzyme-linked immunosorbent assays (ELISAs), and/or flow cytometry were performed. Lm-LLO-E7 upregulated the cytokine-dependent production of TH1-associated chemokines by malignant cells, esp. CXCL9. CXCL9 was the only chemokine whose mRNA and protein production by malignant cells were changed by vaccination after treatment with either anti-IFN γ antibodies or control IgG. IFN γ upregulated TC-1 derived chemokines, esp. CXCL9, by 100-fold, plus another 10-fold with the addition of tumor necrosis factor α (TNF α). Upon vaccination, many E7-specific CD8⁺ T cells expressed chemokine (C-X-C motif) receptor 3 (CXCR3) were found infiltrating the TC-1 tumor, with an increase in *L. monocytogenes* antigen-specific CD4⁺ T cells, whereas the knock down of CXCL9 decreased CD8⁺ T cells and increased CD4⁺ T cells. These results suggest that TC-1 derived, IFN γ -driven CXCL9 is crucial for optimal infiltration of CD8⁺ T cells into tumors of *L. monocytogenes*-vaccinated mice.

Key Terms: Immunotherapy
Cancer vaccine

Listeria monocytogenes

UG-CBB-094

The Journey to Cataracts: A Study of UVB-Induced DNA Damage in Cultured Human Lens Epithelial Cells

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Advisors: Frank Giblin (Oakland University), Vidhi Mishra (Oakland University)

Age related cataracts are the second leading cause of blindness in the United States. Cortical cataract (an opacification in the lens periphery) is a major type of this disease; however, little is known about its mechanism of formation. One cause is known to be solar UVB radiation, possibly through UVB-induced damage to DNA present in the lens epithelium. Here, we investigated DNA damage and repair in cultured human lens epithelial cells (LECs) exposed to two different intensities of UVB light, 0.9mW/cm² and 0.09mW/cm². Following UVB exposure, cells were incubated for various times, and analyzed for DNA strand breaks (TMR Roche Red), reactive oxygen species (CellROX), cell viability (MTT), and fluorescence immunocytochemistry, with the latter assay employing antibodies for the DNA repair enzyme poly(ADP)-ribose polymerase 1 (PARP-1) and poly(ADP)-ribose (PAR) polymers. The results indicated a biphasic mechanism for the higher dose of UVB in which a first phase of DNA strand breaks were repaired immediately after exposure, and then followed by a second phase of strand breaks at 90 min, which were repaired again. For the lower dose of UVB there was only an initial occurrence of DNA strand breaks and repair. Furthermore, it was observed that 90 min after the high UVB dose, PAR polymers migrated from the cell nucleus to the cytoplasm, possibly to induce cell death. The results indicate that PARP-1, along with PAR polymers, assist in the repair of UVB-induced damage to DNA in the human lens epithelium, and may also induce cell death.

Key Terms: Cataracts
UVB light
Human lens epithelial cells

UG-CBB-095

The Effect of Light on Dopamine Synthesis in the Retina

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Dopamine is an important neurotransmitter responsible for a variety of functions in the central nervous system. This chemical messenger is involved in light adaptation of the visual system. Light adaptation is essential to visual acuity in a world where the eyes must instantly adapt to changing light conditions. However, the effect of different light conditions on dopamine synthesis levels in the retina remains unclear. The retina contains three classes of photosensitive cells: rods function mostly under dim light conditions, while cones and melanopsin ganglion cells function under bright light conditions. The objective of this study is to determine how each photoreceptor class contributes to dopamine synthesis levels. To achieve this objective, a western blot protein quantification assay was used to determine relative dopamine synthesis levels in retinas from mice. Single photoreceptor function-only mice were used to represent each photoreceptor's response to various light conditions. We found that rod-function-only mice had the highest TH expression under dim light when compared to bright light and dark conditions. Cone-function-only mice had higher TH expression under bright light versus dark conditions. Melanopsin-function-only mice also exhibited higher TH expression under bright light versus dark conditions. The results suggest that dim light conditions lead to increased dopamine synthesis levels via rods and bright light conditions potentially increase dopamine synthesis levels via cones and melanopsin ganglion cells.

Key Terms: Light adaptation
Dopaminergic neurons
Protein quantification

UG-CBB-096

The Effects of NanI Sialidase Production on Host Cell Attachment and Toxin Expression in *Clostridium perfringens* Type C

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Advisors: Bruce McClane (University of Pittsburgh), Jihong Li (University of Pittsburgh)

Clostridium perfringens is an anaerobic pathogenic bacterium that causes lethal enteric diseases in both humans and livestock. The development of therapies to treat infections by this pathogen has been difficult because of its ability to produce a large arsenal of soluble toxins. Previous research has demonstrated that NanI sialidase, a neuraminidase secreted by the bacterium, contributes to host cell attachment and enhances the cytotoxic activity of several clostridial toxins. However, the relationship between NanI function and expression of toxins specific to human pathogenic strains of this species has not been described. The purpose of this project was to characterize the effects of NanI sialidase on host cell adherence and expression of beta toxin in *C. perfringens* Type C, a human-infecting toxinotype, as part of a pilot study investigating the potential use of sialidase inhibitors as effective treatments for clostridial infections. To accomplish this, we constructed isogenic *nanI* null mutant and mutant complement cultures of Type C strain CN3685 and then assayed each strain for beta toxin expression and adherence to Caco-2 intestinal cell culture. The *nanI* null mutant strain showed significantly less host cell adherence than the wild-type and mutant complement strains. However, no significant difference in beta toxin expression was observed between the three isogenic strains. We conclude that NanI is a major contributor to adherence of *C. perfringens* to the human intestinal epithelium, thereby increasing localized concentrations of secreted toxins at the surfaces of host cells. Our findings demonstrate the clinical significance of NanI sialidase and support testing whether sialidase inhibition reduces host cell cytotoxicity caused by this pathogen.

Key Terms: Microbiology
Cell biology
Genetics

UG-CBB-097**Investigating the Mechanism Underlying the Inhibitory Role of Dietary Flavonoids in Human Cancers**

Vaithish Velazhahan (Kansas State University)
Advisor: Kathrin Schrick (Kansas State University)

Flavonoids are plant-derived secondary metabolites that have been shown to have anticancer properties. However, the molecular mechanism underlying flavonoid action is currently unknown. A key area of research in our laboratory is investigating the regulation of gene expression in development using *Arabidopsis* as a model system. Several regulatory proteins have recently been shown to be stabilized by natural compounds of the flavonoid biosynthesis pathway. This finding, combined with a recent study that shows that the dietary flavonoid fisetin induces apoptosis in human cancers by inhibiting the transcription factor Heat Shock Factor 1 (HSF1), led to the hypothesis that fisetin stabilizes HSF1 by direct interaction. Since trimerization of the HSF1 transcription factor under heat shock is critical for its activation and DNA binding, stabilizing the monomeric form of HSF1 fisetin could interfere with heat-induced activation. Human HSF1 along with transcription factors from *Arabidopsis* and charophycean green algae *Spirogyra* have been chosen as candidates to investigate potential interactions with flavonoids and evolutionary conservation of these interactions. Thermal shift assays and additional biophysical assays, such as surface plasmon resonance, are being conducted to assay flavonoid binding. Since fisetin has chemotherapeutic potential, promising novel drugs that more efficiently stabilize HSF1 could be developed as innovative therapies to combat cancer progression.

Key Terms: Genetics
 Molecular biology
 Medicine

UG-CBB-098**Distinctive Effects of Resveratrol on Hepatocytes and Effector T Lymphocytes as a Likely Mechanism of its Action in Immune-Mediated Liver Inflammation**

Amy Harrington (University of South Carolina)
Advisor: Venkatesh Hegde (University of South Carolina)

Resveratrol (RES) is a natural polyphenolic compound derived from red grapes, known for its anti-aging and anti-inflammatory properties. Hepatocytes comprise the parenchyma of the liver, and carry out normal liver function. Activated T cells are the effector cells, which secrete cytokines resulting in liver inflammation during immune-mediated liver diseases such as autoimmune hepatitis (AIH). AIH affects up to 200,000 people in the US every year. Based on previous studies, treatment of RES can decrease liver inflammation in a rodent model of AIH, and cause apoptosis of activated T cells. This study explores the effects of RES on activated T cells and hepatocytes side-by-side. Normal BNL CL.2 murine hepatocytes, and primary lymph node-derived T lymphocytes from mice were activated polyclonally with Concanavalin A in replicates. Cells were treated with multiple doses of RES (0, 10, 40 micro Molar) for ~16 hours in culture medium and analyzed by light microscopy. Trypan blue dye exclusion method was applied to count viable cells. Activated T lymphocytes showed proliferation with medium where no RES treatment was present, while those treated with increasing doses of Resveratrol exhibited significant sensitivity to RES. With increasing doses of RES, T cell proliferation was markedly decreased. Comparatively, the treated hepatocytes showed normal and similar appearance with all doses of RES, and maintained a relatively consistent cell count with no significant decrease in viable cells with RES. These findings suggest that RES acts distinctively on activated T cells versus hepatocytes. It is likely that while RES induces apoptosis in effector T lymphocytes, the compound at similar doses is safe for hepatocytes. These experiments address the effect of RES on immune-mediated liver inflammation and begin to provide a preliminary understanding of distinctive mechanisms in hepatocytes versus effector leukocytes.

Key Terms: Immunology
 Dietary supplement
 Liver inflammation

STUDENT POSTER ABSTRACTS

UG-CBB-099

Identification of the Genetic Regulators of Plasminogen Activator Inhibitor-1

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Advisor: Randal Westrick (Oakland University)

Cardiovascular disease is the leading cause of morbidity and mortality throughout the world. The formation of intravascular blood clots (thrombi) composed primarily of platelets and fibrin, coupled with a decrease in clot breakdown (fibrinolysis) is a final event in cardiovascular disease progression. Plasminogen activator inhibitor-1 (PAI-1, gene name: *Serpine1*) is an essential fibrinolysis inhibitor produced primarily by platelets. PAI-1 is consistently elevated in plasma from cardiovascular disease patients, but mechanisms driving this increase are unknown. In order to elucidate genetic regulators of *Serpine1* expression, we surveyed 12 mouse strains for platelet PAI-1 antigen. We found that while the C57BL/6J inbred strain had 0.2 ± 0.2 pg/ μ g total protein, the LEWES/EiJ strain had a striking increase in platelet PAI-1 antigen with 1.8 ± 0.8 pg/ μ g total protein ($q = 0.004$). LEWES/EiJ x C57BL/6J crossbreeding experiments produced F1 mice with average platelet PAI-1 levels of 0.8 ± 0.1 pg/ μ g total protein ($q = 0.01$), suggesting a semi-dominant *Serpine1* regulatory effect. We used crosses of the LEWES/EiJ and C57BL/6J strains to generate 24 F2 progeny and through QTL analysis identified a major locus for the regulation of platelet PAI-1 levels that spans a 14.4 megabase interval (128.2-142.6 megabases) on chromosome 5 (LOD score= 4.81). Additional studies are underway on 144 F2 progeny to narrow this region. These proposed investigations of PAI-1 regulation will provide insights into platelet specific gene expression as well as identification of novel therapeutic targets for modulating thrombosis and fibrinolysis.

Key Terms: Genetics
Gene expression
Cardiovascular disease

UG-CBB-100

Extreme Local Recombination Frequency in Compound Heterozygous *Actr2* Mutant Mice

Lena Mishack (Oakland University), Amy Siebert (Oakland University)

Advisor: Randal Westrick (Oakland University)

Venous thromboembolism (VTE) is a major health problem worldwide. Recently, we identified a novel, dominant VTE suppressor mutation in the *Actr2* gene using a lethal VTE mouse model. This missense mutation (*Actr2*^{+/G}) occurs within a highly conserved region of the gene. However, *Actr2*^{+/G} is unlikely a loss of function mutation as a gene-targeted *Actr2* knockout allele (*Actr2*^{+/-}) was unable to suppress lethal VTE. To identify the phenotypic consequences associated with the *Actr2*^G mutation, we performed *Actr2*^{+/G} x *Actr2*^{+/G} crosses to produce *Actr2*^{G/G} mice and also *Actr2*^{+/G} x *Actr2*^{+/-} to produce *Actr2*^{G/-} mice. We found significant departures from expected Mendelian frequencies for the *Actr2*^{G/G} progeny ($p=0.005$). *Actr2*^{G/G} mice that did survive were infertile, developed progressive curvature of the spine, and died of wasting by approximately six months of age. Surprisingly, frequencies of *Actr2*^{G/-} mice were normally distributed and were phenotypically indistinguishable from *Actr2*^{+/G} mice. To investigate this observed phenotypic disparity, further intercrossing and backcrossing of *Actr2*^{G/-} mice was performed. Out of 109 progeny, we observed an astonishing 32 recombination events (29.3%) within a 14.2 kb interval of the *Actr2* gene. As the reported recombination activity at this defined locus should be only 0.02%, our findings suggest generation of a novel, promiscuous recombination site as a result of the *Actr2* knockout gene-targeting event. These results provide a cautionary tale of the unintended consequences of gene knockout technology and how genomes edited with this system may be inadvertently affected.

Key Terms: Genetics
Recombination
Gene-targeting technology

STUDENT POSTER ABSTRACTS

UG-CBB-101

Acidithiobacillus ferrooxidans Differentially Regulates Three Pilus Regions in Response to Growth Phase

Tyler Nardone (Oakland University), Adrienne Williams (Oakland University), James Iordanou (Oakland University)

Advisor: Sara Blumer-Schuette (Oakland University)

Acidithiobacillus ferrooxidans is an acidophilic chemolithoautotrophic bacterium that oxidizes ferrous iron. While acidic environments are typically inhospitable for most microbes, these environments slow the spontaneous oxidation of soluble ferrous to ferric iron. *A. ferrooxidans* has gained interest due to its potential for industrial-scale bioleaching of metals from complex ores, especially in copper mining. Since *A. ferrooxidans* relies on dissolution of metal sulfides for their bioenergetic requirements, adhesion to and colonization of the substrate is important. Previously identified attachment mechanisms include extracellular polymers as well as both type IV and tight adherence pilus systems. This study focuses on a third pilus system that our laboratory identified, a sigma-type chaperone usher pilus (CUP). Our hypothesis is that CUP are directly involved in irreversible attachment to surfaces. To address our hypothesis we used a combination of physiological and functional genomics approaches. Using crystal violet staining, we determined that *A. ferrooxidans* was preferentially attaching to hydrophobic versus hydrophilic surfaces, implicating nonpolar, hydrophobic molecules in attachment. Direct counting by epifluorescence microscopy determined that each culture reached similar cell densities, suggesting that biofilm formation was influenced by the surface not cell density. A majority of *A. ferrooxidans* cells also maintain adherent capabilities throughout growth. Ultimately, we used qRT-PCR to compare the expression of the three pilus systems during exponential versus stationary phases. Expression data shows significant up-regulation of CUP genes during the transition to stationary phase. Overall, we provide evidence for growth-phase dependent initiation of biofilm formation and expression of the CUP system.

Key Terms: Microbiology
 Genetics
 Biochemistry

UG-CBB-102

Understanding RNA-Binding Roles in the Microtubule Organizing Center

Lauren DeMeyer (Oakland University), Michael Stubenvoll (Oakland University)

Advisor: Mi Hye Song (Oakland University)

The centrosome serves as the main microtubule organizing center in animal cells, exhibiting changes in both size and number during the cell cycle. During mitosis, the centrosomes help to form the poles of the mitotic spindle, and are crucial for proper chromosome segregation and maintenance of genomic integrity. Centrosomes must duplicate exactly once per cell cycle. Their duplication is a tightly regulated process, and extensive work in the nematode *C. elegans* has identified five factors that are essential for centrosome duplication, including the kinase ZYG-1. Further work into the regulation of this process identified two RNA-binding proteins (RBPs), SZY-20 and ATX-2, which physically associate to negatively regulate ZYG-1. The role of RNA and RNA binding proteins in centrosome duplication is a largely uncharacterized topic. RNAs serve as intermediate messengers for the processing of genetic information, but can also function as regulators of gene expression or serve structural roles as well. The aim of this project is to identify RNAs involved in centrosome duplication by identifying the RNAs that physically interact with SZY-20 and ATX-2. By using a modified RNA Immunoprecipitation technique called *in-vivo* Photoactivatable Ribonucleoside-Enhanced Crosslinking and Immunoprecipitation (*i*PAR-CLIP), we have isolated RNAs bound to SZY-20 and ATX-2. Following RNA-seq analysis, we will continue characterizing the role of these RNAs in the centrosome duplication process.

Key Terms: Cell cycle
 Centrosome
 RNA-binding

STUDENT POSTER ABSTRACTS

UG-CBB-103

Isolation and Purification of Mycobacteriophage Thespis

David Bushhouse (Hampden-Sydney College)
Advisor: Michael Wolyniak (Hampden-Sydney College)

In continuance with the HHMI Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES) program at Hampden-Sydney College, a lytic bacteriophage, named Thespis, was isolated from enriched soil samples using host organism *Mycobacterium smegmatis*. High titer lysates were produced and used to isolate DNA, which was sequenced and uploaded to the Actinobacteriophage Database at www.phagesdb.org. Genome annotation is underway, and continuing efforts are aimed at examining transcriptional and translational characteristics of Thespis in the host using RNA-seq and LC-MS protein identification.

Key Terms: Mycobacteriophage
 Virology
 SEA-PHAGES

UG-CBB-104

Investigating the Regulation of *Drosophila* HIF α in Neuronal Mitochondrial Retrograde Signaling

Amara Thind (University of California, Irvine), Rachel Hunt (King's College, London)
Advisor: Joseph Bateman (King's College, London)

Inherited metabolic disorders are often mitochondrial, and tissues with high metabolic demands, like the nervous system, are frequently affected as seen with Alzheimer's and Parkinson's disease. Mitochondrial retrograde signaling is a key mechanism of cellular homeostasis and defined as the cellular response to changes in the functional state of mitochondria. This allows for changes in nuclear gene transcription and cellular signaling pathways. Hypoxia inducible factor alpha subunit (HIF α) transcription factor was discovered to regulate neuronal mitochondrial retrograde signaling in *Drosophila*. HIF α controls retrograde response genes to reprogram neurons by stopping protein translation and altering cellular metabolic states. In *Drosophila* larvae, estrogen related receptor (ERR) was found to be required for the full complement of HIF responses under hypoxic conditions. It is hypothesized that ERR is required for some/all of HIF α -dependent neuronal mitochondrial retrograde signals. The aims are 1) to investigate the functional impact of ERR in neuronal retrograde signaling under conditions of mitochondrial dysfunction 2) to investigate if levels of ERR change in neuronal mitochondrial dysfunction. Climbing and wing inflation assays were done to assess functional impact of ERR-knockdown and immunofluorescence staining was conducted to detect changes in ERR levels under mitochondrial dysfunction conditions. ERR-knockdown driven in motor neurons significantly improves both wing inflation and climbing ability under mitochondrial dysfunction conditions and ERR levels appear to be higher in larval glutamatergic neurons with damaged mitochondria. This supports the claim that ERR may be involved in mitochondrial retrograde signaling and can possibly regulate neuronal activity, manipulated to enhance neuronal function.

Key Terms: Neuroscience
 Neurodegeneration
 Molecular biology

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UG-CBB-105

Testing the Function of La-Related Proteins 6 in *Danio rerio* by Genome Editing

Jessica Nevarez- Mejia (University of California, Irvine), Victoria C. Williams (King's College London), Maria R. Conte (King's College London), Simon M. Hughes (King's College London)
Advisors: Simon M. Hughes (King's College London), Victoria C. Williams (King's College London)

Larp6 is an RNA binding protein in the La-related protein (LARP) family. *In vitro*, Larp6 has been shown to interact with Type 1 collagen mRNAs, thereby controlling collagen synthesis and stability, and suggesting that Larp6 activity is vital as mis-regulation of collagen biosynthesis can lead to collagen-related diseases, such as fibrosis. Previous studies using Larp6 antisense morpholinos in zebrafish *Danio rerio* also implicate Larp6 in differentiation of slow twitch muscle fibers, which anchor to a collagen-rich extracellular matrix. Zebrafish have two Larp6 genes: *larp6a* and *larp6b*. We hypothesized that creating a true genetic null for each in the zebrafish via genome editing would cause phenotypic defects in muscle fibers. CRISPR/Cas9 and TALEN systems were used to mutate *larp6a* and *larp6b*, respectively. Heterozygote and mutant fish were identified by using High Resolution Melt PCR, and sequence analysis. *In situ* mRNA hybridization revealed that *larp6a* mRNA was significantly reduced in *larp6a* mutants at 50% epiboly stage, presumably through nonsense-mediated decay, strongly indicating that the mutation is an effective null. After 5-day post fertilization and immunofluorescent staining analysis for muscle myosin, *larp6a* mutant fish appeared healthy and did not show significant signs of muscle fiber defects. We conclude that Larp6a is not essential for normal myogenesis and that the previous morpholino result did not arise purely from knockdown of Larp6a. I identified a total of ten apparently healthy *larp6a* mutant sub-adult fish. Further analysis is needed to determine the phenotype of fish mutant for both Larp6 genes.

Key Terms: Developmental biology
 Molecular
 Genetics

UG-CBB-106

Characterizing a Novel Class of Long Noncoding RNAs Expressed in Cancer

Jonathan Mendez (UCI), Karen Yap (King's College London), Eugene Makeyev (King's College London)
Advisors: Karen Yap (King's College London), Eugene Makeyev (King's College London)

Long noncoding RNAs (lncRNAs) are an abundant class of molecules often found to be over-expressed in cancer. One such lncRNA is encoded in the vicinity of the 45S rDNA sequence and referred to as pyrimidine-rich noncoding transcript adjacent to an rDNA array (PNCTR). Unpublished work in Makeyev lab shows that PNCTR is localized to the nucleus where it interacts with the important RNA-binding protein PTBP1 through several (CU)_n repeats encoded in PNCTR. The highly repetitious nature of rDNA arrays, makes it virtually impossible to deduce the exact PNCTR sequence from the reference genome or next-generation RNA sequencing data. Therefore, PNCTR will be analyzed using Sanger sequencing, focusing especially on the (CU)_n regions.

Reverse-transcription (RT)-PCR primers were designed using primer3 software and hg38 human genome assembly. HeLa cells were cultured in DMEM medium containing 10% FBS. Nucleo-cytoplasmic fractionation was carried out and the total RNA from the nuclear fraction was reverse-transcribed into cDNA using random N10 primers and PCR-amplified using PNCTR-specific primers. Specific PCR products were ligated with pGEM-T Easy plasmid vector transformed into Sure2 *E. coli* using electroporation. Recombinant DNA was isolated using a Qiagen plasmid miniprep kit and sent for Sanger sequencing.

Three PNCTR segments (each ~800 bp) comprising (CU)_n and several smaller segments were successfully sequenced. Primer walking will be done using existing clones to resolve the rest of PNCTR sequence. This provides the groundwork to design antisense oligonucleotides in order to examine functional consequences of altered PNCTR expression on viability and proliferation of cancer cells.

Key Terms: Cancer
 RNA
 Cancer genomics

UG-CBB-107

Role of the Transcription Factor Odd-Skipped in Neural Specification

Kyle Kisor (University of California, Irvine)
Advisor: Camilla Larsen (King's College, London)

The transcription factor Odd-skipped plays a critical role in the specification of the epidermis, gut, leg and eye in both vertebrates and invertebrates. Although Odd-skipped is well characterized in patterning several tissues, the role in the *Drosophila* central nervous system remains relatively unexplored. The aim of this study is to examine neuronal morphology when Odd-skipped is miss-expressed ectopically in engrailed neurons or knocked down using RNAi. This study is extensively built on the Gal4/UAS driver system which allows for expression and knockdown in specific neurons. Genetic crosses were performed at both 25°C and 29°C to allow for different expression levels of the transgenes. RNAi lines were subsequently backcrossed to provide two copies of RNAi to further the effects of the knockdown. Both larvae and adult's central nervous system were dissected, fixed, immunostained, and imaged. Analysis was performed using ImageJ software. We found that when Odd is expressed in engrailed tissue both axonal tracts and positioning of cell bodies in the tissue changed in both the larvae and adults as compared to respective controls. When Odd is knocked down there are completely random ectopic projections of varying phenotypes in both larvae and adults. Our results suggest that Odd plays a role in regulation of axonal projection patterning in the central nervous system of *Drosophila*. The relevance of Odd and its homologs continues to expand as a regulator of development in several tissues critical to a diverse set of eukaryotic organisms including humans.

Key Terms: Neuroscience
Developmental biology
Molecular biology

UG-CBB-108

Investigation the Complexity of Protein-Protein Interactions of Splicing Factors during Pre-mRNA Processing in Plants

Annaliese Riegel (Oakland University), Christian Brigolin (Oakland University), Donya Shodja (Oakland University), Feng Bai (University of Florida)
Advisors: Shailesh Lal (Oakland University), Mark Settles (University of Florida)

Eukaryotic genes contain non-coding regions called introns. The precise recognition and removal of introns from precursor-mRNA is a fundamental process that is required for the expression of eukaryotic genes. Despite the importance, the mechanism of this process is poorly understood in plants. It occurs in a complex and dynamic structure called the spliceosome, which is a conglomeration of multiple splicing factors, all of which participate in a step-wise manner during pre-mRNA processing. Here we report an RNA Binding Motif 48 (RBM48) protein as a novel splicing factor required for normal maize seed development and viability. RBM48 is related to a highly conserved family of Arginine/Serine-rich (SR) splicing factors that play a key role during splice site selection in spliceosomes. Using heterologous transient expression assays in tobacco of fluorescent protein fusion, we demonstrate that RBM48 protein co-localizes with core splicing factors U2 snRNP Auxiliary Factor (U2AF) and RGH3 proteins. We also tagged and overexpressed maize RBM48, U2AF, and RGH3 splicing factors in *E. coli* and raised polyclonal antibodies against the fusion protein to investigate *in vitro* protein-protein interactions of RBM48. Our data using *in vitro* co-immunoprecipitation and pull down assays further confirm the *in vivo* interaction of RBM48 with core splicing factors. This data points to a key role of RBM48 during pre-mRNA splicing and seed development in maize.

Key Terms: Molecular biology
Plant biology
Splicing protein

UG-CBB-109**Investigating the Role of Different 5' Partners in BRAF Gene Fusions in Melanoma**

Jacqueline Turner (University of Colorado at Denver, Anschutz Medical Campus), Kasey Coutts (University of Colorado at Denver, Anschutz Medical Campus), Stacey Bagby (University of Colorado at Denver, Anschutz Medical Campus), Judson Bemis (University of Colorado at Denver, Anschutz Medical Campus)
Advisors: William Robinson (University of Colorado at Denver, Anschutz Medical Campus), Marileila Varella-Garcia (University of Colorado at Denver, Anschutz Medical Campus)

Melanoma development and progression is often driven by activation of the MAP kinase pathway through aberrant activation of the BRAF kinase. *BRAF* is activated by mutations, amplifications, alternative splicing, or recently discovered gene fusions. *BRAF* fusions involving different 5' gene partners have been described in cutaneous melanomas and Spitz nevi, however, oncogenic potential and treatment response between *BRAF* fusions with different 5' gene partners has not been assessed. We used fluorescence *in situ* hybridization to analyze a cohort of 59 melanoma patient tumors and identified two different *BRAF* gene fusions, *AGK-BRAF* and *ARMC10-BRAF*. The *ARMC10* 5' gene partner has not been described in melanoma and treatment response of *ARMC10-BRAF* has not been reported in any cancer type. We generated patient-derived xenograft (PDX) models for the two *BRAF* fusions and treated them with MAP kinase pathway inhibitors specific to MEK1/2 and ERK1/2. Both PDX models responded to the inhibitors, however, the *ARMC10-BRAF* fusion was more sensitive and showed stronger tumor regression. To further understand differences between *BRAF* fusions we used computational modeling to predict the protein structures of wild type *BRAF*, mutated *BRAF*V600E, and six *BRAF* gene fusions with 5' partners including, *AGK*, *ARMC10*, *KIAA1549*, *TRIM24*, *PPFIBP2*, and *ZKSCAN1*. We found large variations in the MEK1/2 kinase binding domain between different 5' partners, and we are currently overexpressing these *BRAF* fusions in a generic background to perform additional experiments and determine the tumorigenic potential and treatment response between these different 5' partners. Patients harboring gene fusions should only be treated if the fusion demonstrates actionable driver potential. Understanding differential responses in *BRAF* gene fusions will improve clinical treatment of patients with *BRAF* gene fusions.

Key Terms: Melanoma
 Gene fusion
 5' gene partner

UG-CBB-110**Diamide Inhibitors of N-acetylglucosaminidases as Tools to Study the Bacterial Cell Wall**

Keyana Roohani (Bryant University)
Advisor: Christopher Reid (Bryant University)

Gram-positive bacterial cell walls are composed of a thick peptidoglycan (PG) layer and teichoic acid. The PG layer is composed of a polysaccharide backbone comprised of *N*-acetylglucosamine (GlcNAc) and *N*-acetyl muramic acid (MurNAc). Adjacent polysaccharide strands are cross-linked via pentapeptide side chains attached to MurNAc providing a dynamic 3-dimensional structure that confers shape and strength to resist turgor pressure. Autolysins, enzymes produced by bacteria, are able to break down the PG of cell walls. These enzymes are involved in processes such as cell growth, division, and motility. Our lab is interested in *N*-acetylglucosaminidases (GlcNAcases).

Previous work with Ugi-derived diamides identified inhibitors specific to GlcNAcases in *Bacillus subtilis*. These inhibitors are being investigated for use as tools to study Gram-positive cell wall physiology in the model organism *B. subtilis*. *B. subtilis* is a non-pathogenic Gram-positive bacteria widely studied in relation to PG synthesis and metabolism. The compound fgkc was the top inhibitor of *B. subtilis* 11774. Treatment with fgkc resulted in incomplete cell division and elongated cell phenotype.

At least one target of fgkc has been identified in *B. subtilis*, GlcNAcase LytG. Potential secondary targets in *B. subtilis* strains were screened using deletion mutants of major autolysins. Results indicate increased sensitivity in deletion mutants when LytG is inhibited by fgkc, suggesting LytG is the sole autolysin targeted. Microscopy revealed changes in cell motility and morphology in mutants. We have employed phenotypic arrays to explore the effect of GlcNAcase inhibition or deletion in osmolyte, pH, and chemical sensitivity panels.

Key Terms: Chemical genomics
 Autolysin
 Peptidoglycan

UG-CBB-111

Essential Oils And Methylglyoxal: A Possible Treatment for Inhibiting the Growth of the Extended Spectrum Beta-Lactamase Producing *Escherichia coli* (ESBL-EC)

Joseph Kellett (Monmouth University)

Advisor: James Mack (Monmouth University)

The overuse and misuse of antibiotics have produced antibiotic resistant bacteria. Infections from these bacteria are therefore difficult to treat. Recent problems in healthcare settings include infections of patients with certain antibiotic resistant bacteria which do not respond to traditional antibiotic treatment. Natural products, including essential oils, derived from plants show promise as strong bactericides, which may be useful for effectively combating the infections from these antibiotic resistant bacteria. *Escherichia coli* is part of the normal flora of the intestines, however, some strains can cause an intestinal infection causing abdominal pain, fever, as well as bloody diarrhea. Other strains of *Escherichia coli* can also cause urinary tract infections. In this research, the essential oils cassia, cinnamon bark, oregano, as well as methylglyoxal (main ingredient in Manuka honey) were used in conjunction with three carrier oils (olive oil, jojoba oil, and coconut oil) to determine their efficacy in inhibiting the growth of *ESBL-EC*. Cassia, cinnamon bark, oregano, and methylglyoxal were chosen because they were used in previous studies at Monmouth University and showed to be effective in inhibiting the growth of MRSA and MSSA. The essential oils were diluted to lower concentrations to determine their minimal inhibitory concentration (MIC) because most essential oils are irritating to the skin in high concentrations. The results were then compared to traditional antibiotics, including colistin, tetracycline, ciprofloxacin, fosfomycin, azithromycin, and nitrofurantoin, to determine their effectiveness. It was determined that the MIC of the essential oils to effectively inhibit *E.coli* is 33% and the MIC of methylglyoxal is 12%. The dilutions were made using the carrier oils listed above, which are known to be safe on the skin. The effectiveness of essential oils and methylglyoxal emollients in carrier oils in inhibiting the bacterial growth was better than the currently used antibiotics for treating *ESBL-EC*. Multidrug-resistant bacteria have become a significant global health threat and the possible treatment of multidrug-resistant bacterial infections with proven bactericidal essential oils may help alleviate this problem.

Key Terms: Antibiotic resistance
 Essential oils
 Escherichia coli

UG-CBB-112

The Hemoglobin Beta Gene

Tyra McKnight (SUNY Plattsburgh)

The Hemoglobin beta gene (HBB) provides instructions for making a protein called beta-globin. Beta-globin, a subunit of a protein called hemoglobin, is located inside red blood cells. Hemoglobin is involved in the transport of other gases to tissues throughout the body, including oxygen. Although *Paramecium*, a unicellular protozoan, is avascular it still has the hemoglobin beta gene. Previous research at SUNY Plattsburgh has shown this gene to be expressed in *Paramecium*. This study investigated the environmental factors that alter the level of expression of HBB in *Paramecium*, these included temperature, pH and presence/absence of oxygen. The hypothesis for this project is if there is a lack of oxygen in the living environment of the *Paramecium* then there will be an increase in the activation of the HBB in order to meet their oxygen level requirement. Preliminary data suggested that the lack of oxygen had the greatest effect on the expression of the Hemoglobin beta gene. *Paramecium* was cultured and its DNA was isolated and amplified. Additionally, RNA was isolated to perform reverse transcription polymerase chain reaction (RT-PCR) experiment.

Key Terms: Genetics
 Hemoglobin
 Paramecium

STUDENT POSTER ABSTRACTS

UG-CBB-113

L2-Syntaxin 18 Binding Motif Necessity in HPV16 Infection

Emma DeGrace (Fordham University), Xavier Simon (Fordham University)

Advisor: Patricio Meneses (Fordham University)

HPV is the most common sexually transmitted infection, and while most mucosal HPV strains are benign, several stains can lead to genital warts and cancers such as cervical, vaginal, and oropharyngeal. HPV 16 and 18 alone account for 50 and 18 percent of all cervical cancer cases respectively. The HPV virus consists of DNA held within a protein shell, or capsid. The protein capsid of HPV is composed of two major proteins: L1 and L2. The L2 protein has been shown to be necessary for infection. In this project, we mutated an L2-syntaxin 18 binding motif to see if the region is necessary for HPV16 infection. We found that by changing just one of four amino acids, of the five amino acid motif, the pseudovirus was not infectious. Not only does this result highlight the importance of this L2-syntaxin 18 interaction in viral trafficking, but the motif could serve as a potential vaccine target.

Key Terms: HPV
Cell biology
Molecular biology

UG-CBB-114

Effects of GSM™ (Global Systems for Mobile Communication) radiation on expression of Heat Shock Protein 20 in *Pieris rapae*

Samuele Weekes (SUNY Plattsburgh)

Advisor: Dr. Nancy L. Elwess (SUNY Plattsburgh)

Would you stop using your cell phone if you knew it had the potential to harm certain cells of your body? Society's current predicament is that most individuals in this age value communication over potential unknown long term health effects. It is known that cellular devices operating on the Global Systems for Mobile communication or GSM™ band frequencies have a phenotypical effect on *Paramecium*. When a text message or phone call is sent or made, or even when a cell phone is at rest, radiation is being emitted and taken in by the cellular device in the spectrum of microwaves. The most common band frequency used in North America is Global System for Mobile

Communication, which operates at 1,900 MHz on the east coast. Cell Phones have only been in use for about 43 years and have been utilizing GSM™ frequencies for less, therefore long term effects are still unknown. With the help of a cell signal repeater in an experimental setup *Pieris rapae* (cabbage white butterflies) were either exposed (experimental) or unexposed (control) to the microwaves given off by the cell signal repeater. Levels of expression for the protein HSP20 (heat shock protein 20) were monitored in both control and experimental groups throughout their lifespans. An increase in expression levels for HSP20 in experimental *Pieris rapae* compared to the control would suggest a greater heat stress environment due to exposure of cell phone radiation

Key Terms: GSM™
Pieris rapae
HSP20

UG-CBB-115

Distinct Spatial Organization for Two Misfolded Proteins during Aggresome Biogenesis in HEK293 cells

Jordan Nelson (Western Carolina University)
Advisor: Robert Youker (Western Carolina University)

Mammalian cells possess multiple mechanisms to deal with misfolded proteins. The cell will first attempt to refold/repair the protein but if that fails then it is targeted for degradation by a cytosolic protease. However, the amount of damaged protein can overwhelm the cytosolic protease leading to the formation of perinuclear aggregates caused aggresomes. Aggresomes are composed of protein aggregates and are a protective mechanism to minimize disruption to cellular processes. Are the mechanisms for aggresome formation the same for different misfolded proteins? The misfolded proteins GFP-250 and mCherry-cBSA were co-expressed in cells to determine if the proteins have the same mechanism of misfolding and aggresome formation. GFP-250 and mCherry-cBSA were coexpressed in HEK293 cells and their location with respect to each other measured during aggresome biogenesis. Interestingly, GFP-250 had a greater propensity to form multiple aggregation bodies compared to mCherry-cBSA at early time points. Also, in the early time points the aggregated proteins were separate as judged by approximately 50% colocalization. Later time points showed higher colocalization of 85-88% for the two proteins. In contrast, Cells transfected with mCherry-cBSA and GFP-cBSA had an average value 78% at all times points. Cells with mCherry-cBSA and GFP showed an initial higher colocalization at early time points that decreased as the mCherry-cBSA began to form aggresomes. Taken together, this data suggests that p115-fragment (250) and cBSA proteins have different mechanisms involved in aggresome formation. Future work will allow for more aggresomes to be analyzed to increase the accuracy of the colocalization values and determine the mechanism for the differences observed.

Key Terms: Aggresome biogenesis
Misfolded proteins
Aggresome colocalization

UG-CBB-116

Analysis Hypervariable Region Within Ancient Mayan Mitochondrial DNA

James Stewart (SUNY Plattsburgh)
Advisor: Nancy Elwess (SUNY Plattsburgh)

Thanks to great advancements in bioinformatics, scientists are now able to sequence human genomes with miraculous speed. By sequencing and cataloging the genome of populations across the globe, researchers have been able to better understand ancient human migration patterns. In theory, the closer populations are to each other, the more genetic similarities they should share. The primary purpose of this study is to show that the ancient Tipu Maya DNA contain unique sequences within the 14-base pair region of their mitochondrial DNA compared to other populations. Mitochondrial DNA (mtDNA) is unique compared to nuclear DNA in that rather than fractions being inherited from both parents, it is solely inherited from the mother. This makes it an exceptionally useful tool in also tracing human migration routes. aDNA was isolated from teeth, and the DNA was amplified and sequenced. The sequenced results supported that within the Maya 14 base pair hypervariable region were unique sequences compared to other populations.

Key Terms: Genetics
Mitochondrial DNA
Tipu Maya

STUDENT POSTER ABSTRACTS

UG-CBB-117

The Catechol-O-Methyl Transferase Gene Analysis: Warrior Versus Worrier

Rebecca Muschio (SUNY Plattsburgh)
Advisor: Nancy Elwess (SUNY Plattsburgh)

The Catechol-O-Methyl transferase (COMT) gene has two different versions, or alleles. These alleles are Valine (Val158) and Methionine (Met158). Research has suggested that the Val158 allele is more often found in those with “warrior” personalities. The hypothesis for this study is that the experimental groups will have a higher frequency of the Val/Val allele, making them warriors. Thus far in this study, a control and experimental group has given DNA samples via saline solution. These samples were then isolated, amplified and sequenced. Each sample could have one of three genotypes: Val/Val, Met/Met or Val/Met. The Val/Val genotype (warriors) has low dopamine in the prefrontal cortex and the Met/Met genotype (worriers) have high dopamine in the prefrontal cortex. Lastly, the Val/Met genotype leans more towards the worrier side because they have high dopamine levels, but not as high as the Met/Met allele. Out of the control group, the Val/Met genotype was the most common (19 samples) and the Met/ Met (2 samples) and Val/Val (4 samples) was the least common.

Currently, expeditionary studies majors are being used as an experimental group to see if the warrior genotype is more common in those in that major. Initial studies support the stated hypothesis.

Key Terms: Genetics
 DNA
 Gene

UG-CBB-118

Determining the Role of the Rb-E2F1 Pathway in Epigenetic Remodeling in Osteosarcoma

Josselyn Pena (University of California, Irvine), Stephanie Wu (University of California, Irvine), Claudia Benavente (University of California, Irvine)
Advisors: Claudia Benavente (University of California, Irvine), Stephanie Wu (University of California, Irvine)

Rb protein is responsible for cell cycle regulation and cell fate specification and differentiation through inhibition of the E2F protein family. E2F deregulation promotes uncontrolled gene transcription. Patients with mutations in the RB1 gene, which encodes for Rb protein, are predisposed to develop osteosarcoma with poorer prognosis. Osteosarcoma is highly metastatic so it is important to identify the molecular basis of its progression and develop more effective therapeutics for faster treatment. Our studies identified higher levels of HELLS and UHRF1 protein, both epigenetic modifiers, in osteosarcoma tumors. HELLS and UHRF1 overexpression increase cell survival and migration rates. The main goal of this study was to determine the relationship between the Rb-E2F pathway and these epigenetic modifiers. A lentiviral knockdown of E2F1 was used to observe changes in four osteosarcoma cell lines. Western Blot analysis of the levels of HELLS and UHRF1 protein in each cell line was used to determine the effect on these epigenetic modifiers. Preliminary results have identified a suitable shRNA E2F1 plasmid to package into lentivirus. Analyzing whether levels of HELLS and UHRF1 are affected by knocking down E2F1 will enable us to determine whether the Rb-E2F pathway is responsible for their upregulation; if their levels are reduced when E2F is knocked down, this indicates that E2F deregulation is necessary for their overexpression. If the Rb-E2F pathway is responsible for the patient’s poorer prognosis through the upregulation of epigenetic modifiers, these modifiers would be good potential therapeutic targets to continue studying.

Key Terms: Cancer
 Epigenetics
 Tumorigenesis

UG-CBB-119

Determining Genetic Diversity of *H. subterraneus* using DNA Barcoding of COI and 16S rRNA Genes

Dragomir Vasilev (SUNY Plattsburgh)
Advisor: Nancy Elwess (SUNY Plattsburgh)

Cave crickets like *Hadenoeus subterraneus* are keystone species within cave systems. Mostly concentrated around the entrances of caves, they can serve as indicators of potential issues within cave ecosystems. Our point of focus is determining whether the proximity of *H. subterraneus* populations affects the amount of genetic diversity between them. Cricket samples (eggs/limbs/full bodies) were obtained from different entrances of the Mammoth caves in Central Kentucky. Once obtained the genetic samples were extracted via minicolumn purification the COI and 16s ribosomal regions were used for DNA barcoding. Our findings of differentiation among populations did not strongly correlate with physical distance between populations being compared. Results falsified our original hypothesis of positive correlation between interpopulation distance and variation. This lead us to believe that there may be an underlying mechanism with either the crickets' ability to move between populations or a relatively low rate of mutation. Further analysis will attempt to determine whether interpopulation variation is related to different factors in addition to studying different cave systems where *H. subterraneus* and closely-related species reside.

Key Terms: Genetics
 Cave crickets
 16s rRNA and COI

GR-CBB-138

Regulating Neonatal Platelet Activation: Role of GPCRs Cross-Talk and Dense Granule Secretion

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Advisor: Owen McCarty (Oregon Health & Science University)

Protease-activated receptors (PAR1/4) signal G-protein-coupled receptors (GPCRs) to promote platelet granule secretion and platelet activation in adults. Adenosine diphosphate (ADP), secreted from dense granules following initial platelet activation, triggers a positive feedback loop that enhances platelet activation and aggregation via GPCRs P2Y1/P2Y12. It has been established that once PARs are activated by thrombin, ADP functions as a positive mediator to enhance platelet activation and amplify thrombus formation in adult whole blood. However, previous studies from our group have demonstrated that platelets from neonatal peripheral blood have an attenuated activation in response to PAR1 agonist (TRAP-6) compared to adults. The diminished response may be a consequence of decreased number of platelet dense granules and lower levels of endogenous ADP, and/or a lack of synergy between ADP receptors and PARs. In this study, small volume, whole blood static adhesion assays coupled with structured illumination microscopy were performed with adult samples, quantifying for CD63. These assays allow for the localization of platelet dense granules, which we are currently using to compare adult and neonatal platelet physiology. Fluorescence-activated cell sorting (FACS) was employed to measure platelet activation in response to PAR1 and PAR4 activation in the presence and absence of exogenous ADP. FACS results suggested that ADP and PAR agonists synergize to activate both adult and neonatal platelets, as evidenced by a 2-fold increase in P-selectin and PAC-1 signals in response to PAR agonists in conjunction with exogenous ADP. Our research demonstrates the utility of whole blood assays to quantify platelet granules and the synergy between PARs and ADP receptors in regulating adults and neonatal platelet activation.

Key Terms: Cardiovascular
 Blood
 Biomedical engineering

GR-CBB-139

Identification of the Calmodulin-binding Domains of Fas Death Receptor

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Advisor: Jamil Saad (University of Alabama at Birmingham)

The extrinsic apoptotic pathway is initiated by cell surface death receptors such as Fas. Engagement of Fas by Fas Ligand triggers a conformational change that allows Fas to interact with adaptor protein Fas-associated death domain (FADD) via the cytoplasmic Death Domain, which recruits downstream signaling proteins to form the death-inducing signaling complex (DISC). Previous studies have shown that calmodulin (CaM) is recruited into the DISC in cholangiocarcinoma cells, suggesting a novel role of CaM in Fas-mediated signaling. CaM antagonists induce apoptosis through a Fas-related mechanism in cholangiocarcinoma and other cancer cell lines possibly by inhibiting Fas-CaM interactions. The structural determinants of Fas-CaM interaction and the underlying molecular mechanisms of inhibition, however, are unknown. We employ NMR, biochemical, and biophysical techniques to elucidate these mechanisms. We have shown that CaM binds to the death domain of Fas (FasDD) with a novel 2:1 CaM:FasDD stoichiometry. The interactions between FasDD and CaM are endothermic and entropically driven, suggesting that hydrophobic contacts are critical for binding. Proteolytic digestion and NMR experiments facilitated the identification of the two minimal binding domains of Fas involved in CaM binding. Characterization of both peptides revealed the CaM-FasDD binding interface, including binding affinity, mode of binding, and thermodynamic properties. Our data suggest that because both Fas-CaM binding regions are involved in extensive intermolecular contacts with the death domain of FADD, binding of CaM to these regions may hinder its ability to bind to FADD, thus greatly inhibiting the initiation of apoptotic signaling pathway. By providing new insight into the molecular basis for a novel role of CaM in regulating Fas-mediated apoptosis, we believe these discoveries will facilitate the discovery of effective yet minimally toxic therapies for debilitating diseases such as cholangiocarcinoma.

Key Terms: Structural biology
 Nuclear magnetic resonance
 Cancer

GR-CBB-140

Role of ZIP8 in the Regulation of Cell Morphology, Adhesion and Migration

Xiangrong Geng (Oakland University), Zijuan Liu (Oakland University)

Advisor: Zijuan Liu (Oakland University)

ZIP8 belongs to ZIP8 superfamily, which has been known to play important roles in normal physiology and cancer progression. ZIP8 is a newly identified membrane transporter to facilitate uptake of important divalent metal substrates including zinc, selenium. Although the biochemical function of ZIP8 is known, the physiological and pathological roles of ZIP8 have not been elucidated. Here we explored the role of ZIP8 in the regulation of epithelial to mesenchymal transition (EMT) and cell adhesion, which are important for cancer metastasis. Through gain and loss of function studies, we discovered that ZIP8 regulates genes regulating cell morphology, adhesion and migration. Overexpressing ZIP8 in mouse fibroblast cells leads to a significant change of cell cytoskeletons; increases cells adhesion, migration and proliferation, and induces the EMT. Loss of ZIP8 function through shRNA knockdown and CRISPR knockout in cancer cells and leukemia cells result a visible morphological and modified the cell properties including adhesion, and migration. Gene expression profiling showed that ZIP8 is involved in the TGF β -induced EMT, characterized by the cytoskeletal reorganization, weakened cell adhesion and increased extracellular matrix proteins expression. Molecular mechanisms involved in the regulation as well as the role of ZIP8 in the prostate cancer progression are under investigation. Overall, ZIP8 plays essential roles in regulating cancer cell EMT and control cell adhesion and migration. Therefore, targeting ZIP8 may become a novel therapeutic approach in cancer treatment.

Key Terms: ZIP8 transporter
 Prostate cancer
 EMT

GR-CBB-141

The Role of Cell Cycle in Neural Crest Cell Migration

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Advisors: Claudia Linker (King's College London),
Zain Alhashem (King's College London)

Cell migration is a fundamental process in multicellular organisms that plays a crucial role in embryogenesis, tissue formation, wound healing, etc. It is important to decipher the mechanisms controlling cell migration as any aberrations in this process would cause serious developmental defects. We use the neural crest (NC) in zebrafish to study cell migration, as it is a multipotent population that migrates extensively giving rise to different cell types. Furthermore, its migration shares features with cancer metastasis. Based on preliminary data in single-cell tracking, we observed a strong correlation between cell division and the initiation of trunk NC (TNC) migration. Therefore, we hypothesized that cell cycle progression plays a role in NC migration initiation. Hence, we have analyzed TNC migration upon inhibition of different phases of the cell cycle. Two different drugs were tested to arrest the cell cycle: Teniposide and Aphidicolin. Teniposide showed no effect on arresting the cell cycle in zebrafish embryos. On the other hand, Aphidicolin successfully arrested S phase causing migratory phenotypes and halting TNC migration. Next, we will seek to define the time at which TNC migration are dependent on cell cycle progression by performing Aphidicolin treatment at different embryonic stages. Understanding of the mechanistic effect of cell cycle on cell migration might help shed some light on therapeutic targets in cancer metastasis and other developmental disorders.

Key Terms: Cell biology
Zebrafish
Aphidicolin

HS-CHM-226

Endogenous Adenosine A₃ Receptor Activation Selectively Alleviates Persistent Pain States

Elise Mochizuki (Jericho High School), Kenneth Jacobson (National Institutes of Health/National Institute of Diabetes and Digestive and Kidney Diseases)

Current standards of care for chronic pain are ineffective, and a new therapeutic target is the endogenous adenosine system for analgesia using the activation of G protein-coupled adenosine A₃ receptor. The ability of A₃ agonists to reverse or prevent chronic neuropathic pain is a significant development in the pain field, since the cardiovascular side effects of A₁AR and A₂AR agonists prevent their clinical applications in pain management. Our null hypothesis was that rodent models of experimental neuropathic pain would not demonstrate any analgesia from adenosine levels increased to activate the A₃AR signalling pathway. Rodent behavior in persistent neuropathic pain models was assessed in 301 male Sprague Dawley rats and 63 wild-type C57BL/6 or A₃AR^{-/-} or female BALB/cfC3H mice. Increased endogenous adenosine levels with analgesic effects were seen with selective inhibition of adenosine kinase as well as administration of a novel, highly selective A₃AR agonist. Using the rodent model of chronic constriction injury (CCI), neuropathic pain was reversed by the adenosine kinase inhibitor ABT-702, and by the A₃AR agonist MRS5698. MRS5698 did not change normal nociception measurements on the tail flick latency and hot-plate test. MRS5698 reversed spontaneous pain behaviors after spinal nerve ligation. Mechano-allodynia was reversed by MRS5698 intrathecal injections and rostral ventromedial medulla (RVM) injections to the spinal and supraspinal sites, respectively. These results suggest that A₃AR activation is an endogenous anti-nociceptive pathway. Prototypical A₃AR agonists currently in clinical trials are promising. Highly selective A₃AR agonists may allow aggressive dosing with reduced spill over effect on A₁AR and A₂AR.

Key Terms: Bioorganic chemistry
Chronic pain
A₃AR

UG-CHM-238

Preparation and Characterization of Silver Nanoparticle-loaded Textiles

Samuel Underwood (National Institute of Standards and Technology and Reed College)
Advisor: Justin Gorham (National Institute of Standards and Technology)

Silver nanoparticle (AgNP)-loaded textiles were prepared and used as test materials in an effort to develop measurement methodologies and high-throughput data analysis protocols for detection and characterization of textiles loaded with nanosilver. Aqueous silver nitrate was reduced by sodium citrate in the presence of cotton or nylon fabrics to give AgNP-loaded textiles with varying silver concentration according to the amount of silver nitrate initially added to solution. The textiles were then characterized using X-Ray photoelectron spectroscopy (XPS), scanning electron microscopy (SEM), and inductively coupled plasma mass spectrometry (ICP-MS). An automated method for generating a particle size distribution from SEM images was developed, with results indicating a mean particle diameter of 40 nm, with a standard deviation of 15 nm. SEM and XPS data indicate AgNP are heterogeneously loaded onto the textile surface, with some aggregation present. Data also indicate that AgNP have a high affinity for surface loading, with especially high surface concentrations observed on nylon.

Key Terms: Nanomaterials
 Textiles
 Chemistry

UG-CHM-239

DNA-Binding Studies of the Natural β -carboline Eudistomin U

Patrick Tate (Providence College)
Advisors: Seann Mulcahy (Providence College),
Bongsup Cho (University of Rhode Island)

β -carbolines are high-interest molecules due to their diverse biological activity. These molecules are naturally occurring tricyclic, aromatic indole alkaloids. A subclass of β -carbolines, known as the eudistomins, is reported to have a high binding affinity to DNA. After studying the toxicology of a specific eudistomin compound, eudistomin U, we examined its DNA-Binding properties. The structure of eudistomin U is unique since it contains an indole ring at the 1-position of the pyridine ring. While simple β -carbolines are reported to intercalate DNA, an examination of the mode of binding of eudistomin U has been lacking. We report preliminary spectroscopic (UV-Vis, thermal denaturation, CD) and calorimetric (DSC) data on the binding of eudistomin U to DNA, which suggest that eudistomin U binds weakly according to a mechanism that is more complicated than other members of its class.

Key Terms: Medicinal chemistry
 DNA binding
 Bioorganic chemistry

GR-CHM-250**Phytochemical and Antifungal Evaluation of *Vernonia glabra* Leaves in the Management of Fungal Pathogens Affecting Staple Cereal Production in Kenya**

Catherine Kitonde (University of Nairobi), Dossaji Fidahusein (University of Nairobi), Catherine Lukhoba (University of Nairobi), Maina Wagacha (University of Nairobi)

Advisors: Carla Klittich (Dow AgroSciences), Don Hahn (Dow AgroSciences)

At least 70-90% of global food production is lost to plant diseases. In Kenya, yields from staple cereals such as corn, wheat and rice have reduced drastically due to disease infections and mycotoxins contamination caused by fungal plant pathogens. Chemical sprays used as an immediate method for management of plant diseases, pose adverse health effects in humans and animals, environmental hazards and high cost to farmers in Kenya. Leaves of a pesticidal plant; *Vernonia glabra*, were tested for alternative biopesticide properties. 10g of the leaf extract were isolated using bioassay-guided fractionation and structure elucidation was determined using Nuclear Magnetic Resonance at 600MHz. A novel sitosteroid compound, Glabrol-A, 3-O-Glucopyranoside, was identified. 33 µg to 0.28 µg/100 µl of the compound were evaluated using 96-well plate antifungal-assay against *Septoria tritici*, *Pyricularia oryzae*, *Ustilago maydis*, *Fusarium graminearum*, *F. verticillioides* and *F. oxysporum*. 5 ppm of Azoxystrobin (standard) and 2µl of Dimethyl sulfoxide (control) were tested for antifungal comparison. In the greenhouse, the compound was sprayed at 200 and 50 ppm against *Septoria tritici* in wheat. *In vitro* antifungal-assay results revealed 38% growth inhibition against *Septoria tritici* at 33 µg/100 µl. In the greenhouse 0% disease control was evaluated. *Vernonia glabra* compounds have fungicide characteristics which can be used by farmers as cheap alternative biopesticides. However, further research on chemical modifications of the compound is required for new modes of action for significant antifungal activity. In addition, toxicology studies of Glabrol-A, 3-O-Glucopyranoside are needed for verification and documentation of its safety.

Key Terms: Plant fungal diseases
Food security and safety
Alternative biopesticides

GR-CHM-251**Aspect Ratio Controlled Copper Nanowires Synthesis**

Srikar Rao Darmakkolla (Portland State University), Mitra Ghobadi (Portland State University), Amanda Figueiredo Pereira (Portland State University)
Advisor: Shankar Ranavavare (Portland State University)

Nanomaterials possess significantly improved physical and chemical properties when compared to bulk counter parts. Morphology and dimensions of nanomaterials play an important role in determining its unique properties such as optical, electronic and catalytic, etc. Over the past two decades, numerous efforts have been devoted for developing nanomaterials synthesis methods and controlling its morphologies. Especially controlling the aspect ratios of one dimensional (1D) nanomaterials, which is very challenging. High aspect ratio copper nanowires (Cu NWs) have been widely explored for making transparent flexible thin films, flat panel solar cells, sensor and catalytic applications. Our current work adopts a solution based approach developed by Ye Shengrong *et.al.* and optimized the reaction conditions for synthesis of monodispersed and aspect ratio controlled Cu NWs in a solution based approach. Also, we report synthesis of high surface area copper nanowires (nanosheet decorated Cu NWs) and nanospheres. Scanning Electron Microscopy (SEM), Energy dispersive x-ray spectroscopy (EDS), XRD and UV visible spectroscopy are employed for the characterization.

Key Terms: Materials chemistry
Nanomaterials
Nanowires

GR-CHM-252

Isolation and Structural Elucidation of the Secondary Metabolites from *Calea urticifolia*

Vedanjali Gogineni (University of Mississippi)
Advisors: Christopher McCurdy (University of Mississippi), Stephen Cutler (University of South Carolina)

Calea urticifolia (Juanislama) is native to El Salvador and belongs to the family, Asteraceae. *Calea* is widely known for its folkloric use as a tropical bacteriocide, and for the treatment of gastric ulcers, diarrhea, diabetes, and liver problems. Since my main focus is on the discovery of small molecules to treat various neurological disorders through isolation of secondary metabolites from medicinal plants that have folkloric use, we studied *Calea urticifolia*. Our preliminary data showed that the chloroform extract of *C. urticifolia* exhibited potent inhibition of monoamine oxidases (MAO's) A and B. Bioassay-guided fractionation has been implemented for the isolation of the secondary metabolites from *C. urticifolia*. The structures of the isolated compounds were determined on the basis of HR-MS and 1D- and 2D-NMR studies; configurations were partly established by ECD calculations. Molecular modeling and molecular dynamic studies were used to predict the binding modes on the active sites of the MAO isoenzymes. One of the isolated compounds showed possible potential in the treatment of depression, Alzheimer's and/or Parkinson's disease. Acacetin, a known compound that has not been reported from this plant source, has been isolated and exhibited a 2.5 fold greater preference towards MAO-B vs MAO-A. Acacetin was found to inhibit MAO isoenzymes with IC_{50} values of 121 nM against MAO-A and 49 nM against MAO-B. Molecular modeling studies were also performed on acacetin to interpret its interaction with the MAO enzyme active sites, illustrating the high importance of ligand interaction with negative and positive free energy regions of these active sites. Additionally, three sesquiterpene lactones namely 2,3-epoxyjuanislama, calealactone B and calein C along with three novel bisabolones named caleanolanes A-C were also isolated.

Key Terms: Medicinal chemistry
Neuroscience
Phytochemistry

HS-EEB-276

Nest Box Orientation Impacts Songbird Nest Success in Savannah, Georgia

Harold Parsons (Islands High School), Krzysztofer Philips (Islands High School), William Parsons (Islands High School), Lucas Argo (Islands High School)
Advisor: Megan Heberle (Islands High School)

Many environmental factors, such as temperature and wind direction, influence nest success in songbirds. These factors influence the direction in which birds orient their nests, but vary between regions based on seasonal weather patterns. Songbirds exhibit preferences for specific directional orientations of nest boxes placed by humans. The campus of Islands High School in Savannah, GA borders a fragmented forest, grassy athletic fields with 3 water retention ponds, and has a forested edge along the back perimeter. Nest boxes were placed around the campus spaced 24 meters apart. We observed a significant difference in the number of eggs laid per nest between cardinal and intermediate directions (oneway ANOVA, $p=0.0071$). Conservation efforts to help passerine populations can better be established with the knowledge this study provides.

Key Terms: Songbirds
Conservation
Behavior

STUDENT POSTER ABSTRACTS

HS-EEB-277

Nest-box Visibility Impacts Songbird Reproductive Success

Brittany Bailey (Islands High School), Katherine Gilson (Islands High School), Matthew Shippy (Islands High School), Lauren McGeeney (Islands High School)

Advisor: Megan Heberle (Islands High School)

The visibility of a nest is a crucial factor in the number of eggs per nest and the survivability of songbirds. The visibility of a nestbox can influence whether birds select that location for their reproductive event. Greater visibility can lead to increased predation and exposure to inclement weather. In this study, we observed Eastern Bluebirds (*Sialia sialis*) and Carolina Chickadees (*Poecile carolinensis*) in Savannah, Georgia. The percent visibility was determined by standing five meters away from each nestbox in the four cardinal directions (north, south, east, west). The mean of those percentages, the number of eggs per nest, and the number fledged per nest were used for statistical analyses. Significant differences were observed between the visibility of nestboxes that were unsuccessful compared to nestboxes that were successful (two-sample tTest, $p=0.04233$). It is important to understand beneficial nestbox placement in order to maximize reproductive success in local songbirds that may be impacted by habitat loss.

Key Terms: Songbird
 Reproduction
 Habitat

HS-EEB-278

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. Temperature fluctuation can negatively impact the growth and development of songbird nestlings. 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 a Carolina Chickadee (*Poecile carolinensis*) for 32 days using a thermocouple and data logger (Lascar ELUSBTC). Time from hatching to fledging was divided into two groups based on feather growth: 06 days and 7 days fledging. Significant differences were detected when comparing daytime and nighttime nest temperatures between developmental stages (two-sample tTests; $p=0.000007$ and $p=0.00069$, respectively). In Eastern Bluebirds (*Sialia sialis*), nest cup diameter and the number of nestlings fledged were strongly positively correlated (Pearson's correlation; $r=0.6298$, $p=0.02817$). 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 additional knowledge on avian developmental stages.

Key Terms: Songbird
 Development
 Nest microclimate

STUDENT POSTER ABSTRACTS

HS-EEB-279

Seasonal Time-Budget Comparisons of Adult Songbirds in Savannah, GA

Rebekah Watts (Islands High School), Jocelyn Calvo (Islands High School), 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 one minute accumulated behavioral observations of our study species. Behaviors observed were grouped into three main categories: foraging, resting, and vigilance. Linear models were used to compare the percentages of each behavior observed during breeding and nonbreeding seasons. Time budgets differ between seasons as resource needs for survival fluctuate.

Key Terms: Songbirds
 Behavior
 Seasonal

HS-EEB-280

Orientation of Songbird Nest Boxes Toward Various Habitats Types in Savannah, GA

William Porter (Islands High School), Benjamin Wood (Islands High School), William Stamper (Islands High School)
Advisor: Megan Heberle (Islands High School)

Reproductive success in local songbirds is affected by the orientation of nest boxes toward grass, water, and forests. The habitats near or around the nest boxes create an environment that allows the birds to be successful. The study site contained a large grassy area, three water retention ponds, and a natural mature forest around the perimeter. Nest boxes oriented toward these habitat types vary in reproductive success, as measured by the number of eggs and fledglings per nest box. There was a significant difference in the number of eggs between the three nest box orientations toward habitat types (one-way ANOVA; $p < 0.001$). Post hoc comparisons using the Tukey HSD test indicated that nest boxes oriented toward the forest had significantly more eggs than boxes oriented toward grass and water. The combined importance of orientation with regard to habitat type suggests that nest boxes facing mature trees will have greater success.

Key Terms: Songbirds
 Reproduction
 Habitat

STUDENT POSTER ABSTRACTS

HS-EEB-281

Anthropogenic Noise Impacts Songbird Reproductive Success in Savannah, GA

Carlee Skarin (Islands High School), Zoe Adams (Islands High School), Horace Broadnax (Islands High School)

Advisor: Megan Heberle (Islands High School)

Anthropogenic noise can interrupt essential songbird communication as well as possibly cause damage to embryos and nestlings. Many human activities interfere with bird communication frequencies, as birds communicate between a frequency range of 1.5-4.0 kHz. Noise pollution can limit a bird's ability to communicate with other members of its species. Anthropogenic noise negatively impacts the bird's ability to make calls for mating and reproduction, foraging, and alerting others about predation. We recorded anthropogenic noise at various breeding sites using the Decibel 10th application on an iPhone 6. We compared the number of eggs and anthropogenic noise levels in each breeding site. The number of eggs per nest was significantly greater in the grassy habitat than the forest edge and water habitats (one-way ANOVA; $p < 0.0002$). Anthropogenic noise was significantly lower in the grassy habitat (one-way ANOVA; $p = 0.0015$). Post hoc comparisons using the Tukey HSD test indicated that the grassy habitat was significantly different than the forest habitat with regard to both number of eggs and noise levels. However, the water habitat did not significantly differ from the grass or forest edge. This study can lead to important decisions about songbird and habitat conservation and protection from negative human influences.

Key Terms: Anthropogenic noise
 Songbirds
 Reproduction

UG-EEB-297

Use of Citizen Science Data to Determine Trends in Density and Sighting Frequency of Parrotfish in Belize

Robert Lewis (Georgia State University), Christy Visaggi (Georgia State University), Amy Reber (Georgia State University)

Advisors: Christy Visaggi (Georgia State University), Amy Reber (Georgia State University)

A key functional group of organisms within all coral reef ecosystems are the herbivorous grazers (HGs), which feed on macroalgae. The Scaridae (parrotfishes) are thought to be the most effective HGs within the Caribbean. Unlike other herbivorous fish, Scaridae show no preference for particular types of algae, consume the entire algal stratum, and expose bare reef surfaces, promoting settlement of a wide variety of benthic organisms. Research has indicated that Scaridae are overfished and declining in population, while concurrently, percent cover of macro algae has increased across the Caribbean. In response, in 2009, Belize enacted legislation to ban the harvest of Scaridae. To evaluate whether this legislation has been effective, we utilized citizen science data (provided by REEF.org), to compare the density and sighting frequency of four species of parrotfish in four zones throughout the waters of Belize. Two common concerns with citizen science data are reliability and validity. To increase our confidence in the data, we compared data recorded by novice and expert observers for the given zone and found similar patterns in most instances. This gave us cautious optimism to use the full data set to assess changes in parrotfish density and sighting frequency in different regions of Belize before and after the enactment of the fishing ban.

Key Terms: Coral reef ecology
 Citizen science
 Parrotfish

STUDENT POSTER ABSTRACTS

UG-EEB-298

Scleral Ossicles in Reptilia: Structures Correlated to Taxonomic Diversity

Kevin Wanniarachchi Kankanamalage (State University of New York at Oswego)
Advisor: Poongodi Geetha-Loganathan (State University of New York at Oswego)

Scleral Ossicles (SO) are plates of dermal bones that provide stability and protection to the optic system in many vertebrates, whose morphology, anatomy, development and patterning differ in distinct groups of vertebrates. Although several studies have examined various aspects of SO in vertebrates, to date, comprehensive analysis of scleral ossicle ring for the class reptilia has not been provided. Here, we present a surface and internal morphology of SO in the following family belonging to class reptilia: Agamidae, Chamaeleonidae, Varanidae, Iguanidae, Scincidae, Emydidae, Gekkonidae, Ananidae and, Phasianidae were imaged using Scanning Electron Microscope (SEM). The objective of this study is to examine and compare the number, overlay patterns, shape and arrangement of each individual ossicle in the sclerotic ring. Further we also summarize the phylogenetic relationship of these reptilian families analyzed with reference to SO anatomy. The significance of this study is to understand the homology of SO among reptiles and we propose, based on our analysis on SO that the members of the class reptilia exhibit evolutionary conservatism of the scleral ring structure.

Key Terms: Developmental biology
 Reptiles
 Scleral ossicles

UG-EEB-300

Genetic Exploration of Invertebrate Diversity in Great Salt Lake

Oscar Bedolla (Weber State University)
Advisor: Jonathan Clark (Weber State University)

Great Salt Lake (GSL), in northern Utah, is the largest salt-water lake in the Western Hemisphere, with a total surface area of 4400 square kilometers. Great Salt Lake is the center of one of the world's most important migratory bird habitats, supporting an estimated population of over 7 million individuals. The ecology of GSL is influenced by three invertebrates: brine flies, the brine shrimp, *Artemia franciscana*, and the bug, *Trichocorixa*. There are no published studies on the distribution or identification of other invertebrates in the GSL ecosystem. DNA barcoding has become the international recognized standard for species identification and uses universal DNA sequence comparisons to differentiate species on the basis of genetics. The DNA barcode database includes information from thousands of samples from ecosystems around the world. This study examines the *cytochrome c oxidase* gene to establish DNA barcodes for samples of invertebrates associated with the GSL ecosystem. Data on interspecific and intraspecific sequence variation are considered and sequences are used to examine local species phylogenies. The results of this study can be compared to those from other saline environments to provide insights into the distribution of invertebrates in these important and underappreciated ecosystems.

Key Terms: DNA barcoding
 Ecology
 Phylogeny

STUDENT POSTER ABSTRACTS

UG-EEB-301

Tendencies of Gastropod Drillhole Predation on Infaunal Bivalves Across Different Latitudes in Argentina

Jesse Saldana Arias (Georgia State University-Perimeter College), Christy C. Visaggi (Georgia State University), Patricia Kelley (University of North Carolina Wilmington), Danielle Perez (Georgia State University)
Advisor: Christy C. Visaggi (Georgia State University)

The fossil record of naticid gastropod predation can be used to study the history of predator-prey relationships. However, availability of modern assemblages allows for an examination of latitudinal variation in drilling predation. Work by Visaggi & Kelley (2015) in South America found that drilling frequencies (DF) increased equatorward across Brazil (6°S-34°S). It was unknown whether DF continues to decline to the south moving poleward. This project helped clarify that question by extending the research into Argentina. Drilling predation on infaunal bivalves was recorded across the coastline from 36°S-52°S. Over 5,000 infaunal bivalves were studied from samples collected on beaches in 2010. Specimens were checked for whole vs. fragmented shells and nearly 3,500 “whole” (>85% of the valve intact) shells were analyzed for evidence of drillholes by naticid gastropods. Data collected on whole valves were used to calculate DF (= #drillholes/half of all valves). DFs fluctuated depending on the localities examined. There was an overall ~12% DF for the Argentinean Province to the north and ~6% DF for the Magellanic Province to the south. Taxa drilled across Argentina included *Amiantis*, *Clausinella*, *Glycymeris*, *Mactra*, and *Protothaca*. Broadly speaking, DFs were higher in lower latitudes and lower in higher latitudes for this stretch of coastline. Future work will include analyzing potential factors that may influence this pattern such as variations in the substrate from where samples were collected (as related to the suitability of these habitats for naticid gastropods).

Key Terms: Predator-prey
Marine biology
Latitudinal trends

UG-EEB-302

The Effect of Antagonistic Coevolution on Cyanophage Fitness and Host Range

Jonathan Abebe (University of California, Irvine), Richard Puxty (University of California, Irvine)
Advisor: Jennifer Martiny (University of California, Irvine)

Marine cyanobacteria are primary producers that use sunlight to convert carbon dioxide into organic compounds. Cyanophages infect and lyse cyanobacteria and are thus important players in ecosystem cycling. However, rapid coevolution influences the interactions between cyanophage and their host bacteria and therefore the dynamics of these populations. We hypothesized that coevolution will lead to a tradeoff between host range and fitness in the phage such that as a coevolved phage's host range broadens, its fitness on the ancestral host would decrease. To address this hypothesis, we performed a coevolution experiment in the lab. A cyanophage and its susceptible host were cultured together, being transferred to new media every week for 19 weeks. As a control, we also transferred a phage culture onto the original ancestral host every week. To determine the difference in fitness between the two treatments, we measured plaque size (a composite measure of how fast the phages adsorb to its host, the time it takes to lyse the cell, and burst size). Host range (the breadth of infection on a range of host bacteria) was assessed by counting how many different hosts each phage was able to lyse. Phage isolates from the coevolution treatment produced significantly smaller plaques than the control treatment (2.2 mm versus 3.4 mm). Thus, coevolution led to a fitness cost in the phage. However, this cost was not correlated with host range as expected. Phage isolates from the coevolution treatment infected a narrower range of hosts as compared to isolates from the control (28% versus 40%).

Key Terms: Bacteriophages
Microbial diversity
Virus-Host interaction

STUDENT POSTER ABSTRACTS

UG-EEB-303

Foraging Efficiency and Learning in Capuchin Monkeys (*Cebus capucinus*)

Daniel Herrera (Augustana College)

Advisors: Grace Davis (University of California, Davis), Stephanie Fuhr (Augustana College)

Primates have relatively large brain to body ratios and spend a substantial period of their life in the juvenile development stage. Large brains suggest long juvenile stage, hypothesizing that primates require long juvenile periods to learn complicated foraging techniques. Critics of this hypotheses argue that foraging efficiency increases primarily as a function of increased muscle mass, not learning. We set out to determine if the juvenile period is in fact used to learn complicated foraging techniques by examining food preferencing behavior in white faced capuchin monkeys (*Cebus capucinus*). Individuals of varying ages were observed as they selected fruits from attalea palm trees (*attalea butyracea*). Learning was tested by counting the number of times each individual touched, bit, or dropped individual fruits before eating them. We found that individuals tested fruits less as they aged, indicating that individuals learned how to distinguish a desirable fruit from a non-desirable fruit over time. These results support the previously stated hypothesis and justify the long juvenile period in primates, offering insight to the evolutionary drivers of primate ecology.

Key Terms: Learning
 Foraging efficiency
 Primate

UG-EEB-304

Role of Microbial Communities in the Filtration and Digestion of Microflush Toilet Effluent

Claire Kleinschmidt (Providence College)

Advisors: Laura Williams (Providence College), Stephen Mecca (Providence College)

Throughout the developing world, a lack of sanitation negatively affects the water supply and health of rural communities. The Microflush toilet is a sustainable sanitation solution that separates liquid and solid effluent. Liquid effluent is filtered to remove microbes and solid effluent is digested by earthworms. We analyzed the composition and structure of the microbial communities within the liquid and solid toilet effluent to better understand the bacterial contribution to waste processing and the pathogens present. Solid samples were taken at 0, 4, 10, 15, and 30 days into the digestion process. Three liquid samples were collected: raw outflow, following Solar Disinfection (SOLDIS), and following Slow Sand Filter (SSF) processing. To determine bacteria present in our samples, we extracted genomic DNA and sequenced 16S rRNA amplicons using the Illumina MiSeq System. We used mothur to identify and classify operational taxonomic units (OTUs), or sequences that are 97-100% identical. In our negative controls, we detected <1123 sequences. We detected >115,835 sequences in each solid sample and the most common OTUs were *Chitinophagaceae*, *Algoriphagus*, *Bacteroides*, and *Ohtaekwangia*. In the liquid samples, we detected >106,154 sequences and the most common OTUs were *Rhodobacteraceae*, *Bacteroidetes*, *Flavobacterium*, and *Hyphomonas*. We are currently conducting alpha and beta diversity tests to further analyze the microbial communities over time and as a result of various filtering methods.

Key Terms: Microbiology
 Microbiome
 Bioengineering

STUDENT POSTER ABSTRACTS

UG-EEB-305

Defining Germination Tolerance Ranges for Three Milkweeds (*Asclepias spp.*)

Victoria Lason (Augustana College), Jessamine Finch (Northwestern University)

Advisor: Jessamine Finch (Northwestern University)

Our changing climate is growing as a major variable in plant science as it may have a marked impact upon early life stages of plants including germination and seedling establishment. Both of which have recently been identified as a large potential bottleneck to plant recruitment under climate change, as seedlings will be more sensitive than mature individuals. As an important source of nectar for pollinators, and the obligate host plant for monarch butterflies, three species of milkweed were chosen to forecast species responses to heightened temperatures. Seeds from 9 populations of each species were collected along a latitudinal gradient. Lab-based germination trials occurred in two light and temperature controlled incubators for a period of 32 days at 25/15°F, and for 36 days at 15/5°. After the incubation trials, viability tests were conducted upon non-germinated samples to check for dead or dormant seeds. Our results identified significant differences in milkweed germination among species, populations and regions, in response to simulated winter length and spring temperature changes throughout the Midwest U.S. These findings have the potential to inform best practices in seed sourcing for restoration. Implementing optimal milkweed ecotypes decreases management time and cost, two major limiting factors in restoration.

Key Terms: Seed ecology
 Reproductive biology
 Botany

UG-EEB-306

Analysis of COI Gene Used for DNA Barcoding of Cave Crickets

Francine Francis (SUNY Plattsburgh)

Advisor: Nancy Elwess (SUNY Plattsburgh)

The cytochrome c oxidase subunit I (COI) is one of 37 genes found in the mitochondria. This has been shown to be an ideal gene used for DNA barcoding: the gene codes for an essential protein present in most eukaryotes that is highly conserved across species. Each cell contains 1-1000 copies of the mitochondrial DNA and the rate of gene sequence change is slow enough to show evolutionary history, while fast enough to allow for the differentiation of species. This gene was used to DNA barcode 12 cave cricket eggs found in the Great Onyx cave in the Mammoth Cave National Park. The species has been identified as *Hadenoeus subterraneus*, but they have never been identified using DNA analysis. It is hypothesized that analyzing crickets from geographically-distant caves would yield greater genetic diversity than crickets from closer caves. If the margin of difference is greater than four percent between samples of *Hadenoeus cumberlandicus* collected over the Mammoth Cave National Park, then there may be sufficient evidence to identify a new species. Using DNeasy Blood and Tissue kit as well as QIAquick Gel Extraction kit, the DNA was isolated for the COI gene. The sequences were evaluated using Bioinformatics Protocol.

Key Terms: DNA barcoding
 Cave crickets
 Bioinformatics

STUDENT POSTER ABSTRACTS

UG-EEB-307

Socioeconomic Determinants of Health

Nicholas Malizia (College of Mount Saint Vincent),
Marielle Villanobos (College of Mount Saint Vincent),
Gabirella Mendoza (College of Mount Saint Vincent)
Advisors: Ioanna Visviki (College of Mount Saint
Vincent), Amir Niknejad (College of Mount Saint
Vincent)

Life course epidemiology attempts to identify the biological and social factors, which operate during gestation, childhood, adolescence and adulthood that increase chronic disease susceptibility and affect longevity. In this study, we examined the effects of four socioeconomic factors on the survivorship of a 19th century U.S. population of Irish descent. We selected two conditions from infancy (country of birth), and childhood (education), and two from adulthood (profession and service index). We collected data on 1,480 women that were born during the 19th century and were lifelong members of the Sisters of Charity of New York, a socially active, Catholic congregation. We constructed Kaplan-Meier survival curves using SPSS for the following factors: country of birth, educational level, profession, and service index (years of religious life divided by the number of missions). Contrary to expectations, there was no statistically significant difference in survivorship between women born in the U.S. compared to the first generation Irish immigrants. Educational level and service index, likewise, did not affect survivorship. Profession was the only factor examined that had a statistically significant effect, with teachers experiencing higher longevity than nurses. We attribute our results to the benefits of communal living, which could have protected this population from the adverse effects of socioeconomic factors associated with decreased survivorship in previous studies.

Key Terms: Health
Longevity
Survivorship

UG-EEB-309

Detection of Freshwater Turtle Species Using Environmental DNA

Christopher Smith (SUNY Plattsburgh)
Advisor: Nancy Elwess (SUNY Plattsburgh)

Environmental DNA (eDNA) has recently become a new method to monitor the biodiversity of species within aquatic and terrestrial environments. eDNA can be defined as genetic material left behind from a species, which can be sampled directly from the environment without the physical presence of the biological species. Some scientists have used eDNA from aquatic environments as a method to reduce the cost of detection and for detection of rare species in an environment. The purpose of this study was to test freshwater eDNA to in order determine if turtle eDNA can be successfully detected from various samples of ponds and streams in the region of the Lake Champlain Basin. The freshwater eDNA was tested using conventional polymerase chain reaction (PCR). Exact species was determined through DNA sequencing methods as a mean to detect biological species within the ponds and streams. After the detection of the turtle presence, the speciation of the turtles was also determined within the Lake Champlain Basin. With this, further studies can be conducted to potentially observe the distribution of turtle species in the Lake Champlain Basin.

Key Terms: Ecology and evolutionary biology
eDNA
Biodiversity

STUDENT POSTER ABSTRACTS

UG-EEB-310

Survey of Two Pathogens in Introduced Frogs on Hawaii

Joseph Tyler (Hampden-Sydney College), Dakota Reinartz (Hampden-Sydney College), Rachel Goodman (Hampden-Sydney College), Amber Wright (University of Hawaii at Manoa)

Advisor: Rachel Goodman (Hampden-Sydney College)

Biodiversity is declining worldwide and emerging pathogens are one of the factors causing the decline. Two such pathogens affecting amphibians (and other ectotherms) include *Ranavirus* and *Batrachochytrium dendrobatidis* (Bd), which are known to cause disease and die-offs in amphibians. We surveyed five amphibian species (*Bufo marinus*, *Dendrobates auratus*, *Eleutherodactylus planirostris*, *Rana catesbeiana*, and *Rana rugosa*) in various life stages (tadpoles, metamorphs, and adults) from Oahu, Hawaii for the presence of these two pathogens. Frogs were collected from various areas on the island (Figure 1; Table 1). The intestines, liver, and kidneys were harvested for *Ranavirus* testing and skins swabs were taken for Bd testing and qPCR was conducted to test for the presence of the two pathogens, respectively. 328 frogs were sampled from the species previously mentioned and the *Ranavirus* qPCR was conducted with a stock FV3 ranavirus culture and negative control and the Bd qPCR was conducting using a set of standards extracted from a zoospore stock. No *Ranavirus* was detected in the samples; however, three samples tested positive for Bd. The three positive samples were all located surrounding the James Campbell National Wildlife Reserve, indicating a small, isolated presence of the pathogen on the Hawaii; however, the threat of the two pathogens to have more prevalence on the island – seeing that few studies have occurred regarding the prevalence of *Ranavirus* or Bd on the island – still remains.

Key Terms: *Ranavirus*
 Batrochochytrium dendrobatidis
 Hawaii

UG-EEB-311

An Initial Survey of Terrestrial Tardigrades around Unity College, Maine

Jeanette Gray (Unity College)
Advisor: Emma S. Perry (Unity College)

Maine is the easternmost state in the United States with an extensive tidal coastline, vast forests, and numerous small islands. Although the first tardigrade in North America was found in Maine, only one other paper has documented terrestrial tardigrades in Maine.

The town of Unity is a small town in Waldo County, Maine. It encompasses 41.36mi² of the 853mi² that makes up Waldo County. Much of the county is covered in a hemlock-pine forest. Samples of understory leaf litter were taken from forests around Unity College, Maine.

In total 72 samples of leaf litter were collected. From these samples 626 tardigrades of at least twelve species have been found, several are new records for Maine. These tardigrades were examined using brightfield, phase contrast, Nomarski differential interference contrast and autofluorescence microscopy to aid in their identification.

Key Terms: Tardigrade
 Biodiversity
 Leaf litter

STUDENT POSTER ABSTRACTS

GR-EEB-318

Functional Response and Self-Superparasitism in the Parasitoid Wasp *Cotesia rubecula*

Dhaval Vyas (Colorado State University), Ryan Paul (Colorado State University), Paul Ode (Colorado State University)

Advisor: Paul Ode (Colorado State University)

The number of hosts in a patch influences the rate of attack and host-use strategy of parasitoid insects. This study determined the functional response of the parasitoid wasp, *Cotesia rubecula*, to different densities of its host, the imported cabbageworm butterfly (*Pieris rapae*). Individual female wasps were exposed to one, two, four and eight hosts in a large cage. Each female experienced either an increasing pattern of host densities (1, 2, 4 and 8 hosts) or a decreasing pattern of host densities (8, 4, 2 and 1). A type III functional response was observed for both increasing and decreasing host density patterns. The maximum proportion of hosts parasitized (88%) occurred at the host density of two hosts. Self-superparasitism (multiple attacks per host) was highest (56% of hosts) at the density of two hosts and self-superparasitism occurred even at the density of eight hosts (42% of hosts). A second experiment showed that the mean (\pm SE) clutch size for a single attack was 0.96 (\pm 0.004) eggs, confirming that multiple eggs in a single host were from self-superparasitism. The mean number of eggs for double (1.40 \pm 0.05) and triple (1.60 \pm 0.10) attacks per host showed that females failed to lay an egg during each attack. The type III functional response suggests that at lower host densities, *C. rubecula* has a density dependent response. Self-superparasitism appears to be common, but females seem to limit the number of eggs invested during multiple attacks on the same host.

Key Terms: Animal behavior
 Ecology
 Entomology

GR-EEB-319

Categorization and Effectiveness of Protected Areas: Comparative study of small mammal communities in Nahuel-Huapi National Park, Argentina

Maria Daniela Rivarola (University of Tennessee), Daniel Simberloff (University of Tennessee)

Advisor: Daniel Simberloff (University of Tennessee)

The increment of Protected Areas (PA) at global scale during the second half of the 20th century reflects the growing concern of preserving lands, facing the biodiversity and habitat loss. However, in most cases, there is no clear evidence of the PA effectiveness. Nahuel Huapi National Park is the first and biggest Argentinean PA (750,000 ha); it hosts few big and medium size mammals' species, however, the number and diversity of small mammals equals those found in temperate forest elsewhere. Our goal was to evaluate the conservation status of the small mammals communities in the Nahuel Huapi protection system, accounting for direct and indirect human intervention. In order to achieve this goal, five plots of 60x60 m were established in each level of protection (Strict Natural Reserve, National Park, National Reserve, outside PA), setting 50 traps per plot, over four consecutive nights monthly. Capture effort was 20,600 traps/day. Each individual was identified, marked and released, resulting in 727 individuals (*Abrothrix hirta*, *A. olivacea*, *Oligoryzomys longicaudatus*, *Geoxus valdivianus*, *Chelemys macronix*, *Irenomys tarsalis*, *Loxodontomys micropus* y *Dromiciops gliroides*). Species richness, Shannon-Wiener diversity-index, and abundance were compared by ANOVA, finding only statistical difference for *Loxodontomys micropus* abundance. However, three species were scarcely found; furthermore the unequal distribution of records requires a deeper track in order to elucidate the role that the presence or absence of the PA would be fulfilling in the conservation of these communities.

Key Terms: Conservation
 Small mammals
 Protected areas effectiveness

STUDENT POSTER ABSTRACTS

GR-EEB-320

Cryptic Female Mate Choice and Sperm Competition as Mediated by Sigma Virus in *Drosophila melanogaster*

Meghan Bentz (University of Florida), Marta Wayne (University of Florida)

Advisor: Marta Wayne (University of Florida)

Host-parasite interactions are driven by a competition for resources, during which the pathogen can manipulate host behavior to increase its own fitness. The effect of viral manipulation on host populations can be seen in the model system of *Drosophila melanogaster* and *Drosophila sigma virus* (DMelSV). Despite reproductive costs to the female host, the virus is able to persist in wild *Drosophila* populations via biparental vertical transmission, creating an opportunity for the virus to be a third player in sexual conflict. In this study we experimentally evaluated the effect of DMelSV on cryptic female choice (here, internal selection by the female of which sperm to store, eject, and/or use in fertilization). We also studied whether or not DMelSV infected sperm are better competitors than their uninfected counterparts. We competed uninfected male flies with red fluorescent sperm against DMelSV-infected males with green fluorescent sperm to explore the possibility of differential sperm storage based on infection status. On examining the dissected females' sperm storage organs, there is evidence of second male precedence. In contrast, when looking at the offspring actually produced, there was an overwhelming majority of uninfected offspring produced regardless of mating order, consistent with cryptic female choice. In an answer to the question of which member of the reproductive arms race (male, female, or virus) has the most marked effect on the outcome of reproduction, we have found that to be the female host. While viral manipulation may be occurring at the sperm level, in the end cryptic female choice overrides this advantage when the offspring are produced. If we can learn the mechanism by which female choice aids/hinders vertically transmitted viruses we can potentially manipulate that choice to decrease disease reservoirs.

Key Terms: *Drosophila melanogaster*
Virus evolution
Cryptic female choice

GR-EEB-321

The Effects of Obstacle Placement on Bipedalism in Lizards

Chase Kinsey (Georgia Southern University), Lance McBrayer (Georgia Southern University)
Advisor: Lance McBrayer (Georgia Southern University)

Bipedal locomotion has evolved independently in numerous lizard taxa. Initial acceleration, trunk angle, and the posterior shift of the center of mass contribute significantly to bipedal running. Recent work indicates that bipedal posture is advantageous during obstacle negotiation. However, the effects of obstacle placement on the use of bipedal locomotion has yet to be explored in detail. Whether a lizard runs bipedally solely from increased acceleration (passive bipedalism) or as an applied strategy for navigating obstacles (active bipedalism) is poorly understood. This study quantified the frequency of bipedalism when running with vs. without an obstacle at 0.8 meters from initiating a sprint. Whether bipedal posture is used at the start of a sprint vs. in the stride preceding the obstacle was also quantified. Two species with contrasting body forms were selected (*Sceloporus woodi*, *Aspidoscelis sexlineata*) to assess potential variation in behavioral patterns. Lizards were coerced to run along a 1.4-meter track and filmed with high speed video. *Sceloporus woodi* ran bipedally at the start of the trial in 77.78% of the trials, regardless of obstacle presence. In the strides approaching an obstacle *S. woodi* ran bipedally in 72.73% of trials. *Aspidoscelis sexlineata* ran bipedally at the start of a trial in 50% of trials regardless of obstacle presence. In strides just prior to the obstacle, *A. sexlineata* ran bipedally in all trials. The frequency of bipedalism varies between these two species despite living in similar habitats. Passive bipedalism is less prevalent in *A. sexlineata* than *S. woodi*. Thus, bipedalism may be an active strategy for negotiating obstacles in *A. sexlineata*.

Key Terms: Bipedal locomotion
Biomechanics
Ecology

STUDENT POSTER ABSTRACTS

HS-ENG-361

Assessment of Capacity Degradation and RUL of Flexible Batteries in Wearable Electronics

Rahul Lall (Auburn High School)

Wearable electronics are finding new applications in everyday life. Future adoption of wearable electronics into applications such as medical diagnostics, identity protection, and asset situational awareness requires the development of form factors which are seamlessly integrated into wearable garments and on the surface of skin. Flexible wearable electronics are subjected to a greater deal of mechanical and environmental stresses while attempting to maintain functionality. Wearable applications need thin and flexible form factors for the energy storage to drive sensing, displays, control, and processing. Energy storage of these wearable applications most likely requires the ability to sustain use and recharge cycles. In this paper, the state of art flexible battery technologies commercially available have been studied for their survivability under exposure to environmental loads typical of wearable electronics applications (bending). The charging and discharging cycles were performed on the flexible battery with a custom designed test station. The test station included a linear actuator setup (programmable electronic load), microprocessor, and a data logger. All hardware was controlled using LabVIEW. Additionally, a method for prognosticating the capacity degradation and remaining useful life has been developed using Extended Kalman Filtering (EKF). It is expected that the developed system will expedite the use of flexible electronics and broaden their applications.

Key Terms: Biomedical engineering
 Mechanical engineering
 Electronics reliability

HS-ENG-362

A Survey of Energy-Efficient Techniques for 5G Networks and Challenges Ahead

Elise Mochizuki (Jericho High School), Vincent Poor (Princeton University/School of Engineering and Applied Science)

Without prominent consideration of energy efficiency, the advance beyond 3G and 4G wireless networks to 5G will be challenged by an energy crunch due to increased usage of new services and applications. Associations already announced goals for a 1,000-times energy efficiency improvement and a >40% reduction in CO₂ emissions. Four techniques to increase the energy efficiency of wireless networks were surveyed. First, resource allocation seeks to utilize new mathematical tools to maximize the energy efficiency in exchange for a moderate reduction to energy throughput, where the emphasis would shift from the maximum to the reliable amount of information transmitted. Second, network planning and deployment seek to deploy infrastructure nodes to maximize the covered area per consumed energy, not the covered area alone. Third, energy harvesting and transfer seek to increase the use of renewable and clean energy sources from the environment despite their random availability, and to recycle the energy from the radio signals over the air. Fourth, hardware solutions seek to design hardware with decreased energy consumption, and to adopt architectural changes. Approaches include different designs of power amplifiers to reduce the peak-to-average-power ratio, as well as cloud-based implementation of the radio access network (cloud RAN or C-RAN) to decrease the functions performed in the base station (BS). These survey results suggest all four techniques contain robust and promising approaches supported by the academic literature, but that regulatory, policy, and economic issues present challenges to successful implementation of any of these techniques to eventually result in sufficient energy efficiency.

Key Terms: Energy efficiency
 5G
 Wireless power transfer

UG-ENG-372

Optimizing MMP7 Degradable Hydrogels for Cartilage Tissue Engineering

Marlen Tagle Rodriguez (University of California, Irvine)

Advisors: Stephanie Bryant (University of Colorado at Boulder), Elizabeth Aisenbrey (University of Colorado at Boulder)

Osteoarthritis is the most common chronic condition of the joints in which cartilage breaks down due to injury, overuse or bone misalignment. It debilitates patients because of the pain, inflammation, and swelling around the affected area. Advanced therapies involve cartilage tissue engineering in which cartilage tissue is derived from the patient and is used to replace the damaged cartilage. However, this approach is oftentimes unsuccessful due to aging and patient-to-patient variability. Photopolymerizable poly(ethylene glycol) hydrogels are used to address this challenge because they can recapitulate the complex microenvironment of cartilage tissue and can also be tuned to degrade at the rate needed by the patient's cells. These hydrogels provide a solid foundation for human mesenchymal stem cells (hMSCs) to grow and deposit their own extracellular matrix as they differentiate into chondrocytes. However, it is imperative that the hydrogel is tuned to degrade at a rate that matches matrix deposition of the cells to allow space for the cells to integrate into cartilage tissue. This research proposes an enzymatically degradable hydrogel consisting of a degradable peptide crosslinker specific to matrix metalloproteinase (MMP7) which is associated with chondrogenic differentiation and cartilage remodeling. This allows for the gradual degradation of the hydrogel as the hMSCs differentiate into chondrocytes and should allow the cells the support and time needed for matrix deposition and tissue integration. Results demonstrate that MMP7 hydrogels degrade too quickly. Therefore an additional peptide crosslinker that degrades late in chondrogenesis will be added in future studies to fine-tune the degradation process.

Key Terms: Tissue engineering
 Biomaterials
 Osteoarthritis

UG-ENG-373

A Novel Computational Model of a Total Knee Replacement Implant with Synthetic Ligaments

Taylor Gambon (Clemson University), Michael Stokes (Clemson University), Luke Pietrykowski (Clemson University), Brendan Greene (Clemson University)
Advisor: John DesJardins (Clemson University)

The use of synthetic ligaments has been suggested as a means to offer enhanced total knee replacement (TKR) stability while also maintaining active ranges of motion. However, the placement of the origin and insertion points for such synthetic anterior cruciate and posterior cruciate ligaments could have a significant impact on the stability and range of motion of the implant. A computational model of both an anterior drawer test and induced knee flexion was created using AnyBody Modeling System to explore the incorporation of synthetic cruciate ligaments into a TKR. The model also served to optimize the position and length of the synthetic ligaments with respect to TKR stability. In general, as ACL and PCL lengths increased, the A/P laxity of the TKR system increased linearly. Range of motion was found to be more dependent on ligament attachment location, and laxity was more dependent on ligament length. As ACL insertion location on the femur moved posteriorly, ACL ligament strain decreased during flexion, enabling a higher range of flexion. In this work, TKR stability was clearly affected by changes in synthetic ligament length and location. The TKR design and geometry implicitly contributed to the strains seen in the ligaments, and as such, the results of this work are specific to the TKR design used in this study. By examining the possibility of incorporating ligaments into a TKR system, we have shown that the stability of a TKR system can be increased while maintaining the intended flexion range of motion.

Key Terms: Bioengineering
 Computational modeling
 Knee

STUDENT POSTER ABSTRACTS

UG-ENG-374

Predicting Left Ventricular Assist Device (LVAD) Performance With Human Circulatory System Model

Hieu Nguyen (Trinity College)
Advisor: Joseph Palladino (Trinity College)

LVADs are widely used to provide supplemental pumping in heart failure patients. The LVAD's impeller rotational speed is one of the leading causes of complications and hospital readmission in heart failure patients. Fast speeds might cause blood cell destruction, while slow speeds might not meet the body's cardiac demand, which varies greatly throughout the day. This study modeled the pressure-flow relation for different impeller speeds for each of four different continuous flow LVADs: the Jarvik 2000, the HVAD, the Heartmate II, and the Heart Assist 5. The pressure-flow-impeller performance data were available from the literature. These data were used to create a flow and impeller speed dependent pressure generator. This LVAD model was then coupled in parallel with the left ventricle in a closed-loop model of the human circulatory system (Palladino et al., 2000). The model was formulated as a set of nonlinear, time-dependent differential equations, which were solved numerically using MATLAB. The model permits computation of volumes, pressures, and flows at multiple sites along the circulatory system. In particular, left ventricular output, in the form of cardiac output and ejection fraction, was studied at various LVAD impeller speeds. Pressures and volumes were plotted to facilitate quantitative comparison, particularly as pressure-volume work loops. Preliminary results suggest the impeller speeds necessary for each of the four LVADs to restore cardiac function in the disease state to healthy function. This LVAD-human circulatory system model could assist VAD clinical teams in noninvasively determining the necessary impeller speeds for heart failure patients.

Key Terms: Biomedical engineering
 Cardiovascular
 Mathematical model

GR-ENG-383

Influence of Electrode Design Parameters on the Performance of a Lithium Ion Battery

Meng Xu (Oakland University), Xia Wang (Oakland University)
Advisor: Xia Wang (Oakland University)

The design parameters of electrodes materials such as electrode thickness and porosity usually play an important role in the electrochemical behavior of a lithium ion battery. For instance, increasing the thickness of the active electrode would offer higher energy for a battery cell with fixed geometrical dimensions. However, the thicker electrode tends to lengthen the path for lithium ions to diffuse in the electrolyte, which results in poor rate capability and therefore low power performances. The objective of this research is to study the influence of battery design parameters on the battery performance by developing a one-dimensional electrochemical isothermal model at the cell level. In this model, the composite electrode properties, such as tortuosity and the effective diffusion coefficient were characterized for cells with various electrode thicknesses and porosities. The discharge capacity and rate capability were validated by experimental data from corresponding battery testing samples. The electrode thickness study was conducted with the same porosity and the same particle size. It has been found that the cell discharge capacity faded more when the thickness of positive electrode increases from 45 μ m to 70 μ m at the same discharge rate (2C), which is consistent with the experimental results. This research reveals the effects of design parameters of a Li-ion battery electrode on the battery capacity and rate capability, which are very useful for battery modeling and design.

Key Terms: Lithium ion battery
 Design parameters
 Modeling

STUDENT POSTER ABSTRACTS

UG-ENV-412

The Effects of Carbamazepine and Caffeine on Juvenile Fathead Minnow Swimming Behavior

Caitlyn Patullo (Ithaca College)

Advisor: Dr. Susan Allen-Gil (Ithaca College)

Pharmaceuticals and personal care products have become increasingly popular subjects of toxicological studies due to concerns regarding their potential effects on aquatic ecosystems. Pharmaceuticals pose a major threat due to the fact that wastewater treatment methods have been ineffective in filtering many of them out. Studies have shown that certain pharmaceuticals can impact behaviors such as reproduction, predator avoidance, and food acquisition at concentrations found in effluent wastewater. This study focuses on the behavioral effects of caffeine and carbamazepine on juvenile fathead minnows (*Pimephales promelas*). Caffeine is a well-known central nervous system stimulant. Fathead minnows were exposed to four sublethal concentrations of caffeine: 0.04 µg/L, 9.5 µg/L, 35 µg/L, and 50 mg/L. The first three concentrations were selected by environmental relevance in Ithaca and on the East Coast, and the final concentration was selected as a positive control. Carbamazepine is an anticonvulsant and analgesic that treats seizures, nerve pain, and even bipolar disorder. For this set of experiments, fathead minnows were exposed to four environmentally relevant concentrations: 0.34 µg/L, 2.00 µg/L, 11.5 µg/L, and 1.00 mg/L. We used two experimental designs in this research: one to quantify changes in shelter preference and a second to quantify swimming behavior changes directly through calculating total distance traveled and average velocity. The results of our study to date have indicated no significant change in behavior for either caffeine or carbamazepine at environmentally relevant concentrations; however we have observed notable trends as the dose of carbamazepine increases.

Key Terms: Toxicology
 Hydrology
 Pharmacology

UG-ENV-413

Examining American Propagation of Downy and Powdery Mildew Resistance in *Humulus lupulus*

John Nichols (Hampden-Sydney College), Gannon Griffin (Hampden-Sydney College)

Advisor: Michael Wolyniak (Hampden-Sydney College)

Although a largely commercial crop, there is not much research on the resistance factors of hops. There is large commercial need for such research. In 1999 and 2000, powdery mildew is estimated to have cost hop growers over \$30 million, or 15% of the total crop revenue. Additionally, there is great need for hops research in the American Southeast, as most research has been conducted in the Pacific Northwest. The objectives of this study were: 1) To find the best way to propagate hops plants in Virginia 2) To evaluate hops for resistance to downy and powdery mildew 3) To identify resistance genes within hops strains 4) To establish a method to grow downy and powdery mildew and a controlled environment 5) To establish a hops repository for future research at Hampden-Sydney College.

Key Terms: Botany
 Genetics
 Biology

HS-GSC-431

Geochemical Extraction of Ceratopsian Remains and Opals from Ironstone

Emily Cross (Hammar skjold High School)
Advisors: Clarence Surette (Lakehead University),
Donald Henderson (Royal Tyrrell Museum)

New prehistoric species, ancient hominid bones, potential martian astro-microbiology, and a wealth of soft tissues representing important evolutionary information are among significant specimens trapped within ironstone. Existing mechanical extraction remains time-consuming and causes substantial damage. Little research exists on non-destructive specimen extraction from ironstone. Experimentation generated chemical treatments for ironstone samples containing fossils and opals which removed the stone matrix in a time and resource efficient manner without damaging specimen inclusions. More than 168 samples were exposed to hydrogen peroxide, hydrochloric acid, carbonic acid, sodium hydroxide, and sodium bicarbonate. Changes to samples were assessed using Moh's Hardness, weight, scanning electron microscopy and partial energy-dispersive x-ray spectroscopy. Significant discoveries which maintain targeted specimen quality include four inclusion-specific processes for removing ironstone from fossils or gemstones. Hydrogen peroxide quickly reduces ironstone, but damages soft tissue and minimally affects fossilized bone. Hydrochloric acid is the most effective treatment for opal removal, but destroys fossils and soft tissue. Carbonic acid is the best balance of ironstone removal and preservation of fossilized bone or soft tissue. Sodium hydroxide is moderately effective for fossilized bone and opal removal, but damages soft tissue. The results are highly relevant to many researchers worldwide. These ironstone removal methods provide new, highly effective tools for accessing fossil specimens, potentially closing significant gaps in evolutionary knowledge. Furthermore, application of these processes has potential to drastically improve mining yields and efficiency in the soft gemstone mining industry.

Key Terms: Paleontology
Geochemistry
Geology

GR-MCS-453

Fast Statistical Approximations of Computationally Intensive Finite Element Models

Meiqi Song (Oakland University)
Advisors: Aycil Cesmelioglu (Oakland University),
Dorin Drignei (Oakland University)

This presentation addresses a topic at the interface of applied mathematics, computing and statistics. It uses statistical methods to develop fast approximations of numerical solutions from computationally intensive solvers of differential equations. Accurate expression of the approximation error is an advantage over other methods. The new research, demonstrated on a case study, helps mathematicians to understand the dependence of the solution on unknown parameters. The presentation details the two-dimensional Darcy's equation with homogeneous Dirichlet boundary conditions, modeling the flow of a fluid through a porous medium such as sand or soil and depending on unknown permeability parameters. Its finite element numerical solution is based on the weak formulation and is obtained by solving a large linear system of equations, thus being computationally intensive. The finite element solver generated the numerical solution output data at a sample of permeability parameters. The resulting output data was used to develop the fast statistical approximation and its error, on a grid of new permeability parameters. The number of sampled parameters was increased sequentially from 10 to 30 to 50, and we observed that the approximation surface becomes smoother and more well-defined. In addition, when more points are available, the approximation becomes more accurate since the error surface becomes flatter and closer to zero. The results reveal a nonlinear dependence of the numerical solution on its permeability parameters, which will be characterized analytically and graphically.

Key Terms: Statistic
Applied mathematics
Computing

HS-PHA-466

Test of Rock Salt Model for Suppressed Gross Erosion of High-Temperature Lithium Under Fusion Reactor Conditions

Elise Mochizuki (Jericho High School), Robert Kaita (Princeton Plasma Physics Laboratory)

Plasma facing components (PFCs) protect the underlying walls in a tokamak from high temperatures and high particle fluxes ($>10^{23} \text{ m}^2 \text{ s}^{-1}$) as well as improve plasma performance. Although high-Z materials like tungsten are candidate PFCs, low-Z lithium coatings are increasingly under consideration as sacrificial layers, making important the characterization of the erosion rate of lithium coatings. Most experiments and simulations to date of the temperature limit for a liquid lithium wall only predicted values $<400^\circ\text{C}$, which is too low to be practical for fusion reactor applications. Recent experiments in the Magnum-PSI linear plasma device at reactor-relevant ion fluxes (10^{23} - $10^{24} \text{ m}^2 \text{ s}^{-1}$) and lithium surface temperatures ($\sim 800^\circ\text{C}$), however, indicated that the erosion rate was much lower than expected.^[1] The reason appears to be the formation of a mixed material consisting of both lithium and lithium hydride at the higher flux rates achieved in the Magnum-PSI experiments. This explanation is based on first-principles molecular dynamics (MD) calculations using only three variables: Ion flux, lithium temperature, and lithium thickness.^[2] At high flux rates, MD simulations predict the formation of lithium hydride when hydrogen bombards lithium. With increasing hydrogen flux, the lithium hydride forms a rock salt structure that changes the thermodynamic behavior of the lithium coating. An experiment can be performed with simple rock salt, where the evaporation rates of solutions with different concentrations can be compared as a function of temperature. ^[1] T. Abrams et al., Nucl. Fusion 56 (2016) 016022. ^[2] M. Chen et al., Nucl. Fusion 56 (2016) 016020.

Key Terms: Fusion reactor
 Lithium sputtering
 Ion implantation

UG-PHA-478

Bifrost: Astronomy Data Processing Pipelines Made Easy

Miles Cranmer (Harvard-Smithsonian Center for Astrophysics)

Advisor: Lincoln Greenhill (Harvard-Smithsonian Center for Astrophysics)

Bifrost is an astronomy software framework designed for rapid development of high-performance data processing pipelines, such as for imaging and analysis of telescope data. Bifrost is built on a portable C backend using an efficient ring buffer implementation to handle data flow, with seamless GPU and CPU interconnection, necessary for the computational intensity of modern data reduction. The astronomy community has many efficient analysis programs -- Bifrost serves to connect these algorithms together on a parallel, asynchronous execution model to quicken development of processing pipelines. Bifrost is currently being used to power two large radio interferometers, which require real-time data throughput exceeding 20 Gb/s per CPU.

Key Terms: Astronomical instrumentation
 Radio astronomy
 High performance computing

UG-PHA-479

Operation of a Photomultiplier for Improved Temperature Diagnostics in Non-Neutral Plasmas

Carlos Sierra (University of California, Berkeley)
Advisor: Carlos Sierra (University of California, Berkeley)

A silicon photomultiplier (SiPM) is a device capable of detecting light at the resolution of a single photoelectron. Its compact form, low voltage, low noise, and insensitivity to magnetic fields make it a useful tool for many physics experiments requiring fast and efficient detection of photons. One such experiment is that of the ALPHA collaboration located at CERN. The aim of the ALPHA experiment is to create and trap antihydrogen atoms by mixing positrons and antiprotons, and comparing the trapped antihydrogen to hydrogen through laser spectroscopy and other methods. To successfully confine antihydrogen, the temperature of the constituent non-neutral plasmas (electron, positron and antiproton) must first be very low. In an effort towards ensuring more accurate readings and thus a higher trapping rate, the SiPM's anode output, which corresponds to the total charge accumulated by the detector over a few microseconds, has been used to successfully obtain a temperature for plasmas confined in the ALPHA apparatus. Use of this method removes the necessity for high voltage signals and associated hardware, and improves the signal-to-noise ratio over the previous method used by ALPHA. Additionally, a separate technique that uses the SiPM's fast output to count the arrival rates of single photoelectrons is currently being developed, which could improve these temperature measurements further.

Key Terms: Plasma physics
Electrical engineering
Antimatter

UG-PHA-480

Enhancing Device Sensitivity of Graphene Field Effect Transistor DNA Biosensors via Single Layer Boron Nitride

Christopher Miller (University of North Carolina at Chapel Hill)

Advisors: Ramya Vishnubhotla (University of Pennsylvania), Alan T. Charlie Johnson (University of Pennsylvania)

When it comes to nanoscale devices, graphene continues to demonstrate its great potential as an ideal material for various nanostructures. This is in part due to graphene's physical and electrical properties, which include high electrical conductivity, sensitivity, and flexibility. As such, graphene proves to be useful for developing highly-sensitive sensors and electronics of various kinds. Here we present our progress on developing highly-sensitive graphene field-effect transistor (GFET) sensors capable of detecting single-stranded DNA sequences and providing electrical readouts from these sequences. Here we chose to examine the effects of adding monolayer BN to our GFET devices to improve our GFET device sensitivity and performance. Our devices made with a protective monolayer of BN deposited on top of the graphene layer showed higher sensitivity and a lower Dirac voltage than our standard GFET devices. Furthermore, our fabrication method is scalable and reproducible. These highly-sensitive and accurate bio-sensors show great potential for medical sensing applications such as disease detection and DNA sequencing.

Key Terms: Graphene
Field-effect transistor
DNA biosensor

GR-PHA-490**Creating a Statistically Characterized Reference Data Set to Test 2D Image Registration Algorithms for Testing Automated Portal Alignment for Patient Set-Up**

Afua Dankwa (Oakland University), Edward Castillo (Beaumont Health), Gary McDonald (Oakland University), Thomas Guerrero (Beaumont University) Advisor: Thomas Guerrero (Beaumont Health)

Create and characterize a reference data set for testing image registration algorithms that transform megavoltage portal image (MVPI) to digitally reconstructed radiograph (DRR), which will be used in future studies to test automated portal alignment for patient set-up. Six orthogonal image set anterior/posterior (AP) and lateral (LAT) of head and neck, abdomen and pelvis were selected. Computer assisted manual point selection tool (CAMPST), devoted software created in-house, was used to manually select landmark point pairs by an expert. 58 anatomic landmark points were manually paired between the six images for AP and 52 for the LAT. Approximation of inter- and -intra observer variation was determined by repeat measurement on both images by three other readers as a 2D Euclidean distance. The hypothesis that the mean difference between intra and inter observer registration error equal some critical value between 1mm and 7mm using the test statistic for paired data was tested. The registration error was generally high for the MVPI than the DRR due to the inherent poor quality of images acquired using megavoltage energies. Also the inter observer error was higher than the intra-observer error which is to be expected, as it is more likely for an individual to repeat their own point rather than someone else. The lower limit of the 95% confidence level was higher than 1mm and the upper limit higher 7mm. Our results agree with what has been reported in literature that the accuracies of 2D and 3D registration method fall between 1mm to 7mm.

Key Terms: Image registration
Patient set-up
Set-up uncertainty

HS-PSI-516**Race, Allergen, Methodology, Asthma Diagnosis, and Inflammatory Cells Significantly Alter Reactivity Between Radioallergosorbent and Skin-Prick Testing**

Rahul Krishnaswamy (Forsyth Country Day School) Advisor: Annette Hastie (Wake Forest School of Medicine)

Allergic sensitivity is a chronic problem for millions around the world. Radioallergosorbent testing (RAST) and skin prick testing (SPT) are two widely used methods for testing sensitivity to specific allergens. However, both methods test areas marginally related to airways allergic disease. RAST tests specific IgE-levels in serum and SPT tests reactivity of the external epithelium, leading to possible discrepancies between the two tests. This study aimed to examine the differences in response for individuals tested by both methods, and whether characteristics such as asthma diagnosis, gender, race, or inflammatory cell presence, might influence the differences observed. We examined data for 51 individuals (asthma cases, n=39; healthy controls, n=12) who first underwent SPT and subsequently RAST against 12 allergens by standard statistical tests. Comparison of RAST to SPT did not reveal differences for specific allergens; however, overall greater mismatches between tests occurred between asthma cases and controls ($p=0.001$) and Caucasians and African Americans ($p=0.025$). No significant differences were seen with regards to gender. Significant differences were seen with regards to race between Caucasians and African Americans in *D. farinae* ($p=0.03$), *D. pteronyssinus* ($p=0.019$), and grasses ($p=0.021$) for RAST, and in *D. pteronyssinus* ($p=0.014$) for SPT. Additionally, significant increases were seen in sputum eosinophil levels for subjects testing positive versus negative for specific allergens: for RAST to cat dander ($p=0.022$); for SPT to cockroach ($p=0.041$) and weed mix ($p=0.049$). In conclusion, it appears that race, allergen, test methodology, diagnosis of asthma, and presence of inflammatory cells can alter the reactivity observed.

Key Terms: Allergy
Immunology
Allergy testing

HS-PSI-517

BSU1 Family Mediates Immune Signal to MAP Kinase Cascade

Nicole Xu (San Mateo High School)

Advisors: Chan Ho Park (Carnegie Institution for Science, Stanford University), Zhiyong Wang (Carnegie Institution for Science, Stanford University)

Plants rely on receptor-mediated immune signaling pathways to respond to pathogen attacks. Flg22, a conserved peptide from bacteria flagellin, is recognized by the receptor kinase FLS2 and elicits this immune signaling, leading to MAP kinase (MPK) activation in a model plant *Arabidopsis thaliana*. However, how flg22-induced signal is transduced from FLS2 to MPK is unknown. BSU1 family proteins (BSUf) were suspected to regulate this pathway as they were phosphorylated when plants were treated with flg22, and play a role in the growth-promoting brassinosteroid signaling pathway, which has a similar signaling method as that of immunity. To investigate the function of BSUf in plant immune signaling, we generated an estradiol-inducible artificial microRNA-mediated *bsuf-i* quadruple mutant. We then identified transgenic lines containing single T-DNA insertions based on 1:3 ratio of antibiotic sensitive: resistant in the T2 generation and selected homozygous transgenic plants showing 100% antibiotic resistance in T3. These plants were then treated with flg22 or mock solution, and MPK activation was analyzed using immunoblots. The results showed a decrease of MPK 3/6 activation in these *bsuf-i* mutants compared to uninduced control plants, demonstrating that BSUf is required for flg22-induced MPK activation. To further understand how BSUf mediates immune signaling, we created transgenic plants that express BSUf proteins containing mutations at flg22-induced phosphorylation sites. Confocal imaging showed that these mutations did not affect the subcellular localization of the protein. Future experiments are needed to test if these phosphorylation sites are required for MPK activation and plant immunity.

Key Terms: Plant immune signaling
MAP kinase
BSU1 family proteins

UG-PSI-529

Determining the Role that a Crystallin-Derived Peptide May Play in Nuclear Cataract Caused by Crystallin Aggregation

Anthony Premceski (Oakland University)

Advisors: Frank Giblin (Oakland University), Vidhi Mishra (Oakland University)

Cataract is a leading cause of blindness worldwide. The most common type is nuclear cataract (opacification in the lens center) that is associated with an age-related increase in oxidative stress. Our laboratory has developed a model for nuclear cataract in which guinea pigs are treated with hyperbaric O₂. The treatment causes aggregation of lens proteins, as well as degradation of the lens protein alpha crystallin into products which include alphaA (66-80) crystallin-derived peptide. It is believed that such peptides may induce crystallin aggregation; however, the mechanism needs to be elucidated. This research was conducted to determine whether alphaA (66-80) peptide will bind to guinea pig alphaA crystallin *in vitro*, creating hydrophobic patches that may accelerate aggregate formation. A fluorescence polarization (FP) assay was developed to test peptide binding with increasing amounts of protein. To conduct the *in vitro* FP experiment, recombinant guinea pig alphaA crystallin was expressed in *E.coli* cells and purified using liquid chromatography. A fluorescein-tagged alphaA-(66-80) crystallin peptide was obtained from Genscript. Bovine serum albumin (BSA) served as a control. An unexpected decrease in polarization was observed for alphaA (66-80) peptide with alphaA crystallin, while an expected increase occurred with BSA. Such a decrease in FP can be caused by protein aggregation. An alternative fluorescence intensity assay showed a significant increase in fluorescence intensity for alphaA (66-80) with alphaA crystallin, but not with BSA. The results suggest that alphaA (66-80) peptide can bind to alphaA crystallin, possibly burying within hydrophobic spaces of the crystallin to induce protein aggregation.

Key Terms: Biology
Ophthalmology
Biochemistry

STUDENT POSTER ABSTRACTS

UG-PSI-530

The Role of CXCL17 in a Mouse Model of Diet-Induced Obesity

Carolina Herrera (University of California, Irvine),
Marcela Hernandez (University of California, Irvine),
Albert Zlotnik (University of California, Irvine)
Advisor: Marlene de la Cruz (University of California, Irvine)

CXCL17 is a mucosal chemokine that attracts dendritic cells and monocytes to specific tissues. CXCL17 is mainly expressed in the gastrointestinal tract and has been shown to have anti-inflammatory effects. Its recently described receptor, CXCR8, is a GPCR protein involved in metabolic function. Therefore, we decided to study the role of CXCL17 and CXCR8 in obesity, in which the effect of anti-inflammatory macrophages is essential to maintain tissue homeostasis. To conduct this study, we used a mouse model of diet-induced obesity to compare Cxcl17^{-/-} mice and wild type (WT) C57BL/6 mice. The mice were fed either a 10% or 60% fat diet for four months. They were weighed weekly and a glucose tolerance test was performed after two months. Plasma samples were used to perform an adipokine assay to detect levels of obesity-related cytokines and hormones. After four months, gastrointestinal tract tissue was isolated and isolated RNA was used to measure expression levels of CXCL17 and obesity-associated hormones by qPCR. Our data show that Cxcl17^{-/-} mice fed a high fat diet gained more weight than WT mice. In addition, CXCL17 is highly expressed in the upper gastrointestinal tract in WT mice under homeostatic conditions. Obese Cxcl17^{-/-} mice also exhibited impaired glucose tolerance. Adipokine assay results revealed differences in obesity-associated molecules between WT and Cxcl17^{-/-} mice. These results indicate that CXCL17 influences the development of obesity and systemic metabolic dysfunction. Therefore, we conclude that the CXCL17/CXCR8 axis represents a novel pathway that regulates metabolic responses.

Key Terms: Immunology
Chemokines
Obesity

UG-PSI-531

The Roles of CR3 and CD14 in the Non-Opsonic Phagocytosis of *Pseudomonas aeruginosa*

Alberto Lopez (University of California Irvine), Sally Demirdjian (Dartmouth College), Brent Berwin (Dartmouth College)
Advisor: Brent Berwin (Dartmouth College)

Complement receptor 3 (CR3) and CD14 are receptors that are important for phagocytic clearance of Gram-negative bacteria. Previous studies that employed phagocytes obtained from patients with Leukocyte adhesion deficiency, a genetic deficiency for CR3, indicated that either CR3 or CD14 is involved independently in the phagocytosis of various *Pseudomonas aeruginosa* bacterial strains. However, direct interactions between *P. aeruginosa* and these receptors have never been demonstrated, therefore we propose to test the sufficiency and necessity of these receptors to binding and mediating phagocytic uptake of *P. aeruginosa*. We hypothesize that if CR3 and CD14 directly interact with *P. aeruginosa*, then ectopic expression of these receptors will confer bacterial binding. We tested the sufficiency of these two receptors by performing bacterial association assays with cultured epithelial cells which do not express either of these receptors and for which we have clones that have been transfected to express each of these receptors. To test the necessity of these receptors we performed phagocytosis assays to measure the uptake of different strains of *P. aeruginosa* with murine CR3 and CD14 knockout bone marrow derived dendritic cells. Bacterial association assays with various strains of *P. aeruginosa* suggests that there is no significant difference of bacterial association with the three CHO cell lines. However, a significant difference in phagocytic uptake of specific strains of *P. aeruginosa* by WT versus CD14^{-/-} BDMCs supports a role for CD14. These studies will provide novel insights on the molecular basis for cellular recognition and clearance of *P. aeruginosa* by phagocytes.

Key Terms: Immunology
Host pathogen
Phagocytosis

STUDENT POSTER ABSTRACTS

UG-PSI-532

Are Vaccine Myths and Misconceptions Driving Outbreaks of Infectious Diseases?

Georgiana Kourepenos (Quinnipiac University), Jessica Kuchta (Quinnipiac University), Kristen Bender (Quinnipiac University)

Advisor: Lisa Cuchara (Quinnipiac University)

Vaccines have enabled debilitating and fatal diseases, such as smallpox and polio, to be abated in the United States. This success has been halted due to inaccurate media representation and unreliable internet sources, resulting in negative effects upon public health. Our hypothesis is while scientists and healthcare providers know more *facts* about this issue, they too are often believers (or ambiguous believers) in misinformation. Using a comprehensive survey supported by numerous sources, vaccination knowledge was evaluated in 4,275 individuals with varying backgrounds using a Likert scale for data analysis.

The next step will be to determine if science/health students need to be more versed in debunking vaccine myths misconceptions in order to transmit accurate vaccine knowledge to patients and to the public.

Key Terms: Public health
 Infectious disease
 Vaccines

GR-PSI-540

ZIP8 in the Regulation of Methionine Metabolic Pathway in Liver

Liu Liu (Oakland University)

Advisor: Zijuan Liu (Oakland University)

Membrane transporter SLC39A8 (encoding ZIP8) regulates the influx of micronutrients such as selenium and divalent cations zinc, iron and manganese. As an essential mammalian protein, ZIP8 is found to be associated with inflammation and multiple metabolic disorders including high cholesterol and obesity in humans. However, the pathological effects of ZIP8 on downstream metabolic pathway is unknown. Using recently developed RNA-sequencing technique, we analyzed and compared transcriptome profiling in hypomorphic *Slc39a8^{neo/neo}* fetal livers along with WT controls. We discovered that downregulation of ZIP8 significantly affected two enzymes involved in methionine metabolism: MAT1A and BHMT1. These enzymes are important to maintain homeostasis of essential metabolic intermediates, including methionine, S-adenosyl-methionine (SAM) and homocysteine. Defects in protein expression are associated with liver disorders including inflammation and fibrosis. ZIP8 regulation of MAT1A and BHMT1 is consistent with our observations of 50% haploinsufficiency *Slc39a8^{+/neo}* mice showing visible liver pathologies including liver inflammation and fibrosis, along with decreased expression of *Bhmt1* and *Mat1a* and lowered selenium level. Since BHMT1 is zinc-dependent enzyme, we hypothesize ZIP8 deficiency decreases hepatocytes' access to zinc and selenium, compromising *Mat1a* and *Bhmt1* expression and thus promoting chronic liver disease. In a summary, we identified novel function of ZIP8, a newly identified multiple-functional transporter to play important roles in regulating liver function through controlling downstream enzymes MAT1A and BHMT1. This discovery hold promise to propose ZIP8 as a new molecule to be evaluated in popular liver diseases including fatty liver disease and fibrosis.

Key Terms: ZIP8
 Methionine metabolic
 Liver pathology

GR-PSI-541

Preliminary Examinations of Changes in Intestinal Microbiota Induced by High Fat Feeding in Male Adolescent Rats

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 Advisors: Karen Sweazea (Arizona State University), Corrie Whisner (Arizona State University)

The gut microbiome has a significant physiological impact in both health and disease. In a healthy individual, microbes influence metabolism, offer protection against pathogens, and train the immune system. The dominant bacterial phyla in the human digestive system are gram-positive *Firmicutes* and *Actinobacteria* as well as gram-negative *Bacteroidetes*. Recent metagenomic studies show that obesity is associated with reduced *Firmicutes* and *Bacteroidetes* while an increase in *Actinobacteria* is observed. Additionally, the gut microbiome is implicated in the regulation of host metabolic processes, which include producing the short chain fatty acids (SCFA), butyrate, acetate and propionate. However, previous research has shown that prolonged consumption of a Westernized diet can drastically alter gut microbiota and increase the risk of obesity and other metabolic diseases in adults. Although it is known that energy dense foods can alter microbial diversity, less is known about the physiological effects of diet-induced changes in the gut microbiome on cardiovascular disease risk in adolescents. Six-week old periadolescent male Sprague Dawley rats were divided into two groups (n=6 each) and fed either a standard rodent chow (18.9% protein, 57.33% carbohydrates, 5% fat) or a high-fat diet (HFD) (20% protein, 20% carbohydrates [6.8% sucrose], 60% fat) for 6 weeks. Following the diets, fecal pellets were collected and sequenced at the Microbiome Analysis Lab at Arizona State University. Although not significant, the preliminary fecal taxonomy analyses suggest changes in the relative abundance of *Firmicutes* (Chow: 86.3±4.6%; HFD: 80.8±5.0%), *Bacteroidetes* (Chow: 5.6±2.4%; HFD: 15.0±4.9%), and *Actinobacteria* (Chow: 0.42±0.17%; HFD: 1.62±0.72%) following the HFD protocol. These preliminary data were limited by the availability of fecal samples only at the post-intervention period but serve as a basis for future examination of the effects of a novel fiber treatment on SCFA production, inflammation and cardiovascular disease markers in adolescent rats throughout a more prolonged HFD protocol (10 weeks). Understanding how the gut microbiome is altered with poor nutrition may elucidate potential treatment strategies for adolescent overweight and obesity as well as prevention of cardiovascular disease.

Key Terms: Gut microbiome
 High fat diet
 Physiology

GR-PSI-542

Characterization of Peripheral Blood B Cells in Allergic Asthma and the Effect of Rhinovirus Infection

Tiffany Batarseh (University of California, Irvine), Nadine Upton (King's College London), Yu-Chang Bryan Wu (King's College London), Hannah Gould (King's College London)
 Advisors: Nadine Upton (King's College London), Hannah Gould (King's College London)

Asthma, a chronic, respiratory condition, affects 1 in 12 people in the US, with 60% having allergic-asthma. This is characterized by elevated levels of IgE antibodies, the antibody isotype that causes allergies. Rhinovirus (RV) infection causes 60% of asthma exacerbations, however the mechanism of how RV does so is not established and research is necessary. We hypothesized that RV infection induces IgE-B responses in patients with allergic asthma. In partnership with a clinical study, peripheral blood samples were taken from allergic-asthmatic and non-asthmatic individuals before and after RV infection. Total peripheral blood B cells and peripheral blood memory B cells were sorted out through fluorescence activated cell sorting. Both groups of sorted cells were lysed and cDNA generated. To study changes in gene expression, the total B cell cDNA was used for qPCR. To investigate if B cells increase IgE antibody response, memory B cell cDNA was used for switch circle transcript analysis. Increases in IL-4R gene expression appears to occur in both the allergic-asthmatics and the healthy populations. CD23 gene expression appears to increase in the allergic-asthmatic group at an earlier timepoint than compared to the healthy group. Both of these genes deal with B cell differentiation and IgE responses. After infection with RV, CD27- and IgD- memory B cells have a significant increase in switching from IgM antibody isotype only in allergic-asthmatics. Further investigation is warranted to fully understand the specific mechanism and consequence of this induction in further understanding the pathogenesis of rhinovirus-induced asthma exacerbations.

Key Terms: Immunology
 Asthma
 Allergy

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