
## ABSTRACTS OF STUDENT RESEARCH POSTERS

**Click on the research field below to navigate to that section in the abstract list.**



*Research that encompasses a body of knowledge and methodology from more than one field of research is designated as Interdisciplinary Research and will be evaluated by judges from fields designated by the presenter.

**BC-01**

## The metabolism of black tea theaflavins by human fecal microbiota

Saeed Hayek (North Carolina Agricultural and Technical State and North Carolina Research Campus), Huadong Chen (North Carolina Research Campus), Advisors: Salam Ibrahim (North Carolina Agricultural), Shengmin Sang (North Carolina Research Campus)

Polyphenolic compounds in black tea (*Camellia sinensis*, Theaceae) have been associated with many beneficial health effects, including the prevention of cancer and heart disease. The main bioactive polyphenols in black tea are theaflavins, which are formed by the oxidation and polymerization of catechins in green tea leaves during fermentation. Theaflavins including theaflavin (TF), theaflavin-3-gallate (TF3G), theaflavin-3′-gallate (TF3′G), and theaflavin-3,3′-digallate (TFDG). We and others have found that theaflavins have poor systematic bioavailability. Therefore, it is still unclear how these compounds could exert their biological functions. It has been reported that higher molecular weight polyphenols are metabolized by the gut microbiota and their metabolites may play an important role in chronic disease prevention. In the present study, we investigated the microbial bioconversion of theaflavins in vitro using 3 human fecal slurries which was collected from healthy subjects after 2 days of diet restrictions. Microbial bioconversion was monitored using liquid chromatography/electrospray ionization tandem mass spectrometry by analyzing the $MS^n$ (n = 1–3) spectra. The three subjects displayed the same metabolite profile but in different level of these metabolites. Our results indicated that both TF3G and TFDG can be metabolized by human microbiota to generate gallic acid, pyrogallol, and TF. To our knowledge, this is the first report on the metabolism of theaflavins by human fecal microbiota. In conclusion, this study is first step toward a better understanding of how black tea polyphenols may involved in beneficial health effects.

Key Terms: Biochemistry
Fermentation
Microbial bioconversion of polyphenols

**BC-02**

## Effect of Extracellular Lipoprotein on Localization of Phosphatidylinositol-4,5-bisphosphate and Virulence Functions in *Entamoeba histolytica*

Amrita Koushik (Clemson University), Rhonda Powell (Clemson University), Brenda Welter (Clemson University), Advisor: Lesly Temesvari (Clemson University)

The protozoan parasite, *Entamoeba histolytica*, causes amebic dysentery and liver abscess resulting in 100,000 deaths worldwide annually. Once inside the human host, the parasite's cellular processes such as adhesion, phagocytosis, motility and secretion play a vital role in its pathogenicity. Previous reports have implicated cholesterol in the modulation of *E. histolytica* virulence. For example, severity of infection was more in hypercholesteromic animal hosts. *E. histolytica* also possesses lipid rafts, cholesterol-rich membranes, enriched in signaling molecules such as phosphatidylinositol- 4, 5-bisphosphate ($PIP_2$). Since this pathogen relies on lipoprotein-rich growth medium for propagation, we examined the effect of extracellular lipoprotein on localization and distribution of $PIP_2$. We found an increase in levels of membrane-bound $PIP_2$ and a decrease in downstream calcium levels upon exposure to lipoproteins. This suggested that exposure to lipoproteins could result in preparing the cells for various signaling events. Therefore, we tested various virulence functions including adhesion, phagocytosis and host-cell destruction. We found that lipoprotein treatment increased the adhesion of this parasite to extracellular matrix components such as collagen and fibronectin as well as to host epithelial cells. There was also a dramatic increase in host monolayer destruction upon lipoprotein exposure. However, we did not find significant changes in erythrophagocytosis upon exposure of the parasites to lipoproteins as compared to untreated cells. Together, our data suggests the involvement of lipoprotein in regulating virulence via $PIP_2$- mediated signaling pathway.

Key Terms: Biochemistry
Cell and Molecular Biology
Parasitology

**BC-03**

## Effects of Nicotine on *Caenorhabditis elegan* survival, reproduction, and gene expressions

Michael A. Smith Jr (East Carolina University), Yanqiong Zhang (East Carolina University), Dongliang Chen (East Carolina University), Baohong Zhang (East Carolina University), Advisor: Xiaoping Pan (East Carolina University)

Although much is known about the additive effects of nicotine, the molecular mechanisms of nicotine-induced effects remain largely unclear. Especially, little is known about the effects on gene expression including protein coding genes and miRNA genes. miRNAs could possibly play a key role in regulating protein coding gene expression in response to acute nicotine exposure. This may be the key to understand the addictive nature of nicotine. Our goals are to explore the toxicity effects of nicotine on *Caenorhabditis elegans (C. elegans),* including survival, egg production, and gene expression. We hypothesize that 1) Nicotine affects survival and reproduction *of C. elegans;* 2) The expression of several important genes including the genes of the nicotinic acetylcholine receptor, oxidative stress response will be affected by nicotine exposure; 3) The expression of miRNA genes will be changed and related to the selected protein coding gene expression. In the survival trials, we tested a range of doses in order to obtain a 24- hour dose-dependent pattern. The 24-hour LD20 in *C. elegans* correspond to dose of 3.16 ppm of nicotine. Using qRT-PCR, we have revealed that several protein coding genes are altered by nicotine which may be regulated by miRNAs.

Key Terms: Gene expression
Toxicology
Caenorhabditis elegans

**BC-04**

## Size Dependent Antibacterial Activity of Sugar Encapsulated Gold Nanoparticles

Lakshmisri Vangala (Western Kentucky University), Advisor: D. Raja (Western Kentucky University)

In the present study, antibacterial properties of completely green synthesized dextrose encapsulated GNPs were investigated against both Gram-negative and Gram positive bacteria. Experiments were performed to analyze the growth, morphology and the ultra-structural changes in bacteria. GNPs found to have significant dose dependent antibacterial activity which was directly proportional to increase in the size of nanoparticles. The microbial assays showed the GNPs to be bacteriostatic as well as bactericidal. This special dextrose encapsulated GNPs exert their bactericidal action via disrupting the bacterial cell membrane causing leakage of cytoplasmic content. The cytotoxicity studies suggest the GNPs to be non-toxic towards mammalian cells proving the nanoparticles to be biocompatible. Results of this study clearly suggest that dextrose encapsulated GNPs can be used as a potent antibacterial agent against wide range of bacteria to control and prevent various infections or diseases caused by them.

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Key Terms: Biochemistry
Chemistry
Proteins

**BC-05**

## Effects of Lead on the Blood Proteome of Children in Oswego, NY: the focus on Apolipoprotein E – Lead Interactions

Tamara Nsouli (State University of New York, Oswego), Advisor: Kestutis Bendinskas (State University of New York, Oswego)

Lead exposure in children has been associated with a variety of physiological and neurological problems. Blood plasma and serum samples from 34 children were depleted of their most abundant proteins using antibody-based affinity columns and analyzed using two different methods, LC-MS/MS and 2-D electrophoresis coupled with MALDI-TOF/MS and tandem mass spectrometry. Apolipoprotein E demonstrated a significant negative association with lead concentrations (average being one microgram/deciliter) as deduced from LC-MS/MS and 2-D electrophoresis and confirmed by Western blot analysis. Cloned and serum apolipoprotein E exhibited in vitro binding to IDA columns loaded with lead as determined by Western and the BCA method after the MWCO filter-facilitated buffer exchange. ApoE's three isoforms, ApoE 2, 3 and 4, have shown to have different binding affinities and are strongly believed to attach to lead through cysteine residues. The study is the first in the field of proteomics to study toxicology of heavy metals in blood in a general population of children. It is the first to statistically relate a cardiovascular protein Apolipoprotein E with sub-clinical blood lead levels and to prove apolipoprotein E- lead binding.

Key Terms: Biochemistry
Metal Toxicology
Pediatric Research

**BC-06**

## Gene Network Regulation of Outer Membrane Vesiculation in *Escherichia coli*

Bo Sun (Duke University), Adam Kulp (Duke University), Teresa Ai (Duke University), Amy Schmid (Duke University), Advisor: Meta Kuehn (Duke University)

The membrane of gram-negative bacterial species such as *Escherichia coli* is comprised of an outer membrane, inner membrane, and peptidoglycan-rich periplasm in between. Outer membrane vesiculation, a budding of the outer membrane, is commonly observed and has been implicated in processes such as toxin transport, biofilm production, and resistance to antibiotics. Outer membrane vesicle (OMV) formation may therefore represent a possible target for future antibiotics. The most efficacious antibiotic targeting vesiculation must take into account all the possible effects of the drug – therefore, it is important to understand the gene networks that contribute to vesiculation, networks that still have not been elucidated in *E. coli*. The Keio Collection, a library of approximately 4,000 non-essential single-gene deletion mutants in *E. coli*, has been screened for the vesiculation level of each mutant. Mutants with the most extreme vesiculation phenotypes (both above and below the median) have been selected for further analysis and verification of phenotype in a larger-scale vesicle preparation. Systems biology analysis has been utilized to draw connections among the selected mutants and indicate gene networks that may influence vesiculation. Pairs of select mutants were chosen to generate double deletion mutants whose resulting vesiculation levels were measured to determine possible epistatic relationships between the genes deleted. A group of mutants has also been implicated in the pathway responsible for the biosynthesis of lipopolysaccharide, found on the outer membrane of *E. coli*. Ongoing work focuses on elucidating additional gene networks or pathways that may influence OMV formation.

Key Terms: Biochemistry
Microbiology

**BC-07**

## Proteomic Study of Human Serum Proteins binding to immobilized metals on an IDA column

Christyne Chmil (State University of New York, Oswego), Fengrong Wang (State University of New York, Oswego), Frank Pierce (State University of New York, Oswego), Advisor: Kestutis Bendinskas (State University of New York, Oswego)

Heavy metal exposure in humans has been associated with a variety of physiological and neurological problems. Human blood serum samples were loaded onto IDA metal-affinity columns and analyzed using LC-MS/MS. The metal binding was assessed using ICP-MS. Among the metals screened, only lead, zinc, cadmium, nickel and copper were used in the system under physiological conditions. The distributions of metals in different column washes are reported here along with the protein concentrations, abundance and identities in the EDTA elutions. Several proteins known to bind metals such as alpha-2-macroglobulin have been identified proving the validity of the method. Additionally, a multitude of proteins not known to bind to the studied metals have been identified.

Key Terms: Proteomic Study
Human Serum
Column Chromatography

**BC-08**

## Diverting The Allocation Of Kauralexins To The Roots By Increased Stress Of Above Ground Tissues

Vitor Martins (University of Florida), Kristine Callis (University of Florida), Advisor: Martha Marie Vaughan (USDA Gainesville, Florida)

Global climate change is expected to bring various alterations to abiotic factors such as precipitation patterns. When plants experience stress from diverse factors, optimal defense theory suggests that plants will use their energy on defending the more vital plant tissues. For example, to a plant experiencing drought stress, the roots would be the more vital tissue. Kauralexins are phytoalexins produced in response to infection of fungal pathogens, but, surprisingly, we found that kauralexins were induced in the roots for drought stressed plants. We hypothesized that the plant was reallocating defense resources to the roots because drought stress, the roots were the more vital tissue. We proceeded to design a study to see if we could divert the reallocation of resources to the roots by increasing the importance of the above ground parts of the plant by adding in two additional factors: limited light and pathogen infection. We did this by inoculating the stacked node of some *Zea mays* var. 'Golden Queen' with the pathogen *Fusarium verticillioides* and keeping some of the plants in a more shaded environment, while measuring the production of kauralexins in the roots. The pathogen infection above ground dramatically reduced the drought response, but the difference between the induced effect of pathogen infection alone, compared to pathogen paired with dim-lighting was minimal, leading us to believe that the stress of reduced light is minimal. Our results suggest that different stress factors have varying magnitudes and that plants respond to them accordingly.

Key Terms: Biochemistry
Plant Defense
Global Change

**BC-09**

**Rational Design of Cysteinyl Peptides as Chelators of Mercury(II)**

Matthew Bronson (Winston-Salem State University), Jeremy Brooks, Advisor: Maria Ngu-Schwemlein (Winston-Salem State University)

As a result of industrialization in the modern world mercury exists all around us in various physical forms. Exposure to mercury, especially by ingestion or inhalation, is extremely hazardous to our health. Clinical therapy for mercury poisoning primarily employs two compounds, DMPS and DMSA. Unfortunately, these clinical drugs have limitations and are not optimal for chelation therapy. In this study, we propose to use cysteinyl peptides that mimic the natural metal ion chelators, such as phytochelatins. The thiol groups of cysteine could act as anchors for mercury because of their preferential soft S-donor and soft Hg-acceptor interactions. We propose to incorporate multiple cysteinyl residues on the peptide and vary the distance and amino acid residues between them to optimize efficiency for mercury binding. The present study is undertaken to develop a better understanding of the interactions of cysteinyl peptides containing one to four cysteine residues with mercury(II). These peptides are prepared by microwave-assisted solid phase peptide synthesis. Their mercury (II) binding affinities and associated thermodynamic parameters are evaluated by isothermal titration calorimetry (ITC). The results show that peptide ligands containing three cysteine residues with an adjacent aspartic acid residue in the peptide sequence provide optimum binding affinity for mercury(II). These tricysteinyl peptides may present a more attractive option for mercury chelation therapy, detoxification or remediation.

Key Terms: Mercury poisoning
Chelation therapy
Cysteinyl peptides

**BC-10**

## Elucidation of the Role of RUNX1 Tyrosine Phosphorylation in Hematopoiesis and Megakaryopoiesis

Alvin Shi (Duke University), Advisors: Hui Huang (Children's Hospital Boston), Alan Cantor (Children's Hospital Boston)

RUNX1 is a member of the Runt-related transcription factor family, which plays a critical role in hematopoiesis and megakaryopoiesis. The Cantor lab has identified that Runx1 tyrosine phosphorylation by Src-Family Kinases (SFK) as an important regulator of its activity. Here, we further elucidate the role of RUNX1 tyrosine phosphorylation in GATA switching, and the effects of Dasitinib, a novel tyrosine kinase inhibitor for treatment of CML (Chronic Myelogenous Leukemia) patients, on RUNX1 tyrosine phosphorylation.

Key Terms: Biochemistry
Hematopoiesis
Developmental Biology

**BC-11**

## Rewiring the Genetic Code for Global Protein Footprinting

Johnny Rodriguez (University of California, Irvine), Advisor: Pehr Harbury (Stanford University)

Proteins are molecular machines that generally function in large assemblies to carry out most biological processes. Although NMR and crystal structures have enhanced our understanding of protein function, they only provide “snapshots” of purified proteins and thus fail to reveal conformational changes and partner interactions that are key to the operation of molecular machines. Alternative chemical footprinting techniques can give time resolved pictures of which residues in a protein are solvent accessible. Patterns of residue accessibility are characteristic signatures of different protein conformational states, allowing characterization of conformational changes in real time. Although cysteine’s unique chemical properties are ideal for footprinting, cysteine’s low abundance in naturally occurring proteins limits applicability. One way to overcome this problem is to rewire the genetic code so that, under the control of a genetic switch, any codon can be translated into cysteine. Previous work has shown that non cysteine codons can be rewired to cysteine by expression of a mutant cysteine-tRNA with an anticodon complementary to the desired non cysteine codon, but in many cases has been inefficient. I have designed a pulse chase genetic selection to find mutant cysteine-tRNA and cysteine-tRNA synthetases that rewire the genetic code with high efficiency. Preliminary experiments involved constructing a yellow fluorescent protein containing an intein insertion to serve as a reporter for cysteine misincorporation. Currently, mutant cysteine-tRNA and tRNA synthetase libraries are being screened for efficient misincorporation. Each mutant cys-tRNA/synthetase pair discovered will provide a valuable tool for analyzing protein structure and "action" in protein complex mixtures.

Key Term: Biochemistry

**BC-12**

## The Effect of Iron Uptake on Mussel Thread Strength

Julia Callender (University of California Santa Barbara), YerPeng Tan (University of California Santa Barbara), Advisor: J. Herbert Waite (University of California Santa Barbara)

The marine mussel *Mytilus californianus* utilizes an extraorganismic structure known as the byssus to attach to surfaces along the wave-swept intertidal zone. Individual byssal threads exhibit great strength, durability and self-healing following deformation. Past research proposes a model in which these unique properties are due to the presence of protein-metal crosslinking between 3,4-dihydroxyphenylalanine (Dopa) side chains and $Fe^{3+}$ ions that have been sequestered from the mussel's aquatic environment. Chelated removal of $Fe^{3+}$ from the thread has been shown to cause a decrease in the stiffness of the outer thread covering. We hypothesize that increasing the $Fe^{3+}$ content in a thread will cause an increase in total thread strength under uniaxial tension. A Bionix MTS tensile testing apparatus is used to subject threads to uniaxial tension, yielding mechanical values such as stress, strain, and elastic modulus. Preliminary data indicates that increasing the iron concentrations in the thread affects its mechanical properties. Understanding more about the structure-properties relationships in byssal threads can potentially impact the way we control synthetic polymer stability through the addition or removal of metal ions.

Key Terms: Marine Biomolecular Materials
Biochemistry
Molecular Biology

**BC-13**

## Synthesis and Purification of Meso-Substituted Porphyrin Isomers

Joy Cote (College of Mount Saint Vincent), Advisors: Stephanie L. Widmer and Pamela K. Kerrigan (College of Mount Saint Vincent)

Photodynamic therapy (PDT) is a method of treating cancer cells by use of photosensitizing agents. Porphyrins are light sensitive, organic compounds which absorb light at appropriate wavelengths (630-800 nm) and fluoresce under treatment of radiation. This characteristic of porphyrins allows for the easy detection of tumors and the release of an active form of oxygen, which is suggested to destroy neighboring cancer cells. As part of a larger study on the use of porphyrins in PDT, isomers of meso substituted porphyrins were synthesized using p- anisaldehyde or p-tolualdehyde with p-acetamidoaldehyde. The porphyrins are synthesized by means of refluxing and, when produced are disseminated in a tar mixture. The precipitated porphyrins are collected using vacuum filtration. The porphyrins are separated into different fractions using column chromatography. Nuclear Magnetic Resonance and Thin Layer Chromatography were used in order to determine which isomer is present and insure that the fractions were sufficiently separated.

**BC-14**

## Metabolism of Dietary Fatty Acids that Affect the Growth of Rat Mammary Tumor Cells

Alimatu Dittmann (Purchase College, State University of New York), Advisors: Joanne Tillotson (Purchase College, State University of New York), Joseph Skrivanek (Purchase College, State University of New York)

Omega-3 and omega-6 are essential dietary fatty acids. Omega-3 fatty acids are found mostly in fish and nut oil, while omega-6 fatty acids are abundant in canola, corn, and soybean oil. Over the past few years, research has shown that tumor cells given omega-3 fatty acids exhibit a lower proliferation rate than those given omega-6 fatty acid, but the mechanism for this decreased proliferation is uncertain. For this project, we hypothesized that if the cells were given more omega-6 fatty acid, we would observe an increased rate of production of arachidonic acid, which is a precursor for eicosanoid cell signaling compounds. In our study, rat mammary tumor cells (NMU) were cultured in vitro in medium containing fetal bovine serum (FBS). The omega-3 & 6 fatty acids were then added to cells in medium containing low levels of FBS (1%). Controls did not receive any fatty acids. The cells were harvested after 2, 3, 4, or 5 days. The lipids from the cells were extracted, and separated using column chromatography, in order to analyze how the cancer cells metabolized the omega-3 and omega-6 fatty acids. Thin layer chromatography (TLC) was used to separate and analyze the lipids found in the cells. It was observed that neutral lipids, e.g. cholesterol, did not show relevant changes between cells given omega-3 fatty acid and omega-6 fatty acid. Gas chromatography/mass spectrometry (GC/MS) was used to analyze fatty acids found in the cells. Cells given omega-6 fatty acid contained higher levels of arachidonic acid while cells given omega-3 fatty acid showed higher levels of eicosapentaenoic acid. To demonstrate whether the cells were converting the two essential fatty acids into these metabolites, further analyses were conducted using deuterated fatty acids. Preliminary analysis of those studies indicates that deuterated linoleic acid was converted into deuterated arachidonic acid (both omega-6), while deuterated alpha-linolenic acid was converted into eicosapentaenoic acid (both omega-3).

This project was supported in part by National Institutes of Health, Bridges to the Baccalaureate Grant ##3R25GM62012-09.

Key Terms: Biochemistry
Chemistry
Biology

**BC-15**

## Nanobiosensing Interactions of Bombolitins III and IV with Nitroaromatics through Adsorption onto Single-Walled Carbon Nanotubes

Gayatri Rathod (North Carolina School of Science and Mathematics), Advisor: Dr. Melissa Pasquinelli (North Carolina State University)

Molecular dynamics (MD) simulations were used to investigate how the chemical composition and conformation of Bombolitins III and IV, when adsorbed onto the surface of the carbon nanotube, dictates the selectivity in detecting the nitroaromatics, cyclotrimethylenetrinitramine (RDX) and trinitrotoluene (TNT). The MD simulations revealed that the conformation of the Bombolitin III and IV polypeptide is sensitive to its local environment, and this conformational motion is a key component to the specificity of this nanobiosensor. In the presence of SWNT, bombolitin IV molecules are able to recognize compounds to a certain extent from the class of nitro-aromatics under intense conditions. By situating a system in VMD with SWNT with bombolitin III and IV on its surface, their biosensing properties under high temperatures and pressures were tested, as well as their ability to detect other classes of compounds. While the tbiosensing properties of the two molecules were similar, Bombolitin III was found to have higher targeting abilities for TNT, and Bombolitin IV was discovered to have a higher adsorption ability for the 7-5-CNT type.

Key Terms: Nanoscience
Molecular Dynamics

**BC-16**

## Capillary Electrophoretic Validation of Sequence Motifs for Transcriptional Regulation

Katrina Gutierrez (North Carolina School of Science and Mathematics), Brian Iezzi (North Carolina School of Science and Mathematics), Advisors: Dr. Brian Cooper (University of North Carolina at Charlotte), Dr. Myra Halpin (North Carolina School of Science and Mathematics)

Although entire genomes have been mapped, our understanding of biological processes is hindered because transcription regulatory networks are not yet completely understood. In order to expand the list of known transcription factor binding sites, predictions of these sites must be validated. This research involves detecting binding at multiple sites on the genome where, unlike previous work, the binding conditions are unknown. By utilizing protein fractions prepared from *E. coli* and capillary electrophoresis, we screened predicted binding sequences from a researcher's computational algorithm. Since a cofactor is often required to bind, we included micromolecules obtained from ultrafiltration, solid phase extraction, and metabolite extraction. Our successful detection of the CRP-cAMP binding complex at a known binding site offers promise for detecting binding at predicted sequences. We also found that we could differentiate between the specific and non-specific binding because the latter would be detected around the same time with every DNA sequence. Although specific binding was not yet detected in this set of screenings, continued work includes preparing the samples to more closely reflect the cellular conditions. Successful validation could help us better understand the complex system of gene expression, thus allowing for novel disease treatment development.

Key Terms: Transcriptional Regulation
DNA-Protein Interactions
Capillary Electrophoresis

**BC-17**

## The Effects of Various Stresses on The Growth Rate of *Saccharomyces cerevisiae* and *Kluyveromyces lactis*

Michaelangelo Lucas(Johnston County Middle College), Advisor: Dr. Laura Rusche (Duke University)

In the production of yeast for industrial applications, yeasts rarely encounter the optimal conditions for growing and instead they are exposed to a variety of stresses. The genetic expression caused by the stresses that activate adaptation can vary slightly or extensively between species. To study these types of variations, comparisons of responses between two strains of *Kluyveromyces lactis,* LRY 1506 and LRY 2775, and *Saccharomyces cerevisiae,* 1009 and 1012, were researched under the stresses of osmotic, oxidative, cold, heat, and desiccation. The yeasts were grown in yeast extract peptone dextrose (YPD). For each stress the yeast strains were exposed to the stress and their growth was observed over a period of time. To shock the yeast strains, they are exposed to a stress for a period of time and then taken out to be place onto YPD plates. Growth curves were made for heat and osmotic stress. Statistics showed that there was no significant difference between the two species in osmotic stress and on $H_20_2$/YPD plates, oxidative stress, no difference was seen. *Saccharomyces cerevisiae* showed more growth in heat than *Kluyveromyces lactis*. While *Kluyveromyces lactis* showed more growth in cold stress and desiccation stress than *Saccharomyces cerevisiae*. From the results no difference was identified between *Kluyveromyces lactis* and *Saccharomyces cerevisiae* in osmotic and oxidative stress. However *Saccharomyces cerevisiae* did respond better than *Kluyveromyces lactis* in heat stress and the opposite was shown for cold and desiccation stress.

Key Terms: Molecular Biology
Genetics
Spectrophotometry

**BC-18**

**In virto Characterization of Potential Small Molecule Activators of Procaspase-3**

Avery Young (William G. Enloe High School), Advisor: Dr. Clay Clark (North Carolina State University)

The intent of this project is to develop small molecule activators of procaspase-3 as an anti-cancer strategy. Procaspase-3 is the terminal protease in the apoptotic cascade that, once activated, commits the cell to undergo apoptosis. This is an exciting and novel target that could potentially eliminate the resistance observed after administration of other chemotherapeutic agents which target proteins found further upstream in the apoptotic cascade. Most cancers have a large pool of inactive procaspase-3 due to the inability of the cancer cell to undergo apoptosis. Our strategy is to activate this pool of procaspase-3 in cancer cells which will enable apoptosis to resume thereby reducing tumor size or eliminating the tumor all together. The data presented here are the preliminary characterization of ~1300 small molecules that could potentially activate procaspase-3. Procaspase-3 activity was measured in the presence of each drug candidate. It was found that eighteen of the ~1300 molecules had some degree of activating potential. Several confirmatory assays were performed to ensure that the activity data were real. From these collective data, we found 8 molecules that are good leads candidates with which future preclinical testing will be performed.

Key Terms: Biology
Biochemistry

**BC-19**

## Electron Transfer in Natural Proteins: Evidence of Structure Function Relationships Through Evolution

Myatt Person (North Moore High School), Advisor: David Beratan (Duke University)

Currently scientist are trying to understand how a protein works, specifically focusing on the effects that specific amino acids have on the structure and function of the protein. There is some current knowledge of amino acids in proteins, however, not much knowledge about what amino acids effect electron transfer. Thus my project focuses on trying to find the amino acids that are important in the electron transfer process of certain proteins. History has stated that tryptophan is an important amino acid in electron transfer. This project will focus on the analysis of DNA Photolyase and Ribonucletide Reductase. In analyzing these two protein classes we hope to find amino acids that are important in the electron transfer process. It is hypothesized that if statistics of coevolving amino acids can provide critical structure and function information then we could build a protein through de novo protein design. To get these results we will first identify the protein class. Then the protein will be put into a psi blast to collect homologous sequences related to the protein. Next we will measure the covariance of the amino acids using MATLAB. Finally we will graph the important amino acids onto a 3-D crystal structure using pymol. In this analysis we found that tryptophan was important in electron transfer but it was not found in all sectors. It also did not have a heavy weight meaning it did not affect the protein very much. These findings left the hypothesis inconclusive.

Key Terms: Electron Transfer
Proteins
Computer Science

**BC-20**

# Evaluation of the Performance of Two Proteases for Analysis of Proteomic Samples by Mass Spectrometry

Gabriel Xavier Pauling (Knightdale High School), Dr. Micheal B. Goshe (North Carolina State University Department of Biochemistry)

***Purpose*:** Proteomics is the study of proteins and their interactions within a biological system. The focus of this research is to evaluate the performance of the protease Lys-C against Trypsin, the most commonly used protease for proteomic analysis, for the digestion of a model proteomic system (*E. coli* lysate).

***Methods*:** The procedures used to conduct this research were proteolytic digestion of an *E.coli* lysate sample with the each of two proteases (Lys-C and Trypsin). Liquid Chromatography/Mass Spectrometry analysis ($LC/MS^E$) was used to determine how many proteins were identified with each protease, the average sequence coverage observed with each protease, and the quality of peptide spectral matches obtained with each protease.

***Results*:** Trypsin identified slightly more proteins than Lys-C (170 versus 153, respectively). However some proteins were only identified with Lys-C (3 of 173) and some were only identified in the Trypsin digest (20 of 173) as well. Trypsin provided slightly higher protein sequence coverage than Lys-C (44 % versus 38%). Trypsin and Lys-C provided comparable qualities of peptide matches.

***Conclusion*:** Trypsin will continue to be used as the preferred protease for general proteomic analysis, but analysis of both Lys-C and Trypsin digests together could provide higher proteome coverage than when using one protease by itself.

Key Terms: Protemics
Biochemistry
Proteases

**BC-21**

## DNA Methylation as the Potential Basis of Caste Differentiation in Queen and Worker Honey Bees

Jackson Mower (North Carolina School of Science and Mathematics), Advisor: Amy Sheck (North Carolina School of Science and Mathematics)

The caste system of *Apis mellifera*, (honey bee), is an example of epigenetics. Queen and worker bees both possess similar genotypes, but exhibit different phenotypes. The proposed cause of this dichotomy is DNA methylation, which silences genes. DNA methylation is an epigenetic phenomenon that involves the addition of methyl groups to DNA through DNA methyltransferase (DNMT). A DNMT system has been detected in honey bees, but the activity of the enzyme has yet to be proven in adult worker bees. Studies suggest that the female honey bee genome contains the genes required for both a worker and a queen, but the queen specific genes are suppressed in worker bees through DNA methylation. The goal of this project was to determine if DNMT is active in adult worker honey bees, and to compare the activity of DNMT between queen and worker larvae. One adult worker bee was tested first with an ELISA-based test that analyzed nuclear and cytoplasmic extracts of the bee. The results suggest that adult worker honey bees possess a working DNMT system. Cytoplasmic and nuclear extracts from three queen and two worker age-matched larvae were also subjected to the assay. The results suggest that worker larvae exhibit less DNMT activity than queen larvae. This does not support the hypothesis that queen genes are suppressed in worker larvae, but more data are needed. Honey bees are an attractive model for the study of epigenetics. With further research, epigenetic therapies could be implemented in health care.

Key Term: Epigenetics

**BC-22**

## Hormonal-like Effects Of Bisphenol A (BPA) On Estrogen Receptor (ER) And Tumor Suppressor Protein, p53 In Breast Cancer Cells

Maria Yonan (Oakland Unversity), Alessandra Boufford, Amy Seibert, Advisors: Dana Ruskin and Sumi Dinda (Oakland University)

Estradiol ($E_2$) and progesterone play a crucial role in the growth, development, and differentiation of the breast cells; their actions being facilitated by receptors. The hormone-receptor complex triggers cellular events by activation/inactivation of hormone-responsive genes. Cancer is a balance between the oncogenes and tumor suppressor genes (TS). Activation of oncogenes or loss/inactivation of TS will cause uncontrolled cell proliferation and can lead to cancer. Our lab has been working on the hormonal regulation of tumor suppressor proteins inT47D breast cancer cells. Inactivated TS will lead to uncontrolled cell proliferation due to absence of apoptosis. Bisphenol A (BPA) is a polymerizing agent found commonly in plastics and has been linked to xenoestrogenic activity. In this study, we analyzed the estrogen-like effects of BPA on the expression of ERα and p53 (TS) with hormonal and anti-hormonal treatments in T47D cells. Although estradiol treatment down regulates ERα expression in stripped serum, BPA causes an increased expression of ERα under similar conditions. In comparison to the control, increased BPA concentrations demonstrates decreased expression of ERα,whereas the optimal concentration (500-600 nM) of BPA has shown the increased levels of p53 expression. Expressions of ER and p53 plateaued at 12-48 hrs when treated with optimal concentrations of BPA. Treatment of BPA and $E_2$ has shown to increase the levels of p53 and ERα which was blocked by ERα antagonist and SERM. Our initial observation suggests that these effects may be ER mediated. Further studies are underway to explore the correlation between p53 and ER.

Key Terms: Endocrinology
Biochemistry

**BH-01**

## The Role of Gesture in Second Language Word Learning

Laura Morett (University of California, Santa Cruz; University of Pittsburgh), Advisors: Brian MacWhinney (Carnegie Mellon University), Ray Gibbs (University of California, Santa Cruz)

Recent research investigating the role of gesture in second language (L2) acquisition (cf. Gullberg, 2006; 2010) has revealed that gesture enhances L2 speech perception (Hubbard, 2009) and lexical acquisition (Kelly, McDevitt, & Esch, 2009). Based on this research and work showing that gesture embodies mental representations of events and actions expressed through language (Hostetter & Alibali, 2010), gesture is predicted to facilitate L2 word learning over alternative methods, such as text and images.

The work presented here consists of four related studies examining gesture's effect on L2 word learning. Participants consist of a total of 80 English-speaking undergraduate students at a medium-sized public research university in the US who are unfamiliar with Hungarian (average age=22 years). In each study, 20 Hungarian words and their English translations are presented one-by-one, accompanied by iconic gestures, beat gestures, images, text, and speech representing the word meanings. L2 word recall is tested via production of English translations in response to Hungarian words at 3 time intervals: 5 minutes, 1 week, and 1 month after learning.

The results of this work indicate that text facilitates passive L2 word learning to the greatest degree. Nevertheless, this effect is mitigated by time and modality of test. Current research, the results of which will be discussed in this presentation, investigates whether active L2 word learning can be enhanced via gesture production. Together, the results of this work elucidate the role of gesture in L2 word learning, providing insight into the embodiment of lexical representations in a novel L2.

Key Terms: Psychology
Linguistics
Second language acquisition

**BH-02**

## Omega-6 to Omega-3 Ratio and Higher Order Cognitive Functions in 7-to-9 Year Olds

Kelly Will (University of North Carolina at Chapel Hill), Advisor: Carol Cheatham, PhD (University of North Carolina at Chapel Hill)

Omega-3 and omega-3 fatty acids are found in abundance in the human brain, and omega-3 fatty acids have long been thought to be important to cognitive function. However, omega-6 fatty acids are also important for neuronal functioning including synaptic transmission and synaptogenesis. Moreover, omega-6 and omega-3 fatty acids work together in the brain. We hypothesize that children with a lower omega-6/omega-3 ratio will perform better on tests of cognitive function than children with a higher ratio. Children ages 7 to 9 provided three days of diet recalls and their parents completed a Diet History Questionnaire, a Temperament in Middle Childhood Questionnaire, and a demographic questionnaire. The participants then completed a series of computerized, standardized cognitive function tests using CANTAB software. Preliminary results indicate that the omega-6/omega-3 ratio is a significant predictor of speed and efficiency of processing on the most challenging problems in measures of spatial working memory, $F(11,51)=2.08$, $p=.039$, and planning $F(11,45)=2.24$, $p=.029$, above and beyond covariates such as maternal education and age.

Key Terms: Executive Functions
Fatty Acids
School-Age Children

**BH-03**

## Impaired Associative Learning and Cell Loss in Rats Exposed to an Iron Deficient Diet and Neonatal Alcohol Exposure

Dorothy L. Dobbins (East Carolina University), Iola D. Conchar (East Carolina University), Ellen M. Sheffer (East Carolina University), Advisor: Tuan D. Tran (East Carolina University)

Alcohol consumption during pregnancy is detrimental to the fetus and greatly increases the risk of having children with fetal alcohol spectrum disorder (FASD). Fetal alcohol exposure (FAE) severely damages the cerebellum and hippocampus - structures that mediate learning processes. During development, micronutrient deficiencies synergize with FAE to exacerbate neurobehavioral damage. Indeed, iron deficiency (ID) frequently accompanies alcohol use during pregnancy. It is the most common nutritional deficiency in pregnant women of child-bearing age and 7% of toddlers. Moreover, ID causes behavioral deficits that parallel those seen in FASD, suggesting that these conditions may synergize to heighten alcohol's neurotoxicity. Iron-sufficient (IS) or ID rats were generated from mothers that received 100 ppm Fe or 4 ppm Fe diets, respectively. Pups received alcohol (0, 3.5, 5.0 g/kg) from postnatal days (PD) 4-9. At ~PD 32, they underwent delay or trace eyeblink classical conditioning (ECC). Afterwards, their cerebella and hippocampi were examined for cell loss in key regions important for ECC. Results showed FAE and ID exacerbated learning deficits. However, IS protected against the impact from FAE in rats trained with delay, but not trace ECC. These results elucidate the need for further investigations into the role micronutrients play in minimizing the impact of FAE-induced neuropathology. Research support: NIH 1R21AA017281-01A2to TDT.

Key Terms: Neuroscience
Alcohol Studies
Neurotoxicity

**BH-04**

## Perceived Racial Expectations of Children

Jessica Roesslein (Lindenwood University), Advisor: Michiko Nohara-LeClair (Lindenwood University)

Racial prejudice has been an ever changing issue in society and feelings of prejudice are prevalent among minority Americans of all ages. Racism has been shown to cause a host of stress related health diseases in adults and amongst children causes a variety of psychological issues ranging from depression to attention deficit hyperactivity disorder. Researchers have found evidence that acts of prejudice have been shown to be more harmful than overt acts of racism. The present study investigated prejudice by having children interpret an ambiguous drawing depicting white and black children interacting on a playground. Children between the ages of 5 and 12 years old were asked to narrate what they thought was happening in the drawing. The children's responses were coded as prosocial acts or social conflict and in each case, they were asked to identify the instigator of the behaviors. Chi-squared analysis of the data suggested a trend toward white children depicting their own race more favorably. African Americans, however, were not seen as significantly antisocial by these children, although this trend emerged in the descriptive data. These results do indicate that although more research is needed, prejudice can be found in children as young as five years old. By alerting children, parents, and educators early on about the presence and tangible harm that prejudice creates, we can in turn begin to combat it. By lessening the cumulative stress effects of prejudice in children, we can reduce the frequency of detrimental health effects in both children and adults.

Key Terms: Psychology
Racism
Child prejudice

**BH-05**

## Aripiprazol's Effects on the Linkage Between Repetitive and Restrictive Behaviors and Executive Function in High Functioning Autism

Ryan DeLapp (University of North Carolina at Chapel Hill), Lin Sikich (UNC School of Medicine), James Bodfish (UNC School of Medicine), Gabriel Dichter (UNC School of Medicine), Advisor: Gabriel Dichter (University of North Carolina at Chapel Hill)

There is currently no pharmacological treatment FDA-approved to treat the core symptoms of autism. However, aripiprazole (Abilify ®), an atypical antipsychotic medication originally approved to treat irritability, has also shown efficacy in reducing a core symptom in autism, repetitive and restrictive behaviors (RRBs). The main objective of this pilot study was to replicate prior evidence demonstrating the effects of aripiprazole on RRBs, while also investigating a previously supported linkage between RRBs and deficits in executive function (EF). I analyzed previously gathered data from 13 high functioning autistic individuals, who were assessed before and after receiving aripiprazole for 8-weeks with an assortment of symptom inventories. In the assessment of RRBs, participants significantly improved according to reductions on both the RBS-R subscales ($p<.05$), and the PDD-CYBOCs Compulsions subscale ($p<.05$). Additionally, in assessing EF, participants showed a highly significant improvement ($p<.01$) on the inhibition and shifting subscales of the BRIEF, but did not show significant changes in target latency and accuracy ($p>.05$) on the Oddball Target Detection task. Lastly, a Pearson Correlation Coefficient was conducted to determine the relationship between RRBs and EF during aripiprazole treatment. Results showed a pretreatment positive correlation between the RBS-R Sameness subscale and BRIEF Shifting subscale ($p<.05$). Post-treatment analysis revealed positive correlation between the RBS-R Self-Injurious Behavior subscale and the BRIEF Shifting subscale along with a positive correlation between RBS-R Self-Injurious Behavior subscale and Target Latency on the Oddball task. This study replicates aripiprazole’s reduction of RRBs and provides support for the linkage of RRBs and EF during pharmacotherapy. Lastly, in light of research supporting a connection between aberrant brain function and deficit in EF, this study supports a future investigation of how the relationship between RRBs and EF can be used to explain the neurological impact of pharmacotherapy in autism.

Key Terms: High Functioning Autism
Pharmacological Treatment
Aripiprazole

**BH-06**

**Developing a computerized method for quantifying characteristics of bubble nests formed by *Betta splendens***

Raluca Illinik (Christopher Newport University), Carol Paulson (Christopher Newport University), Kaitlin Ryan (Christopher Newport University), Laura Little (Christopher Newport University), Morgan Warner (Christopher Newport University), Jeffrey Illinik (Virginia Wesleyan College), Brian Roller (University of Arizona), Advisor: Andrew Velkey

Bubble nesting is an important component of the reproductive cycle of *Betta splendens*. Many environmental factors can influence bubble nesting behaviors and nest construction. Specifically, nest size can be an indicator of mate quality, and nest density can be an important factor that influences the viability of eggs that are subsequently deposited in the nest. Previous studies have employed manual grid-counting and pixel-counting strategies to examine bubble nest characteristics; however, grid-counting lacks precision, and pixel-counting, while more precise, is time-consuming when analyzing large data sets. The use of digital image analysis can reduce measurement error and will allow for the quantification of other important characteristics such as intra-nest density variations. The purpose of the present study is to develop and test a computerized image analysis tool to efficiently quantify bubble nest characteristics. Such a method can be used to further behavioral research associated with bubble nesting in *Betta splendens*.

Key Terms: Bubble nesting
Behavioral psychology
Computerized

**BH-07**

## Non-Governmental Organizations and Tomorrow's Nanotechnology

William Reynolds (Ventura College), Cassandra Engeman (University of California, Santa Barbara), Jennifer Earl (University of California, Santa Barbara), Barbara Herr Harthorn (University of California, Santa Barbara)

With possible unknown health and safety risks and no regulation on handling practices, engineered nanomaterials are attracting new research to understand public risk perception and its role in the development of nanotechnology. Non-governmental organizations, or interest groups, serve as self-identified representatives of and advocates for the public. As such, they have the potential to effect public perception and the future governance of nanotechnology. My research asks: 1) what issues are these organizations concerned about? and 2) what actions have they taken in response to those issues? To that end, a matrix of organizations and summaries of data on those organizations has been created through internet search tools and organizational references and then catalogued for future research. Preliminarily, a broad spectrum of eighty organizations has been found globally. These organizations as a whole are focused on the issues of public and environmental health and safety around nanotechnology with the goal of some kind of regulatory change. Currently, their actions are focused on the issuance of publications on nanotechnology and possible solutions to environmental and human health impacts. Future research will examine why these groups are concerned with nanotechnology and what possible impact they may have on governmental regulatory policy and industry practices of engineered nanomaterials.

Key Terms: Nanotechnology
Social Science

**BH-08**

## The Effects of Social Anxiety, Sensation Seeking, and Alcohol Outcome Expectations on Pregaming in College Students

Katie McCaughey (Elon University), Advisor: Dr. Gabie Smith (Elon University)

Read et al. (2010) found that approximately two-thirds of college students that drink alcohol engage in "pregaming" behaviors. Considering the prevalence of this behavior on college campuses and the health concerns associated with the behavior, more research is needed regarding the motives and decision-making factors that influence this behavior. Very little research, however, has been performed to investigate the motives and factors that lead to pregaming. The current study investigated factors that may contribute to pregaming; specifically, we examined the influence of social anxiety (Leary, 1983), sensation seeking (Zuckerman, 1994), and alcohol outcome expectations (Leigh & Stacy, 1993). Previous research has shown that these variables influence alcohol use behaviors, in general. We hypothesized that social anxiety, disinhibitory sensation seeking, and positive alcohol expectancies would combine to predict frequency of pregamining behaviors. We predicted that both sensation seeking and social anxiety would positively relate to pregaming and that alcohol outcome expectancies would mediate these relationships. We further hypothesized that participants' motivations for pregaming would be affected by the variables under study.

College student participants (ages 18-22) completed an online questionnaire assessing each of the variables. Thematic coding of the qualitative data indicated that participants' motivation for pregaming included pregaming to feel more relaxed, to save money, and to become more excited for the upcoming event. Participants' responses show that drawbacks to pregaming include overestimating the amount of alcohol consumed and experiencing negative physical effects.

Key Terms: Alcohol Risk-taking
Social Psychology

**BH-09**

## The Role of Curiosity and Openness in Chinese Peer Relations

Brendan Yorke (University of North Carolina at Chapel Hill, Advisor: Dr. Mitch Prinstein (University of North Carolina at Chapel Hill)

One's self concept in middle school is strongly influenced by peer-perceived norms, therefore culturally homophilic relationships can reduce intercultural competencies later in life. This pilot study compares two types of peer relationships in Chinese youth. We postulate that youth with greater curiosity, openness, and shared activities will have less negative and more positive cognitions about their "different peers" and rate their relationship with best friends as more intimate.

Using a class roster, Chinese youth selected a perceived best friend and a different peer. Participants reported on their relationships with a best friend and a perceived "most different peer" using the Network of Relationship Inventory (NRI). Curiosity was measured through the General Social Curiosity Scale (SCS-G), the Covert Social Curiosity Scale (SCS-C), the CACPI-C, and the CACPI-A. The Big Five Factors Questionnaire for Children (BFQ-C) measured participant's Openness. Shared activities were measured using a list of extra-curricular activities common in China.

Youth rated "best friends" and "most different peers" differently on positive relationship qualities (ie. Instrumental aid). There were no significant effects of negative relationship qualities (ie. Criticism), Openness, or common activities on relationship status. General Social Curiosity was positively correlated with intimacy with a best friend. Developing mutual instrumental aid and social curiosity would help youth find satisfaction in their relationship with diverse peers.

Key Terms: Psychology
Peer Relations
Cultural Differences

**BH-10**

## Group Composition and Male-male Aggression in Wild Howler Monkeys (*Alouatta palliatta*) on Isla de Ometepe

Jordan A. Miller (Duke University), Advisor Amy Schreier (Duke University)

Male-male relationships are a complex component of primate social systems. The multi-male, multi-female groups of *Alouatta palliata* provide a perfect venue for the study of male group composition and agonistic interactions. Male competition over access to females is an important aspect of primate societies that often manifests itself in the form of overt aggressive behaviors. How does the presence of females influence aggression in males? I observed a wild group of mantled howler monkeys at the Maderas Rainforest Conservancy on Isla de Ometepe, Nicaragua, using instantaneous scan sampling of adult males at two minute intervals for thirty minutes. As predicted, when a female was within a 5 meter radius of the focal male, there were a greater number of males in the focal individual's 5 meter radius (1.36±0.44) than when a female was not present (1.22±0.46). Additionally, when at least one female was within the 5 meter radius of the focal male, the male's nearest neighbor was an adult female (90.2±18.7%) more often than it was another male (10.5±18.9%). Finally, males demonstrated exceptionally low rates of aggression, with only 4 instances of aggression recorded in a total of 308 scans. This supports van Hoof & van Schaik's (1994) model that egalitarian male relationships and scramble polygynandry will persist when there is an absence of male dominance, demonstrating the peaceful yet complex nature of *A. palliata* males.

Key Terms: Behavioral Ecology
Evolutionary Anthropology
Aggression

**BH-11**

## Stature Estimation Utilizing the Upper Breadth of the Femur

Tony Fitzpatrick (Georgia State University), Leslie Brown (Georgia State University). Advisors: Frank Williams (Georgia State University), Bethany Turner (Georgia State University)

Forensic stature estimation from fragmented skeletal remains requires the use of non-standard formulae. The proximal femoral breadth, measured along the axis of the femoral neck, has been tested in the past on skeletal populations of known stature, and has been shown to have a high correlation with the length of the femur. Length of the femur is in turn highly correlated with living stature. A measurement that is slightly modified, but simpler to collect has been tested in skeletal populations which lack living stature information, with similar results. The modified measurement, or upper breadth of femur, is taken from the most superior point on the fovea capitis to the inferior aspect of the greater trochanter. In this study, data were collected from individuals housed in the Bass Donated Skeletal Collection at the University of Tennessee of known age and living stature. In a sample of 63 females, the correlation between upper breadth of femur and length of femur is high at .667, similar to previous studies. In the male population of 146 individuals, there is almost no correlation at .203. While this dissimilarity is surprising, differences between males and females in frame-size measurement to stature correlations have been shown in other areas of research. These results suggest that the upper breadth of femur measurement may be useful for estimating the stature of females, but other methods must be utilized for males.

Key Terms: Forensic Anthropology
Stature Estimation

**BH-12**

**The Use of the Prehensile Tail in *Alouatta palliata* (mantled howler monkey)**

Jocelyn Antonio (Duke University), Advisor: Amy Schreier (Duke University)

In different species of New World Monkeys it has been observed that the prehensile tail serves similar functions to those of the arms and legs. As such, the tail aids monkeys in activities to provide balance and is often referred to as a fifth limb. Prehensile tail use was observed in a group of *Alouatta palliata* (mantled howler monkey) in the Coffee Forest on Isla de Ometepe, Nicaragua in August 2011. Data were recorded on the monkeys' activity, tail use, and the level of the forest using a scan sampling technique. I hypothesized that *A. palliata* has a prehensile tail because it is useful during certain activities and in certain layers of the rainforest. *A. palliata* used the tail 35.6% of the time throughout all activities. The prehensile tail was used the most during sitting (41.5%) followed by resting (36.8%), feeding (10.5%), walking (4.3%), standing (3.2%), climbing (2.5%), jumping (0.7%), and foraging (0.4%). Furthermore, the prehensile tail was used more in the lower level of the rainforest (71.2%) than in the upper level (28.9%). *A. palliata* use their tail preferentially for stationary activities and in the lower level of the rainforest.

Key Terms: mantled howler monkeys
prehensile tail
Alouatta palliata

**BH-13**

## The Risk of Obesity Relative to Educational Attainment, Aspirations, and Expectations

Chandni Kazi (University of California, Berkeley), Manisha Rai (University of California, Berkeley), Advisors: Alison Cohen (University of California, Berkeley), Barbara Abrams, DrPH, RD (University of California, Berkeley)

Over the past 20 years, there has been a dramatic increase in obesity in the United States (CDC 2011). The more prominent causes of obesity are credited to a combination of excessive energy intake and lack of physical activity. Although these factors are highly correlated with obesity, there are underlying social factors that may lead to a better understanding of this epidemic and offer other points of intervention. This research focuses on education level as the prime social factor and how it relates to obesity. It is well documented that education is inversely associated with the prevalence of obesity. However, the mechanisms by which this association operates are still poorly understood. This project analyzes data collected from the Bureau of Labor Statistics: National Longitudinal Survey of Youth 1979 to analyze the risk of obesity relative to educational attainment, aspirations, and expectations. This trend implies that socioeconomic status may dictate overall health, such that a low socioeconomic status could be linked to poor health. Since education is a determinant for socioeconomic status, this analysis is pertinent to the social gradient of health. This research concludes that attaining and expecting an education acts as a protective factor for the onset of obesity, whereas aspiring for an education has no statistically significant effect. Furthermore, a multivariable analysis will be implemented in order to further assess this trend with respect to known confounders and effect measure modifiers.

Key Terms: Public Health
Epidemiology

**CB-01**

## Multilocus Sequence Typing and Phylogenetic Analysis of *Campylobacter* Isolated from Conventional and Antimicrobial-Free (ABF) Swine and their Environment

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*Campylobacter* is one of the leading pathogens causing foodborne illnesses in the US. Epidemiological evidence has indicated that food animals, including pigs, act as reservoirs of *Campylobacter* strains that can infect humans. The purpose of this study is to determine the clonality or diversity of *Campylobacter coli* isolated from the conventional and ABF production systems at farm, slaughter and environment using multilocus sequence typing (MLST). A total of 129 *C. coli* isolates were selected from fecal, environmental and carcass samples of ABF ($N$ = 71) and conventional ($N$ = 58) production systems. Seven housekeeping genes (*asp, gln, glt, gly, pgm, tkt, unc*) were amplified using PCR and the amplified product was sequenced. Sequence data was analyzed for the determination of allelic profiles and identification of sequence types (STs). Dendrograms and minimum spanning trees were generated to establish the relationships between the genotyped isolates. Isolates with similar sequence types were found between the pigs and their environment at farm and slaughter (ABF: 13, $I_A$ = 0.1308; Conventional: 20, $I_A$ = 0.1357). Higher genotypic diversity was observed among isolates from the conventional swine production systems (ABF: 0.3455 +/- 0.0901; Conventional: 0.3929 +/- 0.0805). Phylogenetic analysis revealed a genotypically diverse *C. coli* population with the presence of *C. coli* isolates sharing a common ancestry in both production systems. Overall, MLST of *C. coli* isolates from two distinct production systems unveil a weak clonal population and diverse genetic makeup of this species.

Key Terms: *Campylobacter*
MLST
Swine

**CB-02**

## Prevalence, Molecular Characterization and Genotypic Analysis of *Campylobacter* and *Salmonella* from Commercial Poultry Farms

Shivaramu Keelara (North Carolina State University), Zou Ming (QAU,China), Heather Pierce (North Carolina State University), Ashley Whitesell (North Carolina State University), Emma Susick (North Carolina State University), Adivsor: Sid Thakur (North Carolina State University)

The objective of this study was to determine the prevalence, antimicrobial susceptibility and clonal relationship of *Campylobacter* and *Salmonella* from commercial poultry farms and their environment. A total of 900 samples (fecal n=400; environment n=500) were collected from ten poultry farms and tested for the presence of *Campylobacter* and *Salmonella*. All the *Campylobacter* (n=119) and *Salmonella* isolates (n=76) were tested for antimicrobial susceptibility to a panel of antimicrobials. The antimicrobial resistant (AR) isolates were further characterized for the presence of resistance genes, class I integrons by PCR. Pulsed-field gel electrophoresis (PFGE) was used to determine the genetic relationships among *Salmonella* and *Campylobacter* isolates from fecal and their environment. *Campylobacter* prevalence was significantly higher in fecal (29.5%) than the in the environment (0.8%; P=0.003). However, There was no significant difference in *Salmonella* prevalence between fecal (8.8%) and the environment (8.4%; P=0.217). The *Campylobacter* isolates exhibited resistance to only tetracycline (n=66; 55.5%). Whereas, *Salmonella* isolates exhibited wide spectrum of AR with highest frequency of resistance to streptomycin (46%) followed by tetracycline (31.5%). We detected multidrug resistant (MDR) (n=26; 34.2%) only in *Salmonella* isolates. All tetracycline resistant *Campylobacter* isolates carried *tet(O)* gene. *Salmonella* isolates carried different resistance genes i.e., ampicillin ($bla_{\text{TEM}}$), cephalosporins ($bla_{\text{CMY-2}}$), streptomycin (*strA* or *aadA1*), and tetracycline (*tetA* and *tetB*) genes. We also detected class I integrons (1kb) in the MDR isolates. The PFGE patterns of *Campylobacter* and *Salmonella* showed 100% similarity among the fecal and environmental isolates highlighting the potential role of environment in transmission of pathogens to birds.

Key Terms: *Salmonella*, *Campylobater*
Antimicrobial resistance
PFGE

**CB-03**

**Exposure to Host Ligands Correlates with Co-localization of Gal/GalNAc Lectin Subunits in Lipid Rafts and Phosphatidylinositol Signaling in *Entamoeba histolytica***

Amanda Goldston (Clemson University), Amrita Koushik (Clemson University), Rhonda Powell (Clemson University), Advisor: Lesly Temesvari (Clemson University)

*Entamoeba histolytica* is an intestinal parasite responsible for dysentery and liver abscess. Parasite cell surface receptors, such as the galactose/N-acetylgalactosamine lectin (Gal/GalNAc lectin), facilitate attachment to host cells. The Gal/GalNAc lectin is composed of heavy (Hgl), intermediate (Igl), and light (Lgl) subunits. Although, Igl is constitutively localized to lipid rafts, cholesterol-rich domains, Hgl and Lgl transiently associate with this compartment in a cholesterol-dependent fashion. Trophozoites were exposed to biologically relevant ligands to determine if ligand-binding influences the submembrane distribution of the subunits. Exposure to host red blood cells or collagen, Gal/GalNAc lectin ligands, was correlated with enrichment of Hgl and Lgl in lipid rafts. This enrichment was abrogated in the presence of galactose, suggesting that direct lectin-ligand interactions are necessary to influence subunit location. Exposure to fibronectin, a control extracellular matrix (ECM) component, did not affect the localization of subunits. The colocalization of the subunits in lipid rafts after ligand-binding may facilitate signaling; therefore, the submembrane distribution of another signaling molecule, phosphatidylinositol (4,5) bisphosphate ($PI(4,5)P_2$), was also assessed after exposure to ECM. $PI(4,5)P_2$ was localized to lipid rafts prior to exposure to ECM; but, $PI(4,5)P_2$ levels decreased in this compartment only after incubation with collagen. In other systems, ligand binding induces hydrolysis of $PI(4,5)P_2$ to inositol trisphosphate and diacylglycerol, which facilitates increases in cellular calcium. Calcium levels also increased in after exposure to collagen but not fibronectin. Therefore, in *E. histolytica*, $PI(4,5)P_2$–based signaling may be activated after interaction with host components, and lipid rafts may regulate this event.

Key Terms: Parasitology
Molecular Biology
Biochemistry

**CB-04**

**Anchoring the dog to its relatives reveals new evolutionary breakpoint regions across 11 species of the Canidae and provides new clues for the role of B chromosomes.**

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Evolutionary breakpoint regions (EBRs) may reflect naturally occurring fragile regions that have been reused as part of evolutionary related translocation events. In human cancers, common translocations often span EBRs and it has been theorized that the chromosomal reorganization events leading to speciation may also be associated with cancers. In this context, we study genome organization in the Canidae, a group with chromosome numbers ranging from 2n=34+Bs (red fox) to 2n=78 (domestic dog). This karyotypic range developed via breakage-fusion events involving whole-arm segments during speciation, reflecting a high rate of karyotypic evolution since their divergence from a common ancestor 10MYA. We explored canine EBRs using multicolor fluorescence *in-situ* hybridization analysis to physically map groups of dog-derived bacterial artificial chromosome (BAC) clones to the karyotypes of eleven species of wild canid. As the panels were hybridized to test species, the order of hybridization signals revealed the orientation of the dog-syntenic regions. Shared EBRs were narrowed to ~1-3Mb regions and compared across each species. Our findings suggest that the EBRs associated with speciation in the Canidae are compatible with recent phylogenetic groupings and provide evidence that these breakpoints are also recurrently associated with spontaneous canine cancers. We identified several regions of domestic dog sequence that share homology with canid B chromosomes, including additional cancer associated genes, suggesting that these supernumerary elements may represent more than inert passengers within the cell. We propose that the complex karyotype rearrangements associated with speciation of the Canidae reflect unstable chromosome regions described by the Fragile Breakage Model.

Key Terms: Cytogenetics

**CB-05**

## BAF57 Deregulation: Turning on the SWI/SNF Switch for Advanced Prostate Cancer

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(Department of Cancer Biology, Kimmel Cancer Center, Department of Urology, Department of Radiation Oncology, Thomas Jefferson University)

Prostate cancer is one of the leading causes of male mortality in the United States. Androgen receptor (AR) signaling, necessary for disease development and progression, is targeted for therapy. However, remission is not durable and a majority of patients eventually develop refractory castration resistant prostate cancer (CRPC), due to inappropriate androgen-independent AR activation. Therefore, it is crucial to investigate the signaling components in advanced disease for identifying new therapeutic targets. BAF57, a component of the multisubunit SWI/SNF chromatin remodeling complex, has been previously shown to be critical for androgen dependent AR activity. However, the consequences of BAF57 deregulation in CRPC remain unstudied. Here, we demonstrate that BAF57 is aberrantly elevated in a small cohort of advanced prostate cancers. Mimicking BAF57 aberrations *in vitro* and using unbiased microarray analyses, we have identified certain genes whose upregulation confers a migratory phenotype to prostate cancer cells. Preliminary chromatin immunoprecipitation analyses indicate that BAF57 deregulation serves to direct, significant enrichment of the core ATPase subunits of the SWI/SNF complex along with histone acetylation, at discrete gene loci. These data implicate SWI/SNF chromatin remodelers as novel modulators of metastatic signaling in prostate cancer and offer the promise of newer, more effective platforms for therapeutic intervention.

Key Terms: Prostate cancer
Chromatin remodeling
Metastasis

**CB-06**

**Repression of miR-199a and miR-125b By Reactive Oxygen Species Promotes Ovarian Tumor Growth and Angiogenesis through ERBB2 and ERBB3**

Jun He (Thomas Jefferson University), Yi Jing, Qing Xu, Faton Agani, Richard Carpenter, Ling-Zhi Liu, Advisor: Bing-Hua Jiang (Thomas Jefferson University)

Elevated reactive oxygen species (ROS) are strongly associated with cancer; however, the role of ROS in cancer development remains elusive. Our study previously showed that ovarian cancer cells have much higher level of ROS than normal cells and the excessive ROS promote tumor angiogenesis. However, the underlying mechanism remains to be elucidated. Here we demonstrate that two microRNAs, miR-199a and 125b, are ROS-regulated miRNAs. The excessive ROS inhibited expression of miR-199a and miR-125b in ovarian cancer cells and ovarian cancer xerograph model in nude mice. We further established that these two miRNAs directly targeted ERBB2 and ERBB3. Collectively, the repression of miR-199a and miR-125b by excessive ROS relieves the inhibition of ERBB signaling, leading to the activation of downstream Akt/p70S6K1/HIF signaling and induction of angiogenesis and tumor growth. These results provide the direct link between ROS and tumorigenesis, and potential therapeutic application of miR-199a and miR-125b in the future.

Key Terms: ROS
miRNA
angiogenesis

**CB-07**

# Canine Oral Melanoma – Cytogenetic Characterization of Fresh Tissues, Cell Lines, and Archival Tissues

Kelsey Poorman (North Carolina State University), Luke Borst (North Carolina State University), Matthew Breen (North Carolina State University)

Canine oral melanoma is a common and aggressive tumor with poor life expectancy. Molecular cytogenetic characterization of these tumors is sparse. There are numerous biological resources available for researchers, including fresh and archival primary tumors, established cell lines, and a series of genomics tools. While it is widely accepted that cell lines may be used to represent the primary disease, they often evolve *in vitro* beyond what is seen in primary tumors. Additionally, DNA obtained from archival specimens can be degraded, leading to decreased data quality. The purpose of this study was to characterize genome-wide numerical and structural aberrations in canine oral melanomas, using a cohort comprising fresh-frozen tissue, formalin-fixed paraffin embedded (FFPE) tissue and cell lines.

We assessed fresh primary tissues (n=5), primary cell lines (n=8), and FFPE archival tissue (n=20) using a combination of high resolution genome-wide array based comparative genomic hybridization (aCGH) and multicolor fluorescence *in situ* hybridization (FISH).

aCGH analysis revealed numerous DNA copy number aberrations in all melanoma samples evaluated. Most notable were characteristic patterns of gain followed by loss on dog chromosomes (CFA) 10, 26, and 30. Various chromosome instabilities were observed and confirmed by FISH. Cell lines recapitulated aberrations evident in primary tumors, suggesting their importance in melanoma pathogenesis. However, cell lines also showed cytogenetic aberrations not evident in primary tumors, suggesting these were secondary events as a result of culture. Among archival FFPE cases, it was evident that the ability to detect copy number aberration declined with the age of the specimen.

Key Terms: Veterinary Oncology
Cytogenetics
Molecular Biology

**CB-08**

# Characterization of Recombinant *Metallosphaera sedula* Msed_1072 to Augment Production of Microalgal-Derived Biofuel

Rushyannah Killens (North Carolina State University), Rachel Turner (North Carolina State University), Advisor: Amy Grunden (North Carolina State University)

**Background:** Lipid-producing microalgae are emerging as the leading platform for producing alternative biofuels in response to diminishing petroleum reserves. Optimization of fatty acid production is required for efficient conversion of microalgal fatty acids into usable transportation fuels. Microbial lipases can be used to enhance fatty acid production because of their efficacy in catalyzing hydrolysis of esters into alcohols and fatty acids while minimizing the potential poisoning of catalysts needed in the biofuel production process. Although studies have extensively focused on lipases produced by mesophilic organisms, our knowledge of lipases produced by thermophilic, acidic tolerant microbes, such as *Metallosphaera sedula*, is limited. It is likely that enzymes produced by *M. sedula* will exhibit high specific activities at extremely high temperatures (>70C) and acidic pHs (<5). These characteristics will be important for the conversion of microalgal fatty acids/lipids into transportation fuel because of temperature and pH conditions used for fuel conversion. The primary goal of this study was to recombinantly express the *M. sedula* gene encoding Msed_1072 in *Escherichia coli* to enable its biochemical characterization. It is hypothesized that this lipase will be more stable at elevated temperatures and acidic pHs compared to homologous mesophilic lipases, which has important implication for their use in the lipid to fuel conversion process.
**Methods:** The gene encoding *Msed_1072* was cloned into the pET-28a plasmid. Recombinant protein was expressed in *E. coli* strain BL-21, purified using affinity chromatography, and biochemically characterized.
**Results:** The gene encoding *Msed_1072* was successfully cloned and used for recombinant protein expression. Purified protein was evaluated for lipase activity over a range of temperature and pH conditions.
**Conclusion:** The objectives of this study were to purify and characterize Msed_1072 from *M. sedula*. This enzyme hold the promise of being highly stable at elevated temperatures and acidic pHs which are attractive attributes for use in algae-based biofuel production.

Key Terms: Biofuel
Lipases

**CB-09**

## A Dissection Of Mcm10's Functions In *D. melanogaster*

Michael Reubens (East Carolina University), Advisor: Tim W. Christensen (East Carolina University)

Highly efficient DNA replication is essential for the accurate transmission of genetic material from cells to their progeny; likewise, the maintenance of epigenetic chromatin states is essential for the faithful reproduction of the transcriptional state of the cell. Improper regulation, and coordination, of these essential processes can result in genomic instability, which can manifest in disease or potentially the death of the organism. It is becoming more apparent that these two processes are linked through interactions between DNA replication proteins and chromatin associated proteins. Recently our lab conducted an analysis of two *Drosophila* Mcm10 mutants which demonstrated that *Mcm10* not only plays a role in DNA replication, but also has a role in heterochromatic silencing and chromosome condensation; thus the *D. melanogaster* homolog Mcm10 provides an excellent subject to study the connections of these two essential processes. Interaction studies in yeast, as well as both phenotypic and genetic analyses in *Drosophila*, imply that the conserved C-terminus is important for the many interactions carried out by this promiscuous protein. Therefore, our investigation of Mcm10 in *Drosophila* has continued using a collection of 35 isolated strains which contain various point mutations, or deletions, within Mcm10 coding sequence; allowing for an in-depth dissection of this conserved protein using both phenotypic and genetic analysis in *Drosophila*. Throughout this study, we intend to elucidate the regions of the protein responsible for its biological functions, in hopes of better understanding Mcm10's role in these essential biological processes, as well as replication and chromatin biology in general.

Key Terms: DNA Replication
Chromatin Biology
Molecular Biology

**CB-10**

## The ubiquitin Ligases CHIP and MuRF1 inhibit physiological cardiac growth (hypertrophy) in response to exercise

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The regulation of muscle size depends upon the balance of protein synthesis and the protein degradation of the sarcomere. We have recently identified 2 ubiquitin ligases which are have roles in degrading sarcomere proteins, as well as roles in regulating hypertrophic signaling processes in pathologic cardiac hypertrophy. In the present study, we investigated the response of CHIP -/- and MuRF1 -/- mice to 5 weeks of voluntary running, a common model used to induce physiologic cardiac hypertrophy. We identified that exercise-induced cardiac growth was significantly increased 28.8% and 21.0% in CHIP-/- and MuRF1-/- mice, respectively, compared to strain-matched wildtype controls. Since the insulin-like growth factor (IGF-1)-Akt signaling pathway mediates this running-induced increase in cardiac mass, we next investigated these signaling pathways in CHIP -/- and MuRF1-/- hearts by Western blot analysis. In both strain-matched wild type controls, we identified activation of Akt-1 and the downstream effector GSK3-β activity (by increased phosphorylation) compared to age-matched sham wildtype animals. While the CHIP -/- hearts demonstrated an exaggerated Akt-1 and GSK3-β activation (phosphorylation) after running, as expected with their exaggerated cardiomyocyte size, these signaling pathways were reduced in the MuRF1 -/- mice compared to their sham controls. These studies demonstrate for the first time a role for cardiac CHIP and MuRF1 in inhibiting the development of physiologic cardiac hypertrophy, by regulating different signaling processes. CHIP interacts with Akt directly to inhibit its activity in vivo, while MuRF1 enhances cardiac hypertrophy by some other, yet to be identified signaling pathway(s).

Key Terms: ubiquitin ligase
hypertrophy
cardiac

**CB-11**

## Resequencing of *Clostridium beijerinckii* SA-1 / ATCC 35702

Satya Makwana (North Carolina State University), Advisors: Michael Thon (Unversidad de Salamanca), Andrea Azcarate-Peril (University of North Carolina, Chapel Hill), José M. Bruno-Bárcena (North Carolina State University)

The most recent crisis in rising oil prices has reinvigorated interest in solvent producing *Clostridia*, well-known for its ability to produce acetone/butanol/ethanol using plant biomass feedstock. Butanol has been considered a viable option as an alternative high energy content molecule. However, butanol's toxic effects on solvent producing *Clostridia* have restricted final butanol concentrations in the broth. To overcome this challenge butanol tolerant strains were selected by Lin and Blaschek by applying stress directed evolution experiments on *C. beijerinckii* NCIMB 8052 (NC_009617). The offspring strain, *C. beijerinckii* ATCC 35702/SA-1, was selected and further characterization by our group established the added ability of this strain to co-utilize D-glucose, and D-xylose. In our quest to determine the original source of higher butanol tolerance we compared the genomes of the *C. beijerinckii* NCIMB 8052 parent and SA-1 offspring. Here, we provide evidence for point mutations, insertions, deletions and translocations that have occurred in the offspring *C. beijerinckii* SA-1 strain. This work not only provides insight into the SA-1 genome but also examines the efficiency of assembling the sequences obtained by the Illumina GAIIx platform. The reference genome of *C. beijerinckii* NCIMB 8052 provided a suitable "*in-silico*" template for identifying genetic variations present in SA-1. *In silico* analysis using MAQ version 0.7.1 and Breakdancer indicated a 47% rate of false positive genetic alterations that were discarded when confirmed though further evaluations using PCR and sequencing.

Key Terms: Butanol
Clostridia
Genome assembly

**CB-12**

## Psf2: A Role In Chromosome Condensation

Jeffrey Chmielewski (East Carolina University), Advisor:Tim Christensen (East Carolina University)

In *D. melanogaster*, the CMG complex is a group of proteins that function as the DNA helicase during replication. The CMG complex is composed of cdc45, MCM2-7, and the GINS complex. The GINS complex is a heterotetrameric complex composed of the protein subunits Psf1, Psf2, Psf3, and Sld5. Recent research in human dermal fibroblasts shows GINS is essential for the initiation and elongation stages of chromosomal replication. Working with a null mutation, I have designed a series of experiments aimed at elucidating the function of Psf2 *in vivo*. Using phosphoH3 immunostaining and M-phase indices, I have shown that heterozygous mutants exhibit a significant M-phase delay. EdU incorporation assays show no significant difference in the number of cells in S-phase. However, the pattern of EdU incorporation indicates cells take longer to replicate euchromatin than WT; possibly resulting in the improper packaging of euchromatin as heterochromatin. To corroborate the data seen in the pattern of Edu incorporation, we designed a novel technique to establish the packing ratio of salivary gland polytene chromosomes. Using this novel technique, we are able to show that heterozygous mutants exhibit a significant increase in packing ratio compared to WT. Additionally, in the later stages of egg chamber development, nurse cell nuclei display overly condense polytene chromosomes during the suedo M-phase. We have evidence that indicates these instances of overly condensed chromosomes results in apoptotic egg chambers, seen later in development. This data, when combined, suggests Psf2 has a role during replication that ultimately determines how DNA is packaged.

Key Terms: Molecular Biology
DNA Replication
Chromosome Condensation

**CB-13**

## Arabidopsis Defense Transcriptome At The Transcript Isoform Level

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Tair10 annotation (Nov 2010) indicated that 5,886 Arabidopsis genes (~18%) generate multiple transcript isoforms mostly via alternative transcription starting sites (TSS) and/or alternative splicing (referred to as AS genes). However, the extent of the transcriptome that is regulated at the isoform level is still poorly investigated. To contribute to fill in this knowledge gap and establish a possible functional significance for differential alternative transcript abundance during stress exposure, we characterized the Arabidopsis defense transcriptome via RNA-Seq experiments. In particular, we used Illumina 75 bp paired-end sequencing to study resistant and susceptible Arabidopsis response to inoculation with virulent (vir, DC3000) and avirulent (avr, avrRPS4) bacterium *Pseudomonas syringae* pv *tomato*. By aligning the reads to the TAIR10 gene models using Bowtie and TopHat and determining transcript abundance using the open-source software program Cufflinks and a conservative cut-off of 1000 reads/transcript, we identified 802, 737 and 473 AS genes with at least one transcript isoform differentially accumulated in the pair-wise comparisons mock/avr, mock/vir and avr/vir, respectively. Among them, 161, 141 and 84 genes had two or more isoforms significantly regulated, respectively. We will discuss functional categorization of the regulated AS transcriptome and the impact of alternative TSS and/or AS on the gene products.

Key Terms: Genomics
Bioinformatics
Plant Pathology

**CB-14**

## Apolipoprotein (ApoC-1) Induces Aortic Smooth Muscle Cell Apoptosis

Jennifer Hou (The Johns Hopkins Medical Institutions), Nezar Alsaeedi (The Johns Hopkins Medical Institutions), Advisor: Subroto Chatterjee (The Johns Hopkins Medical Institutions)

About 1.2 million people suffer from heart attacks, in the United States each year (National Heart Lung and Blood Institute, NHLBI). One cause of heart attacks is the apoptosis of aortic smooth muscle cells (ASMC), leading to plaque rupture and afterwards blood clots that can obstruct the artery (NHLBI). We investigated whether novel, human Apolipoprotein (ApoC-I) isoforms contribute to marked apoptosis of ASMC, by activating a membrane-bound neutral sphingomyelinase (NSMase), and whether inhibiting NSMase may inhibit apoptosis and plaque rupture.

To test this hypothesis, first, wild-type and NSMase knock-out mouse aortas were isolated, incubated with treatments: control, ApoC-I and/or NSMase inhibitor, GW4869. Next, the aortic rings were stained with Annexin V-FITC, Propidium Iodide, and Hoechst and subject to confocal microscopy.

We found in wild type, mouse aortic rings, ApoC-I induced a concentration-dependent increase in apoptosis; and, this was mitigated by pre-incubation with GW4869. In NSMase -/- aortic rings, ApoC-I did not induce apoptosis. These results suggest that NSMase plays a crucial role in the ApoC-I induced apoptosis of ASMC *ex vivo,* in mouse aortic rings. These findings were consistent with those of Kolmakova A, et al. (2004) Apolipoprotein C-I Induces Apoptosis in Human Aortic Smooth Muscle Cells via Recruiting Neutral Sphingomyelinase. *Arteriosclerosis, Thrombosis, and Vascular Biology* 24: 264-269. For future studies, if novel ApoC-I isoforms are truly and solely responsible for causing plaque rupture *in vivo*, then this tenet has immense potential for early screening and detection, and the development of more specific inhibitors.

Key Terms: Cardiovascular Disease
Confocal Microscopy
Cell Signaling

**CB-15**

## Site-specific Isolation, Screening, and Genetic Characterization of Antibiotic Producing Microorganisms

Yvon Woappi (University of Pittsburgh at Bradford), Advisor: Dr. Om V. Singh (University of Pittsburgh at Bradford)

The low-molecular-mass microbial products of secondary metabolism, antibiotics, carries an important role in human health. It is thus of high necessity to search for novel antibiotic producing microbial strains. We hypothesize that site-specific soil samples will have diversity of antibiotic producing microorganisms. Soil samples from residential and recreational areas were collected locally and examined for microbial antibiotic producing abilities on Potato Dextrose Agar (PDA), Nutrient Agar (NA), and Tryptic Soy Agar (TSA) media. The soil samples were sprinkled against 19 pathogenic microorganisms (obtained from ATCC) lawned across 114 solid medium plates in duplicate (38 of each PDA, NA and TSA). The antibiotic producing zone generating microorganisms were observed after 48 hrs of incubation at 37ºC. A total of 52 microorganisms were observed with zone formation from residential soil sample on NA medium followed by 9 organisms from recreational soil sample. A total of 7 and 12 microorganisms from residential soil sample revealed clear zone on TSA and PDA medium, respectively. The square plate method was developed and used for secondary and tertiary screening. All from residential soil, tertiary screening revealed 6, 4 and 4 microorganisms on NA, TSA and PDA medium, respectively with wider antibiotic producing zones. Microorganisms were purified by subculture and re-tested for antibiotic producing ability. DNA isolation was then performed on the isolates. Our results revealed robust presence of antibiotic producing microorganisms with pDNA in residential soil samples- pDNA could carry antibiotic producing genes. The isolated microorganisms will be of tremendous aid to pharmacology and medicine of infectious diseases.

Key Terms: Micrbiology
Antibiotics
Genetic Engineering

**CB-16**

## Oxygen Deprivation Disrupts Phospholipids And Upregulates Phospholipid Scramblase 1 In Endothelial Cells

Emily Archer Slone (Kansas State University), Mary Roth (Kansas State University), Ruth Welti (Kansas State University), Advisor: Sherry D. Fleming (Kansas State University)

Ischemia, a lack of blood flow, initiates cellular injury which is exacerbated by reperfusion, the return of blood flow. Ischemia/reperfusion (IR) events, including heart attack and stroke, are major health concerns. The mortality rate associated with IR of the intestine is 60 to 80%. This high mortality rate is due to: 1) sensitivity of the intestine to IR, 2) systemic activation of the innate immune response resulting in damage to other organs, and 3) lack of suitable therapeutic targets. Previous studies indicated involvement of a lipid moiety in intestinal IR-induced pathology. Three classes of translocators are responsible for maintaining the asymmetry of the phospholipid bilayer. Scramblase proteins are ATP-independent, bi-directional transporters with relatively low specificity that localize to the plasma membrane. These characteristics support PLSCR1 activity as a likely mechanism for exposure of neoantigens for antibody recognition in our IR model. We hypothesized that similar to ischemia, hypoxia induces phospholipid bilayer disruption exposing neoantigens via PLSCR1 activity. Lipids were analyzed by mass spectrometry and a significant increase in free arachidonic acid found following IR treatment. In vitro studies found similar results by subjecting the endothelial cell line, MS-1, to hypoxia to mimic ischemia. Like the tissue, MS-1 cells showed an increase in arachidonic acid, Cox-2 transcription, and prostaglandin $E_2$ production following oxygen deprivation. Furthermore, PLSCR1 transcription significantly increases following hypoxia treatment. We conclude that hypoxic treatment of MS-1 cells induces similar lipid changes as IR treatment and that further investigation of PLSCR1 as a mechanism of exposing neoantigens is warranted.

Key Terms: Hypoxia
Phospholipids
Neoantigens

**CB-17**

## Exocytosis in Mast Cells

Adolfo Lara (University of Houston-Downtown), Advisors: Alfredo Davalos (MD Anderson), and Ruth Heidelberger (University of Texas-Health Science Center at Houston), M.D./Ph.D.

Mast cells or mastocytes play an important role in the inflammatory response process. The main characteristics in mast cells are their numerous highly regulated and calcium-dependent granules. These granules release histamine and cause inflammation through the process of exocytosis. Mast cells are ideal to study exocytosis due to these characteristics and large secretory granules. It was previously found that several syntaxins, which are calcium sensors in neuronal exocytosis, are found in a mast cell line. In this experiment we specifically looked at syntaxin 4 which is part of the SNARE (soluble N-ethylmaleimide-sensitive-factor attachment protein receptor) protein machinery which forms networks to create intracellular fusion between the vesicle and the plasma membrane. It is hypothesized that in the absence of syntaxin 4, exocytosis would not be possible. By using patch-clamping techniques, we attempt to study the electrophysiology in the syntaxin 4 knock-out and normal mast cells. Patch-clamping allows us to record the capacitance changes in the mast cells which will indicate exocytosis activity. So far, we have found capacitance changes in different phenotypes of mast cells. These capacitance changes occur within the first 200-350 seconds. This preliminary data supports that the rise in capacitance changes in a few cells indicates exocytosis.

Key Terms: Electrophysiology
Neurobiology
patch-clamp

**CB-18**

# Analysis of Differentially Expressed Blood Protein Isoforms as Biomarkers for Alzheimer's Disease

Ana Corcimaru (University of North Carolina at Chapel Hill), Robert DeKroon (University of North Carolina at Chapel Hill), Advisor: Oscar Alzate (University of North Carolina at Chapel Hill)

Alzheimer’s disease (AD) is the most common neurodegenerative disorder in the elderly and represents the seventh-leading cause of death in the United States. Currently, a definitive diagnosis for Alzheimer’s disease is only possible through prost-mortem pathological studies of the brain. This study evaluates how the differential types, presence, and abundance of protein isoforms of *ApoE* and *ApoM* in human blood serum can be used as blood biomarkers in a noninvasive method for diagnostics of AD.

Blood serum samples were collected from patients that had been diagnosed with AD (n=8) and control subjects who did not meet any DMV-IR criteria for AD diagnosis (n=8). Two-dimensional polyacrylamide gel electrophoresis was used to identify differentially expressed isoforms of the aforementioned proteins between AD patients and controls.

Significant differences were identified in the number and distribution of *ApoE* protein isoforms between AD and non-AD patients. Two patient specific *ApoE* isoforms with isoelectric points of 6.0 and 5.7 were consistently expressed in the AD patient population only. The *ApoM* isoforms identified were in non-glycosylated form (at 23KDa), with patterns that were similar between patients and controls.

Future research work includes additional investigation of changes in *ApoE* isoform distribution according to age and disease progression in a larger sample population. Additionally, identified protein isoform will be characterized by mass spectrometry. The identification of noninvasive methods of establishing AD biomarkers is of great importance for proper and timely diagnosis of this disease and for possible understanding of the molecular mechanisms underlying its pathology.

Key Terms: Alzheimer's Disease
Biomarkers
ApoE

**CB-19**

## Development of a Calcium Dependent *Gaussia Luciferase*

Brittany Hollister (Rollins College), Advisors: David Kochman and William Joiner (University of California San Diego)

Due to its genetic tractability, the fruit fly *Drosophila melanogaster* has become a useful model system for studying the molecular basis of sleep regulation. However, the inability to perform multi-electrode recordings in the fly brain currently limits efforts to define sleep-regulatory circuits and the roles of specific genes expressed within them. To overcome this limitation, we are developing genetically-encoded calcium-dependent luciferases with long half-lives to serve as reporters of neuronal activity. We chose to modify the properties of bioluminescent *Gaussia* luciferase (Gluc) because this enzyme has a higher activity than other luciferases and an intrinsic decay rate that is genetically modifiable. To increase the stability of Gluc we generated a double mutant that is known to increase the half-life of enzyme activity in a cell-free system. When we transfected *Drosophila* S2 cells with this construct, bioluminescent lifetime increased by over eight-fold relative to wildtype controls. To confer calcium sensitivity to Gluc, we split the molecule such that its two functional halves flanked a fusion of calmodulin to the M13 domain of myosin light chain kinase. This split luciferase maintained bioluminescent activity but did not show any apparent response to calcium in S2 cells. We hypothesize that calmodulin/M13 does not separate the two domains of Gluc sufficiently to prevent them from reconstituting enzymatic activity in the absence of calcium. Future efforts will focus on optimizing linkers connecting the two split domains of Gluc to the central calmodulin/M13 core to improve the calcium sensitivity of the fusion protein.

Key Terms: Molecular Biology
bioluminescence

**CB-20**

## Effects of Lipopolysaccharide-induced Inflammation on Hypoxia-inducible factor-1 Expression in the Rat Testis

Dharm Patel (Monmouth University), Advisor: Michael Palladino (Monmouth University)

Bacterial and viral infections of the human male reproductive tract are known to reduce fertility through decreased sperm mobility, blockage of the tract and reduced androgen output. Identifying molecular changes following inflammation within tissues is a topic of intense research. Hypoxia-Inducible Factor-1 (HIF-1) is a transcription factor that is considered the master regulator of hypoxia. We hypothesize that HIF-1, in the rat testis is up-regulated following lipopolysaccharide (LPS)-induced inflammation through an activation pathway involving NF-κB, a key transcriptional regulator of inflammation, that stimulates HIF-1α transcription. Induction of inflammation in rats was accomplished via intraperitoneal administration of LPS from *E. coli* and *P. aeruginosa* for 1, 3 and 6 hours (n = 3-5 animals/time point) at a dosage of 5mg/kg body weight. Western Blot analysis of testicular cytoplasmic and nuclear protein extracts demonstrated an increase in HIF-1α protein levels and no change in NF-κB and IκB protein levels following LPS treatment. Electromobility shift assays, performed to determine NF-κB binding activity to HIF-1α promoter, suggest a decrease in NF-κB binding activity following LPS treatment. Further experiments will be performed to determine if the mechanism affecting levels of HIF-1α is via transcriptional regulation. This work will shed light on the crosstalk and signaling pathways between NF-κB and HIF-1, two major transcriptional regulators. This relationship may be useful in studying disease states at the molecular level in which hypoxia and inflammation are a feature of the microenvironment.

Key Terms: Immunology
Reproductive Biology

**CB-21**

## Determining anterior gradient homology 2 (AGR2) in estrogen receptor alpha (ER-α) positive etiologies

Diana Xie (Duke University), Advisor: Donald McDonnell (Duke University)

Anterior gradient homology 2 (AGR2), an estrogen receptor (ER) target gene, has recently been shown to be induced by tamoxifen (4-OHT) and estradiol (E2) in the MCF7 breast cancer cell line. Tamoxifen is used as an effective mainstay therapy for ER(+) primary breast cancer. However, the majority of breast cancer tumors develop endocrine resistance to tamoxifen. AGR2 over-expression, particularly in primary breast cancer cell lines, has been linked to this resistance. AGR2 is also strongly expressed and potentially involved in common cancers of other tissues, yet whether it plays a similar role in these cancer types remains to be seen. In this study, AGR2 expression in cell lines breast, ovarian, lung, endometrial, and colon cancers were measured to determine its basal expression in representative ER(+) cancer cell models. AGR2 expression was also examined in these cell lines pre-treated with E2 and 4-OHT, to examine potential patterns of induction. Results concluded that in all cell lines, there was no significant AGR2 induction in response to E2 and/or 4-OHT treatment, compared to control. However, breast cancer cell line BT-483 expressed unusually high levels of basal AGR2. For future direction, the link between AGR2 levels and ER expression will be explored in BT-483.

Key Terms: Pharmacology
Cancer biology
Cell biology

**CB-22**

## The Role of Myosin VI in Epithelial Cell Migration

Kayley Hake (Meredith College), Advisors: Debbie Frank (Washington University), Kathryn Miller (Washington University)

Myosin VI is an actin-based motor protein that has the ability to move processively on actin to transport cargoes or anchor tightly to actin to stabilize structures or localize cargoes. Myosin VI participates in cell migration, but its role and mechanism are unclear. We are investigating this role using two developmental processes in Drosophila: border cell migration, in which somatic epithelial cells migrate past germ-line nurse cells to reach the developing oocyte; and dorsal closure, a process in embryogenesis during which two sheets of epithelial cells migrate dorsally to encase the embryo. In both cases knocking down myosin VI only in the migrating cells affects migration and myosin VI works in concert with cell adhesion molecules. Unexpectedly, when myosin VI is completely absent from the whole animal, migration occurs normally. We propose that the relative levels of myosin VI expression in neighboring tissues are critical for successful migration. If levels of myosin VI are significantly greater or less in one tissue, migration is disrupted due to different levels of stabilization of actin and cell adhesion complexes. To test this hypothesis, we are generating flies in which myosin VI is over-expressed or knocked down in different populations of cells involved in these movements. If the differential adhesion hypothesis is correct, then we should see a defect when neighboring cells have different amounts of myosin VI. By comparing these two developmental cell migration processes, we hope to better understand the mechanisms of myosin VI action in cell adhesion and motility.

Key Terms: Cell Migration
Cell Structure
Microscopy

**CB-23**

## Effects of Netrin-1 on Developing Tectal Neurons in *Xenopus laevis* Tadpoles

Monica Andrawes (University of California, Irvine), Sonia Marshak (University of California, Irvine), Advisor: Susana Cohen-Cory (University of California, Irvine)

Netrins, a family of bifunctional proteins, guide axonal growth in the developing nervous system. A concentration gradient of netrin protein attracts axons expressing DCC and repels axons expressing UNC-5 alone or with DCC. Netrin-1 is also present in the developing visual system of *Xenopus laevis*, our model, increasing retinal axon terminal arborization and formation of presynaptic specializations. A number of invertebrate studies have recently implicated netrin in modulating dendritic differentiation as well. We used *Xenopus laevis* to investigate the role of netrin-1 in the development of postsynaptic tectal neurons as they form connections with presynaptic retinal axons. We showed that at this developmental period, netrin-1 mRNA is expressed in the optic tectum along the ventricle wall, implying the presence of a medio-lateral netrin gradient. In vivo confocal imaging of individual tectal neurons showed that altering tectal netrin levels by microinjection of recombinant netrin-1, or by sequestration of endogenous netrin with an UNC5 ectodomain fusion protein, induced rapid reorganization of tectal dendrites and changed the direction of dendritic arbor growth. Finally, we found both netrin receptors, UNC5 and DCC, expressed in developing *Xenopus* tectum: immunostaining experiments revealed UNC5 receptor localized to cell bodies of a large subpopulation of tectal neurons, while DCC receptor is present in both cell bodies and dendrites of tectal neurons. Together, our results support a model wherein netrin participates in the directional growth of tectal neuron dendritic arbors; this effect might be mediated by both of netrin receptors.

Key Terms: Neuroscience
Development

**CB-24**

## Characterization of Dar1 Interacting Proteins Essential for Differential Cellular Localization and Regulation of Class-specific Dendrite Development

Myurajan Rubaharan (George Mason University), Srividya Chandramouli Iyer (George Mason University), Eswar P.R. Iyer (George Mason University), Advisor: Daniel N. Cox (George Mason University)

Dendrite morphogenesis represents a critical process in the establishment, maintenance and modulation of neural connectivity that is the basis of a functional nervous system. Dendrites, as the primary sites of synaptic and/or sensory input largely determine the size and range of the neuronal receptive field. A recent study has identified *dar1*, a Krüppel-like transcription factor, as an essential regulator involved in controlling dendrite development and growth via microtubule modulation. The *Drosophila melanogaster* peripheral nervous system (PNS) has emerged as an excellent model system for studying molecular mechanisms underlying class specific dendrite development. Dendritic arborization (da) neurons are grouped into four distinct classes (I-IV) based upon increasing orders of dendritic complexity. Interestingly, Dar1 protein localization is primarily nuclear in the morphologically simple class I neurons, whereas in contrast largely cytoplasmic in the highly complex class IV da neurons. This observation led us investigate putative protein-interaction partners of Dar1 that potentially regulate this complexity-dependent differential localization, and the result of perturbing this localization. A targeted mutant screen for nineteen genes identified as direct interactors of Dar1 by protein-protein interaction studies recovered genes responsible for its differential localization in class IV da neurons. This study sheds novel insights on mechanism of differential localization of Dar1 protein, and its effect of dendrite development. The broader implications of these studies are understanding the molecular mechanism of *dar-1* transcriptional regulation at a class-specific level and how this regulation ultimately contributes to acquisition of distinct neuronal morphologies that underlie the establishment of complex neural networks.

Key Terms: Molecular Biology
Neurocience
Developmental Genetics

**CB-25**

## Characterizing Mutants in the Self Versus Non-Self Recognition Pathway of *Proteus mirabilis*

Daniel Sandoval (University of California Irvine), Nora Sullivan (Harvard University), Advisor: Karine Gibbs (Harvard University)

*Proteus mirabilis*, a mobile gram-negative bacterium, is an opportunistic pathogen that causes urinary tract infections. Upon meeting a solid surface, *P. mirabilis* short cells differentiate into swarmer cells; these swarmer cell migrate rapidly across the surface, exhibiting a behavior termed swarming. Swarming requires cell-to-cell contact and communication. When identical swarms meet, they merge; however, boundaries form between non-identical swarms of *P. mirabilis* indicating that the bacterium can recognize self versus non-self. To investigate pathways that may be involved in self versus non-self recognition, *P. mirabilis* mutants that were previously identified to be deficient in self versus non-self recognition were swarmed against each other to determine their relationship with each other. Cluster analysis of the mutant strains revealed four different groups. We are currently mapping the location of the disrupted genes and will next complement the disrupted genes with the wild-type alleles. These identified genes may be novel members of the self versus non-self recognition pathway in *P. mirabilis.*

Key Terms: Bacteria
Recognition

**CB-26**

**Effects of the Hormone Melatonin and Caffeine on the Mitochondrial Function of a Neuronal Cell Line Modeling Alzheimer's Disease.**

Emily Nickoloff (Rollins College), Mira Janjus (University of South Florida), Vedad Delic (University of South Florida), Advisor: Patrick Bradshaw (University of South Florida)

Mitochondria dysfunction is a hallmark of many neurodegenerative diseases, including Alzheimer's Disease (AD). AD is associated with a decrease in mitochondrial respiration, reflecting the inability of the mitochondria to provide adequate energy for proper neuron function as well as a host of other deficiencies. Our lab and others have previously shown that both caffeine treatment and melatonin treatment rescue oxidative respiration of mitochondria in mouse neuroblastoma cell lines and decrease cognitive impairment in mouse modeling AD. Using respirometry experiments, we established melatonin at 10 μM concentrations rescued mitochondria respiration in our cell line. We demonstrate when paired with melatonin treatment, caffeine has an antagonistic effect on AD, indicating the melatonin pathway and caffeine pathway interact at some unknown location. Previous studies have shown caffeine has an antagonistic effect on phosphodiesterase only at high concentrations (100 μM or greater). Using a phosphodiesterase assay from Enzo Sciences we measured cAMP activity and found a significant decrease in cAMP activity at 10 μM concentrations of caffeine. Notably, there was no significant difference between cAMP at 10 μM and 100 μM concentrations. This indicates the levels of caffeine needed to impair phosphodiestarase activity are much lower than previously thought. We also show antagonistic rather than synergistic effects when combining two treatments previously demonstrated to rescue cells from AD. In order to help determine the melatonin pathway we plan on using proteomic and transcriptomic techinques.

Key Terms: Alzheimer's Disease
Neuroscience
Mitochondrial respiration

**CB-27**

## Osteogenic Differentiation of hMSCs by 1,25$D_3$ Cultured in Serum Free Media

Kayla Cline (Winston Salem State University), Hayley Whitlock (Winston Salem State University), Advisor: Carly Kemmis (Winston Salem State University)

Human bone marrow-derived mesenchymal stromal cells (hMSCs) are progenitor cells that can differentiate into various tissues, such as bone, and are currently studied for use in regenerative medicines. Thus, hMSCs should be cultured in serum free media. In addition it has been found that vitamin D plays an important role in osteogenic differentiation (OD). Therefore, it is important to study the impact of 1,25 dihydroxyvitamin $D_3$ (1,25$D_3$) and serum free media on the growth and OD of hMSCs. In this study, we characterized the proliferation and OD of hMSCs in response to 1,25$D_3$ by differentiating cells at low and medium densities in serum free media. We hypothesized that hMSCs seeded at a higher density exhibit more proliferation and that 1,25$D_3$ will induce OD. To characterize the amount of growth and differentiation, the amount of proliferation, alkaline phosphatase activity, and mineralization were examined on days 7 and 14. In comparison to control, hMSCs cultured with 1,25$D_3$ showed a slight increase in cell proliferation at day 14; improved alkaline phosphatase activity between day 7 and 14; and strong alizarin red staining on day 14 . In addition, the control cells cultured in low density showed more alkaline phosphatase activity than cells cultured at medium density. Our work demonstrates that 1,25$D_3$ impacts osteogenic differentiation and proliferation of hMSCs. This is an important stepping stone to creating an efficient cell culture medium for hMSCs used in regenerative medicines and provides insight to the effect of 1,25$D_3$ *in vivo*.

Key Terms: human mesenchymal stromal cells
1,25 dihydroxyvitamin D3
osteogenic differentiation

**CB-28**

## Differential Gene Regulation in *Zea mays* Stem in Response to *Ostrinia nubilalis* feeding

James Thomas (University of Florida, USDA Center for Medical, Agricultural, and Veterinary Entomology), Advisor: Nicole Dafoe (USDA Center for Medical, Agricultural, and Veterinary Entomology)

In the United States, the European corn borer (ECB), *Ostrinia nubilalis*, is a prevalent pest of corn, *Zea mays*. The mechanical damage associated with ECB feeding weakens the plant and introduces sites for pathogen infection. The corn responds to this feeding by synthesizing defensive compounds, such as benzoxazinoids and terpenoids that can have anti-nutritive effects on the insect. However, previous studies have shown that although defensive compounds are induced by ECB feeding, they do not have a significant impact on ECB growth. Interestingly, when comparing proteins collected from control and ECB treated tissues, a number of glycolytic enzymes were upregulated. These enzymes are involved in the production of energy required for many metabolic processes. Their upregulation provides a possible explanation as to how ECB acquire nutrition despite the defensive response. Using semi-quantitative PCR, we have observed that genes encoding these proteins are induced at the site of ECB feeding. The induction of these genes is higher in ECB damaged stem tissue when compared to mechanically damaged tissues, suggesting that factors other than mechanical damage may be involved in the plants response. When the plant hormones auxin and jasmonic acid are added to the damage site, the genes encoding glycolytic enzymes are induced at levels similar to that of ECB feeding, and combinations of these hormones have synergistic effects. The results of this research provide insight into how genes encoding glycolytic enzymes may be regulated by ECB and plant hormones.

Key Terms: Plant Biology
Plant-insect Interactions
Molecular Biology

**CB-29**

## Understanding the Genetic Mechanisms of Cold Tolerance in *Drosophila melanogaster*

Lauren Sanchez (Barry University), Jessica Tsai (Stanford University), and Thomas Clandinin (Stanford University)

Insects are ectotherms with limited ability to regulate body temperature. However, in response to cold environments, insects have multiple adaptive strategies to ensure survival, including freeze tolerance and freeze avoidance. Currently, genetic mechanisms underlying cold survival in insects are unknown. We examined the cold tolerance of *Drosophila melanogaster* isolates obtained from different climates and found that they displayed significant variation in their ability to survive at 4 C. Strains from Nagano, Japan and Ica, Peru displayed increased survival relative to an isogenized control line *(IsoDG)*. Given the phenotypic variation, we wanted to examine whether there was a genetic basis for increased cold tolerance. To do this, we crossed different isolates, and examined the survival of F1 and F2 animals. Survival curves were generated for the F1 and F2 progeny of *IsoDG* mated with flies from Nagano, Japan and Ica, Peru. F1 flies showed enhanced cold tolerance similar to the Ica and Nagano parental strains, suggesting that increased cold tolerance is dominantly inherited. Subsequently, F2 flies were selected for the increased cold tolerance phenotype. DNA from selected flies was pooled for whole genome sequencing, an approach that will allow us to determine which genes are associated with increased survival. Future directions include characterizing the genes responsible for cold tolerance and mating lines from different locations with varying cold tolerance to establish whether increased cold tolerance has a common genetic origin.

Supported by: NIH-NIGMS RISE Grant, R25 GM059244-11, Barry University

Key Terms: Genetics
Drosophila Melanogaster
Whole Genome Sequencing

**CB-30**

## Phylogenetic Analysis Of The Unusual Chromosomal Telomeres Of *Drosophila*, A Model Genetic Organism

Haylie Cox (Weber State University), Advisor: Jonathan Clark (Weber State University)

In most eukaryotes, telomeres are formed by a short nucleotide sequence that is repeated many times at the chromosome end. In contrast, the chromosome ends of *Drosophila* consist of at least two different transposable elements, *HeT-A* and *TART*, which are tandemly arrayed in multiple copies. In *D. melanogaster*, these transposable elements are confined to the ends of chromosomes and are not found at any other sites in the genome. This is the most striking example of a eukaryotic transposable element that performs an essential cellular function. A molecular study has been initiated that examines the phylogeny of the *HeT-A* transposable element among eight species within the *melanogaster* species subgroup, which includes *D. melanogaster*. Multiple *HeT-A* sequences were obtained from each species and these sequences are compared to an expanded dataset of *HeT-A* sequences available from the *Drosophila* genome projects. The phylogeny of the *HeT-A* sequences is compared to the phylogeny of the host species, determined by *ADH* gene sequences. For some comparisons, the extent of *HeT-A* nucleotide divergence exceeds 50%. The phylogeny reveals that multiple sequences from each species are not always monophyletic. This suggests that multiple subfamilies, each with their own evolutionary history, exist in all genomes examined. Alternative explanations, including lateral transfer of *HeT-A* elements between species, are discussed. Additional comparisons of the rate of synonymous and nonsynonymous nucleotide substitutions suggest that there is no selection operating on the *HeT-A* coding region, surprising finding given the importance of telomeres for cellular stability.

Key Terms: Genetics
Drosophila
HeT-A

**CB-31**

# Therapeutic Modulation of Cerebral Microscopic Bleeding in a Mouse Model of Cerebral Amyloid Angiogpathy

Christopher Ventura (University of California, Irvine), Vitaly Vasilevko PhD (University of California, Irvine), Advisor: David Cribbs, PhD Professor of Neurology (University of California, Irvine)

**Problem Statement/Hypothesis:** Aging brains often display MRI and pathological evidence of cerebral microbleeds, which are frequently coupled with cerebral amyloid angiopathy. . Cerebral amyloid angiopathy (CAA) is a disease of the blood vessels of the central nervous system, in which beta amyloid (Aβ) peptide, also associated with the Alzheimer's disease (AD), pathologically deposits in the walls of the brain vasculature. . The goal of this project was develop new therapeutic strategies for this disorder, we did this by studying cerebral microscopic bleeding in a well-characterized mouse model of cerebral amyloidosis. **Methods.** . Dipyridamole is prescribed medication, used as a blocker of platlet aggregation. It has also been used as a secondary prevention of ischemic stroke and has been known to potentially reduce the risk of further vascular deterioration after cerebral ischemia. Tg 2576 mice were studied at ages ranging from 2 to 21 months. Tg2576 enhances ß-secretase cleavage and promotes extensive amyloid beta production and accumulation. Spontaneous and induced microscopic bleeding were analyzed with and without passive anti-amyloid immunization regimen (immunotherapy). **Results:** Areas of microscopic bleeding were demonstrated without difficulty and the oldest mice had the most profound bleeding. Anti-Aß immunotherapy tended to worsen microhemorrhages. Dipyridamole treatment did not worsen frequency and size of cerebral microscopic bleeding. **Conclusions:** The Tg2576 mouse is a useful model to study progression and modification of spontaneous and immunotherapy-induced cerebral microscopic hemorrhage. Due to the lack of microscopic hemorrhage with dipyridamole treatment can play potential therapeutic role of this agent when ischemic and microhemorrhagic pathologies exist together as they often do in elderly patients.

Key Terms: Neuroscience
Cerebral Amyloid Angoipathy
Alzhiemer's

**CB-32**

## β-catenin Down Regulates *Inha* during Granulosa Cell Tumor Formation

Ashley Franklin (Rollins College), Advisor: JoAnne S. Richards and Zhilin Liu (Baylor College of Medicine)

Ovarian cancer remains a deadly threat to women. One aggressive subtype of ovarian cancer is granulosa cell tumors (GCTs). Two mouse models develop GCTs in response to altered oncogene expression. In one, a target of the WNT pathway, CTNNB1 (β-catenin) was stably expressed and an inhibitor of the PI3Kinase pathway, *Pten*, was disrupted selectively in GCs (*Ctnnb1/Pten*). In the other, inhibin α (*Inha*), a negative regulator of activins that are known to promote granulosa cell proliferation, was knocked out. Interestingly, GCTs from the *Ctnnb1/Pten* mice expressed low levels of *Inha*, indicating the two models may have some intrinsic relationship.

To test this, we compared microarray gene expression profiles of the two mouse models and confirmed by qPCR, 13 mis-regulated genes in *Ctnnb1;Pten* and $Inha^{-/-}$ GCs, indicating they did regulate a subset of common genes. However, whereas the levels of *Inha*, as well as the levels of activins (*Inhba* and *Inhbb*) were down-regulated in *Ctnnb1;Pten* GCs, CTNNB1 was not activated in the $Inha^{-/-}$ ovaries as demonstrated by immunohistochemical analyses. These results indicate that β-catenin appears to suppress the expression of inhibin and activins but inhibin/activin have no effect on activation of β-catenin.

In summary, constitutively active CTNNB1 results in the repression of *Inha* and this, along with other mis-regulated genes contributes to GCT formation.

This work was funded by the Cancer Prevention & Research Institute of Texas.

Key Terms: Ovarian cancer
Granulosa-theca cell tumors
WNT and PI3Kinase Pathways

**CB-33**

## Mobility of micro-RNAs in *Arabidopsis thaliana*

Victoria Hanna (University of California, Irvine), Damianos Skopelitis (Cold Spring Harbor Laboratory), Advisor: Marja Timmermans (Cold Spring Harbor Laboratory)

MicroRNAs (miRNAs) are endogenous ~22nt RNAs with critical roles in plant development that silence endogenous mRNAs. Results from the Timmermans Lab have shown that miRNAs miR390 and miR166 can move intercellularly, acting outside their domain of biogenesis. These results propose a novel function for miRNAs as mobile signals in development. I investigated the parameters of miRNA mobility, such as tissue specificity, direction, and range. GUS reporter activity was analyzed in transgenic lines that ubiquitously express the cell autonomous GUS reporter as well as an artificial miRNA targeting GUS transcripts (miRGUS) from promoters with distinct expression profiles. GUS silencing in these lines was compared to expression domains of the specific promoters used. The chosen promoters are *pATML1*,*pRbcs*, and *pFIL*, which are active in the leaf epidermis, the sub-epidermal layers, and the abaxial domain of the leaf respectively. These promoters will test miRNA mobility between different cell layers in young leaf primordia. Moreover, I tested *pSUC2 pATHB8*, and *pSCR*, which are active in vascular tissue and the cells surrounding the vasculature, respectively, and thus will test movement from the vasculature into adjacent cell types. The effects of miRNAs were partially proven to be dose dependent; a silencing effect was only seen when the promoter was exceptionally strong. The results indicate that miRNAs can move from the leaf epidermis into the sub-epidermal layers. Further analysis is required to test additional parameters of miRNA mobility. Supported by NSF-URM Grant DBI-0731655.

Key Terms: Plant Sciences
Molecular Biology
Development

**CB-34**

## Co-treatment of Ferric Ammonium Citrate (FAC) with Ebselen Decreased FAC Induced PC-3 Cell Invasion

Wenji Guo (University of Illinois at Chicago), Michael Schlicht, Teresa Kucynda, Ping Zhou, Klara Valyi-Nagy, Advisor: André Kajdacsy-Balla (University of Illinois)

PC-3 prostate cancer cell invasion with iron was investigated using Neuroprobe filter membrane transmigration assays. PC-3 cells were pre-incubated with 100 μM ferric ammonium citrate (FAC) for 6 hours. Excess iron was removed before the assay. The PC-3 cells were placed on an extracellular membrane preparation (Matrigel ®) in the upper wells of the chamber and allowed to migrate onto the underside of a porous membrane that allowed cell transmigration. The number of cells migrating to the underside of the membrane is a direct measure of cell invasion. Pre-treatment with 100 μM FAC caused a 4-fold increase in PC-3 cell invasion when measured at 24 hours ($P < 0.05$). The FAC concentrations that induced PC-3 invasion were 100 times smaller than concentrations which interfered with cell viability or proliferation rate. The effect of FAC exposure on PC-3 cell invasion was associated with p42/44 MAP kinase activity by Western blot analysis. Furthermore, co-treatment of FAC with antioxidant ebselen, a hydrogen peroxide inhibitor, decreased FAC-induced PC-3 cell invasion. We also examined the mRNA expression of invasion-related genes using a cDNA array and found a positive correlation between the exposures to FAC and the invasion phenotype of prostate cancer cells. The data demonstrated that the upregulation of genes, such as fractalkine and plasminogen, after FAC treatment may be associated with iron-induced invasion of prostate cancer. Our data suggest iron overload may be detrimental to patients with prostate cancer and that the effect of iron on invasion may be inhibited by ebselen.

Key Terms: cell biology
pathology
cancer biology

**CB-35**

## Characterization of the Radial Excision Repair Model: an *in vivo* Assay for Dedifferentiation

M. Duran (University of California, Irvine), C. Aguilar, Advisor: D.M. Gardiner (University of California, Irvine)

The Urodele amphibians are the only adult vertebrates able to fully regenerate lost limbs. This regenerative response begins with the formation of a mass of multipotent cells, called a blastema, after injury, which then directs the development of a new fully functional limb. The mechanisms through which the blastema achieves this are not fully understood, however if we are able to fully characterize the events which take place, then we can hopefully use that knowledge to enhance human regenerative ability. One of the ways in which this can be accomplished is by manipulating non-blastema cells in an effort to make them "blastema like," however this in turn requires an assay which will allow you determine whether or not your cells in question are actually regenerative competent. To this end our lab recently devised a model for determining regenerative competency termed the radial excision repair model. This model is based on the observation that the axolotl cannot regenerate a 2mm surgically created bone defect in the radius of the forelimb. We discovered that regeneration could be induced by grafting cells from a blastema into the defect area. This gives us an effective assay with a well defined readout (regenerative response), with which we can assay how closely experimentally manipulated cells can match a blastema regeneration response. To enhance the viability of the assay, we characterize the levels of cell proliferation and apoptosis which occur as a result of a blastema graft at 2, 10, and 20 days.

Key Terms: Limb Regeneration
Axolotl

**CB-36**

**Hedgehog Signaling Controls Intestinal Malrotation and Epithelial Cell Development in *Xenopus Laevis***

Jordan Ferguson (North Carolina State University), Advisor: Nanette Nascone-Yoder (North Carolina State University)

During the development of the digestive tract, the intestine must rotate in a specific direction in order to create proper anatomy. Intestinal malrotation affects 1 in 500 births, and predisposes affected babies to life-threatening complications. It has been shown that disruption of hedgehog signaling can cause intestinal malrotation in mouse models. However, the specific mechanism by which Hedgehog affects intestinal rotation is still unknown. The morphogenesis of the intestinal epithelium occurs coincident with intestinal rotation. I hypothesized that Hedgehog is a controlling gene in epithelial cell arrangement, shape and viability during intestinal rotation. In order to assess the role of Hedgehog in epithelial cell development, developing *Xenopus laevis* embryos were exposed to either cyclopamine, a chemical which inhibits Hedgehog signaling, or purmorphamine, which activates inappropriate Hedgehog signaling, to generate model s of intestinal malrotation. Immunohistochemistry was then used to visualize the development of abnormally rotating guts at a molecular and cellular level. Both compounds affect the formation of the intestinal lumen, as well as intestinal epithelial cell shape, and adhesion. Cyclopamine caused an enlarged lumen with an abnormally wide gut tube, while those embryos treated with purmorphamine had a narrow gut tube with a loss of lumen. These results suggest that Hedgehog signaling controls intestinal rotation by regulating the size of the gut lumen, and the shape and adhesion of intestinal epithelial cells. Therefore, one of the root causes of intestinal malrotation may be changes in cell shape, adhesion, and lumen development, possibly caused by abnormal Hedgehog signaling.

Key Terms: molecular biology
Hedgehog signaling
intestinal malrotation

**CB-37**

**A Genetic Study of the Chromosomal Region of the tdc gene in *Lactobaccilus sakei* and the glutamase decarboxylate gene in *Staphylococcus carnosus***

Camille Warner (SUNY College at Old Westbury), Blanca de las Rivas (Instituto de Fermentaciones Industriales CSIC, Madrid, Spain), Advisor: Dr. Alfonso V. Carrascosa (IFI-CSIC)

Tyramine and phenylethylamine are biogenic amines that have been associated with food poisoning. Characterization and detection of these enzymes and their products is critical to monitor food safety. Tyrosine decarboxylase (*tdc*) and glutamate decarboxylase (*gdc*) catalyze the conversion of tyrosine and phenylalanine into tyramine and phenylethylamine. This study aims to sequence the *tdc* genes of *Lactobacillus sakei* responsible for the conversion of the amino acid tyrosine to tyramine and to determine whether the *gdc* gene in *Staphlococcus carnosus* is responsible for the conversion of phenylalanine to phenylethylamine. In order to know the chromosomal region of the *tdc* gene in *L. sakei*, the chromosomal and plasmid DNA were cut with restriction enzymes and a ligation was done. A polymerase chain reaction (PCR) was done using specific primers. Afterwards the samples were run with gel electrophoresis, purified, and sequenced. We were able to elongate the 12kb fragment that is known. To determine whether glutamate decarboxylase gene in *S. carnosus* is responsible for the production of the amine, the gene was cloned in a plasmid and transformed into competent *E. coli* cells. Thin layer chromatography (TLC) was used to verify the production of the amines. The TLC image suggested that the gene was inactive or producing a small quantity of the protein. *Lactobacillus sakei* and *Staphlococcus carnosus* should be considered biogenic amine producers; this should be taken into account in the food and health industry when choosing bacteria for starter cultures and in cases of food poisoning.

Key Term: Cellular Biology

**CB-38**

## Osteogenic Differentiation in Human Mesenchymal Stomal Cells

Hayley Whitlock (Winston-Salem State University), Kayla Cline (Winston-Salem State University), Advisor: Carly Kemmis (Winston-Salem State University)

Mesenchymal stromal cells are unique cells that are derived from bone marrow, adipose, and other tissues, and can be differentiated into various cell types such as osteogenic, adipogenic, endothelial, and smooth muscle. As they are being used for regenerative medicine it is important to understand how they respond to factors circulating in the body. This study characterizes growth and osteogenic differentiation of human bone marrow-derived mesenchymal stromal cells (hMSCs) in the presence of 1,25 dihydroxyvitamin $D_3$ ($1,25D_3$). $1,25D_3$ is a key factor for cell growth and differentiation *in vivo*, including bone formation. We hypothesized that hMSCs cultured in media treated with $1,25D_3$ will stop proliferating and undergo more osteogenic differentiation compared to untreated hMSCs. We also expected that differentiating cells at a low cell density would result in more osteogenic differentiation since high cell density studies have previously demonstrated decreased differentiation to bone. In order to test our hypotheses, hMSCs plated at low and medium densities were treated with 10nM $1,25D_3$. Cell proliferation and differentiation was observed on days 7and 14 using crystal violet to quantify growth, fast blue to visualize alkaline phosphatase activity, and alizarin red to detect mineralization. We compared hMSCs treated with $1,25D_3$ to control and observed a significant increase in cell proliferation, cell density, and mineralization as well as crystal violet, alkaline phosphatase, and alizarin red dye intensities with the presence of $1,25D_3$. In conclusion, $1,25D_3$ promotes a substantial amount of cell growth, along with osteogenesis in hMSCs.

Key Terms: Osteogenic differentiation
Mesenchymal stromal cells
1,25 Dihydroxyvitamin D3

**CB-39**

## Yeast as a Model for Familial Parkinson's Disease

Alexa Hartman (Rollins College) Advisor: Susan Walsh (Rollins College)

A neuron's inability to complete mitophagy plays an integral role in the pathogenesis of familial Parkinson's disease. One mitophagy pathway requires the protein Parkin, an E3 ubiquitin ligase, and the protein kinase PINK1. Based on mislocalization of PINK1 in damaged mitochondria, Parkin ubiquitinates target substrates and, thus, mediates the selective degradation of dysfunctional mitochondria. Here we sought to reconstitute this pathway in yeast. Yeast serves as an ideal system for testing this model because they can ferment in a mitochondria-independent manner or respire. We can then measure mitophagy by an inability to grow on nonfermentable media. We hypothesized that the expression of human Parkin in yeast would not be sufficient to induce mitophagy, as previous studies in human cells suggest that PINK1 is also necessary. However, we saw that after transformation with the human Parkin gene alone, growth was unaffected on fermentable media, but respiration-dependent growth was inhibited at 30°C. Furthermore, the addition of CCCP, a drug that causes mitochondrial depolarization, also inhibited growth in Parkin-expressing yeast, but not controls. From this we believe that Parkin may be causing an increase in protein degradation, specifically of the mitochondria. We are continuing this research to investigate the precise mechanism underlying this process. Overall, this yeast model may provide a simple system to study the role of Parkin in Parkinson's disease.

Key Terms: Parkinson's disease
autophagy
mitochondria

**CB-40**

**DCPS as a Tumor Suppressor in Cutaneous Squamous Cell Carcinoma**

Kelsey Gray (The Ohio State University), Amy Dworkin (The Ohio State University), Jessica Fleming (The Ohio State University), Advisor: Amanda Toland (The Ohio State University)

*DCPS* is a candidate cutaneous squamous cell carcinoma (SCC) susceptibility gene as determined by allelic imbalance mapping of SCC and genomic blood DNA samples. *DCPS* shows no protein expression in 23% of human SCCs on a tissue microarray. DCPS, a decapping scavenger enzyme, influences the pool of available cap-binding proteins and, in turn, impacts aspects of mRNA metabolism like pre-mRNA splicing and decay. The hypothesis driving this research is that *DCPS* is a tumor suppressor and that the tumor suppressor allele is preferentially lost in SCC. To test this hypothesis, functional effects of increasing and decreasing expression of *DcpS* in mouse keratinocyte cell lines have been studied. Pre-mRNA splicing was examined by determining size differences of mini-gene transcripts between low, normal, and overexpression cell lines by gel electrophoresis. Unexpectedly, preliminary data suggests that splicing is less efficient in both *DcpS* knockdown and overexpression cell lines. This suggests that normal splicing occurs within an optimal range of *DcpS* levels. The difference in mRNA stability between the three cell lines has been studied by preventing translation and tracking mRNA levels over 24 hours. *DcpS* knockdown cell lines were found to have more stable mRNA than normal and overexpression cell lines. DcpS knockdown cell lines exhibit more growth than normal and overexpression cell lines between 24 and 48 hours, but not between 48 and 72 hours. Future studies include examining apoptosis, migration, and cell cycle in these cell lines. This research has the potential to impact cancer susceptibility screening and therapeutic targets.

Key Terms: Cancer
Genetics

**CB-41**

## Characterization of Downstream Effectors Mediating Cut Transcriptional Regulation of Class-Specific Dendrite Morphogenesis

Luis Sullivan (George Mason University), Eswar P.R. Iyer, Madhu Karamsetty, and Daniel N. Cox (School of Systems Biology, Krasnow Institute for Advanced Study)

Neuronal form dictates function and in a circuitry as complex as the human brain the post-synaptic properties of the neuron are established in large part by dendritic morphology. Transcriptional regulation has emerged as a pivotal mediator of class specific dendrite morphogenesis; however, the downstream effectors of these transcription factors remain largely unknown as are the cellular events that direct morphological change. Recent studies have implicated the *Drosophila* homeodomain transcription factor Cut and it's vertebrate homolog in mediating dendrite morphogenesis in the peripheral and central nervous systems. To characterize putative transcriptional targets of Cut regulation, a genetic suppressor screen has been performed in which Cut overexpression has been coupled with target gene-specific *in vivo* RNAi knockdown. Preliminary analyses have identified >400 genes that represent potential direct targets of Cut regulation in *Drosophila* dendritic arborization (da) neurons. Here we report the discovery of target genes that either suppress or enhance Cut-mediated effects on da neuron dendritic morphology. The molecules uncovered in our screen cover a broad range of biological functions. Collectively, these analyses reveal novel transcriptionally regulated pathways and cell biological processes essential to the specification of class specific dendritic morphologies.

Key Terms: Neuroscience
Genetics
Molecular Biology

**CB-42**

## Positive Feedback – A Means Of Maintaining The Robustness Of Cell-cycle Oscillations?

Rong En Tay (Duke University), Advisor: Steven Haase (Duke University)

Cyclin/CDKs are commonly thought to be a core regulatory component of the eukaryotic cell-cycle; however, the Haase lab has proposed an alternative model in which the cell-cycle transcriptional program is regulated by a network of serially-activating transcription factors functioning as a cyclin/CDK-independent oscillator. In the absence of cyclin/CDKs, transcriptional oscillations are dampened, suggesting that cyclin/CDKs promote oscillation robustness. Because cyclin/CDKs positively feed back into several transcription factors in the oscillator network, we propose positive feedback maintains the robustness of cell-cycle transcriptional oscillations.

To test this hypothesis, I replaced cyclin/CDK-mediated positive feedback with transcriptional positive feedback in *Saccharomyces cerevisiae* strains lacking B-cyclin/CDK activity. This was done by placing two distinct transcription factors (*SWI5* and *HCM1*) within our network oscillator under the control of promoters of their respective target genes, *SIC1* and *NDD1*. Thus, positive feedback loops independent of cyclin/CDKs were engineered into the transcription network. Changes in oscillation period and amplitude were then examined in synchronized yeast populations over time courses.

My data show that oscillations in *S. cerevisiae* strains with engineered transcriptional positive feedback exhibit decreased periods and increased amplitudes relative to oscillations in strains without transcriptional positive feedback. The partial restoration of oscillation robustness by transcriptional positive feedback is consistent with my hypothesis that positive feedback contributes to the maintenance of robust cell-cycle oscillations. Furthermore, my data also support the idea that a transcriptional network serves as the fundamental oscillator of the *S. cerevisiae* cell-cycle, and may be relevant to the study of cell-cycle oscillations in other organisms.

Key Terms: Cell Cycle
Transcription Factor Network
Positive Feedback

**CB-43**

**Naturally Occurring Resistant Mutations in HCV NS5b RdRp In Chronic HCV Treatment-Naïve Patients**

Nancy Lopez (University of California, Irvine), Karina Salvatierra (Centro Superior de Investigación en Salud Publica) ), Advisor: Dr. F. Xavier López-Labrador (Centro Superior de Investigación en Salud Publica)

The current treatment for hepatitis C virus (HCV) chronic infection consists of peglyated interferon alpha plus ribavirin inhibitors. This treatment is unspecific, generates important side effects and is only effective in 50% of patients. New treatments based in inhibitors aimed at targeting virus-specific enzymes, such as the HCV NS5b RNA dependent RNA polymerase (RdRp), are being developed. Previous studies have identified emergence of viral resistance in vitro for this compounds, but few have provided information regarding natural variation of polymerases from different infected individuals. We collected viral isolates from different patients with chronic HCV infection from reference hospitals in Valencia, Spain. Natural variability and the presence of resistance or compensatory mutations to NS5B RdRp nucleosidic (NI) and non-nucleosidic (NNI) inhibitors was determined through direct Sanger sequencing of NS5B gene, and by cloning and sequencing individual clones. Signature mutation patterns were deduced in the polymerase at various sites hypothesized to be naturally polymorphic. This clonal analysis was performed on 4 additional treatment-naive chronic HCV patients, and we expect to obtain at least 10 clonal HCV NS5B sequences from each of them. The data will assist in determining the likelihood of HCV resistance upon the administration of new NS5B polymerase inhibitors and will aid in the development of genotypic resistance testing assays.

Key Terms: Hepatitis C virus
resistant viral variants
mutations

**CB-44**

# Rapamycin, an mTOR Inhibitor, Increases OPC to Premyelinating Oligodendrocyte Differentiation *In Vivo*

Ben D. Hobson (University of Colorado, Boulder), Advisors: Kathryn K. Bercury (Department of Cell and Developmental Biology, University of Colorado Denver Health Science Center), Wendy B. Macklin (Department of Cell and Developmental Biology, University of Colorado Denver Health Science Center)

Oligodendrocytes are the myelinating glial cells of the central nervous system (CNS). Throughout postnatal development in the mouse brain, an oligodendrocyte progenitor cell (OPC) transitions into a premyelinating oligodendrocyte before becoming a terminally differentiated, myelinating oligodendrocyte. Many cellular processes regulate transitions through this lineage – but the translational regulation of differentiation within the lineage remains elusive. Understanding the developmental regulation of oligodendrocyte differentiation is clinically relevant because of diseases such as Multiple Sclerosis (MS). MS patients suffer from cognitive and motor deficits; the pathology of the disease is defined by lesioned areas of myelin, oligodendrocyte cell death, and damaged axons. It is known that OPCs and premyelinating oligodendrocytes persist in human MS lesions but the efficacy of remyelination is poor, leaving many axons unmyelinated. Identifying signaling pathways that might be therapeutic targets for remyelination is of interest because there is currently no cure for MS.

Our lab has shown that mTOR is critical in regulating myelination *in vivo*, and other studies have shown that it is critical for regulating OPC to premyelinating oligodendrocyte differentiation *in vitro*. In order to determine the developmental stage at which mTOR acts *in vivo*, we used rapamycin, an mTOR inhibitor, at early postnatal time points in mice. Unexpectedly, blocking mTOR from postnatal days 3-7 *in vivo* resulted in an increased number of premyelinating oligodendrocytes, an opposite effect relative to the published *in vitro* studies. Our findings indicate that mTOR may play a role in both intra- and inter-cellular signaling mechanisms that regulate oligodendrocyte differentiation *in vivo*.

Key Terms: Cellular Biology
Developmental Biology
Neuroscience

**CB-45**

## Directed Evolution of *Cryptococcus neoformans* in Low-Nutrient Media Generates a Stable Phenotype that Differentially Interacts with Murine Macrophages

William B. Zhang (Duke University), Anastasia P. Litvintseva (Duke University), Advisor: Anastasia P. Litvintseva (Duke University)

*Cryptococcus neoformans* var. *grubii* is an opportunistic human pathogen that causes significant morbidity and mortality among immuno-compromised patients, particularly those with HIV/AIDS. Infection is acquired by inhalation, and if not contained by the local immune response, spreads from the lungs to other parts of the body, preferentially to the central nervous system, where it causes meningitis. Other researchers utilized methods of reverse genetics and identified several factors that are required for virulence, but have not uncovered the fundamental mechanisms that enable *C. neoformans* to infect and colonize mammals. Here, we employ a forward genetic approach and apply experimental evolution to study virulence of *C. neoformans*. To test our hypothesis that ability to adapt to a nutrient-limiting environment can enhance virulence, we selected several avirulent strains and propagated them for approximately 250 generations in microbiological media containing limiting amounts of the essential nutrients, such as glucose, nitrogen, iron and copper. We then tested the stability of the acquired phenotypes by growing these evolved strains on rich media for one week (five passages), and assayed their ability to grow in the nutrient-limiting conditions to which they were originally adapted. Our results indicate that these strains retain their superior ability to proliferate in nutrient-poor media even after propagation on rich media. Further, results from *in vitro* murine macrophage assays suggest that our evolved strains may be preferentially phagocytized and/or have an enhanced ability to proliferate within macrophages. Our ongoing work focuses on separating these two potential effects and studying each in isolation.

Key Terms: Cellular/Molecular Biology
Directed Evolution

**CB-46**

**Class-specific dendritic morphology is alternately affected by induced hyper-excitability and suppression of neuronal activity in *Drosophila* sensory neurons**

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Activity-dependent remodeling of dendritic architecture represents a critical process in the formation and modulation of functional neural networks. Understanding how this mechanism manifests itself on the molecular scale can lead to new clues as to how the environment influences the form, and ultimately function, of neurons. The dendritic arborization (da) neurons of the *Drosophila melanogaster* peripheral nervous system (PNS) have proven a powerful model system in which to investigate the molecular mechanisms governing class specific dendrite morphogenesis, however, to date, the role of neuronal activity in regulating dendrite development in these neurons has not been reported. Here we investigate this question directly in two complex da neuron subclasses, class III and IV. The bipartite GAL4/UAS system was used to drive class specific da neuron transgene expression resulting in either sustained neural hyper-excitability (*UAS-Ork1-ΔC*) or inhibition of neural transmission (*UAS-TnT*) to explore the role(s) of neuronal activity in mediating da neuron dendritic morphology. Inactivated forms of these transgenes were likewise used as controls for the specificity of activating or inhibiting neuronal activity on dendrite development. Selectively increasing the intrinsic excitability or selectively disabling synaptic transmission in these da neuron subclasses, thereby allowed for analyses of the effects of neural activity on dendritic morphology via live image confocal microscopy.

Key Terms: Molecular Neuroanatomy
Developmental Neurogenetics

**CB-47**

## Aging Associated Changes in Intestinal Epithelial Stem Cells

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Aging is associated with decreased nutrient absorption and impaired barrier function, which may result from changes in intestinal epithelial stem cells (IESC) located at the base of the intestinal crypt. IESC produce differentiated cells that perform digestive and absorptive functions of the intestinal epithelium. Sry-box protein family member 9 (SOX9) is expressed in distinct cell populations within the intestinal epithelium, including IESCs. A transgenic mouse expressing EGFP under control of SOX9 regulatory sequence can be used to identify IESC, progenitor, and enteroendocrine cells (EEC) based on different levels of SOX9-EGFP expression. SOX9-EGFP sub-low level marks progenitor cells, SOX9-EGFP low level marks IESCs, and high SOX9-EGFP expression marks EECs (Gracz et al., 2010). Previous studies from our lab have used flow cytometry to show that old mice to have an increased number of SOX9-EGFP low IESC. This study tested the hypothesis that increases in SOX9-EGFP IESC result from increased IESC proliferation. The jejunum was isolated from young (3-4 mos.) and old (16-24 mos.) SOX9-EGFP mice. S-phase marker, 5-ethynyl-2'deoxyuridine (EdU) was used to quantify/localize proliferating cells. Results show that there is no difference in crypt depth in old vs. young mice; however, old mice have longer villi (263.2μm ± 26.1 vs. 361.7μm ± 30.0). Preliminarily, old mice exhibit an increase in SOX9-EGFP low IESC, but a decrease in EdU-positive, proliferating cells, and a decrease in SOX9-EGFP high EEC. These data suggest that aging may require an expansion of SOX9-EGFP low IESC to maintain a higher functional mass of villi.

Key Terms: Cell Biology
Molecular Biology
Physiology

**CB-48**

## An Investigation of SOX and FBN Gene Expression in Costal Cartilage of Chest Wall Deformities

Julianna Pryor (Old Dominion University), Advisor: Michael Stacey, Ph.D. (Old Dominion University)

Chest wall deformities, pectus carinatum (PC) and pectus excavatum (PE), are congenital malformations causing a sternal protrusion or depression. These inherited diseases affect 1 in 1000 live births, primarily males, and are often linked to other connective tissue disorders. The biological basis of chest wall deformities is unknown, although their costal cartilage is often described as abnormally grown and weak. Cartilage research focuses primarily on load-bearing cartilage; insufficient research regarding costal cartilage prompted this investigation of genes known to be essential for chondrogenesis with respect to chest wall deformity. SRY (sex determining region Y)-box 5, -6, -9 (SOX5, SOX6, SOX9) are transcription factors necessary for chondrogenesis. Fibrillins (FBN) are large glycoproteins that form microfibrils found in cartilage. Thus, both genes sets are of interest regarding the abnormal growth and strength of this cartilage. The objective of this investigation is to determine expression of SOX5, SOX6, SOX9 and FBN1, FBN2, FBN3 genes within costal cartilage of 4 PC samples compared to that of controls. RNA was extracted from human costal cartilage, and complementary DNA (cDNA) synthesized. Real-time polymerase chain reaction (RT-PCR) was used evaluate gene expression. The positive control was β-actin (ACTB). Melting curve data was generated for quality control, and Ct values determined as a measurement of gene expression. Our preliminary data so far has not shown abnormal gene expression, suggesting these growth factors and structural proteins are not directly causative of these abnormalities, however downstream effects of the SOX-trio and distribution of the FBN proteins still need to be determined.

Key Terms: Molecular Biology
Inherited Disorders of Cartilage

**CB-49**

## Inter-alpha-trypsin Inhibitor Heavy Chain 4: Domain-based Functional Effects on Immune Cell Activation and Migration

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ITIH4, a serum protein, has been shown to have elevated concentrations in patients with diseases such as early stage ovarian cancer, breast cancer, and chronic obstructive pulmonary disease (COPD). Recent studies have therefore identified ITIH4 as a potential biomarker for these diseases. The goal of this study is to better understand the role of ITIH4 as a biomarker and specifically, how it affects the immune response to lung injury.

Wild type mice (ITIH4+/+) and ITIH4 knockout (ITIH4-/-) mice were exposed to lipopolysaccharide, an endotoxin used to induce inflammation in the lungs. Based on immunohistochemistry, we found that ITIH4 is expressed in the lung in bronchial epithelia and in alveolar macrophages and neutrophils. Tissue injury levels, cytokine and cell counts, and cell migration data were analyzed. These indicate that ITIH4 slows the migration of inflammatory cells to the site of an infection. Results suggest that ITIH4 is a biomarker of containment: it serves to localize the immune response to an infection. This information adds to the growing body of knowledge about ITIH4 and may also allow physicians to learn more about the unique immune response in an individual based on the concentration of ITIH4 present.
Recently, we have focused on the mechanisms behind the effects of ITIH4. We hope to clone fragments of the protein in order to assess the effects of three important ITIH4 domains on immune cell activation and migration. Results have the potential to provide a specific target for disease intervention.

Key Terms: Immunology
Biomarkers
Disease Mechanism

**CB-50**

**Biomarkers for Early Prognosis of Lung Cancer in a Lung Tumor Model**

Mark Mckay (Wakefield High School), Advisor: Sheela Sharma (The Hamner Institutes for Health Sciences)

***Purpose:*** This year it is estimated that 156,940 people will die of lung cancer in the United States. The purpose of this research is to reduce the risk of developing cancer through chemo-preventive techniques. Chemotherapy, along with radiotherapy and surgery, has been proven to be inefficient in completely destroying cancerous cells and tumors. However, detecting biomarkers at an early stage can lead to an early prognosis of lung cancer and thus prevent its proliferation.

***Methods:*** The procedures that were used to conduct this research were immunostaining and scoring techniques to give a numerical value for the expression of PCNA and evaluate the translocation of NF-kB biomarkers.

***Results:*** After these experiments were run, the expression of PCNA for all time points in the alveolar and bronchial region were substantially higher in the Benzo[*a*]pyrene (B[*a*]P) treated group than the vehicle control group. Also, there were higher translocation rates of NF-kB for all the time points in the lung tissue cells in the B[*a*]P treated group than the vehicle control group.

***Conclusions:*** The conclusions that were drawn were that there was a positive correlation between the increased expression of PCNA (proliferation) and the translocation of NF-kB (inflammation) in the B[*a*]P treated lung tissue cells.

Key Terms: Preclinical
Safety

**CB-51**

## Analysis Of Simian Virus 40 Infected CV-1 Cell Chromosome Content

Emily Kragel (J. H. Rose High School), Advisor: John Lehman (Brody School of Medicine at East Carolina University)

Simian virus 40 (SV40) has been studied extensively since its discovery as a contaminant in the polio vaccine. Infection of permissive cells results in viral replication and cell lysis. This study looked at specific chromosomal amplification in SV40 infected permissive cells. CV-1 cells were infected with SV40. The progression, confirmation and nature of the infection were studied using an SV40 bioprobe, laser scanning cytometry analysis of DAPI staining for cellular DNA and Pab101/ Alexa Fluor 488 to staining for T-Ag expression. Human chromosome paints for chromosomes 2,4, 17 and 19, which have been shown to identify simian chromosomes when hybridized to the DNA, were used to quantify the number of copies of these chromosomes in infected CV-1 cells. The infected cells had nearly double (41% versus 24%) the number of cells in greater than G2 phase, and the difference in the chromosome contents of infected versus non-infected cells was statistically significant. The infected cells showed increased chromosome numbers as detected by FISH, which were often not diploid or tetraploid, and chromosome 19 showed marked hyperploidy. SV40 infection in CV-1 cells results in DNA cycle and chromosomal abnormalities. The significance of these abnormalities is unclear. Additional studies may help us understand the causes and effects of these chromosomal changes associated with infection.

Key Terms: Cellular Biology
SV40 Infection
Chromosome Analysis

**CB-52**

**Microsatellite Changes Gene Expression in Vocal Nuclei in the Dual Specificity Phosphatase 1 (dusp1) Promoter**

Yue Zheng (North Carolina School of Science and Mathematics), Advisors: Jason Howard (Duke University), Erich Jarvis (Duke University).

Vocal learning, a complex behavioral trait once thought to be unique to humans, is crucial for language acquisition. This behavior is also similarly found in three orders of birds: parrots, hummingbirds, and songbirds. The genetic causes of this rare trait are still being elucidated; for example, the dusp1 gene has been found to be highly up-regulated in response to vocalization learning in the song nuclei of vocal learners, and studies suggest that microsatellites— short repeating DNA sequences found in the genome that alter gene expression significantly—have an effect on dusp1 gene expression. To identify microsatellites and determine their effect on the dusp1 promoter, I compared the dusp1 promoter sequences of vocal learning and non-vocal learning avian models. After isolating, cloning, and sequencing the dusp1 promoter sequence from various species, I found that the length and number of microsatellites varied significantly across both species and individuals of the same species. These results were supported by gel electrophoresis and computational analysis of the sequences and have implications for updating the phylogenetic tree of bird evolution, increasing knowledge about avian vocal learning, validating sequences in the Genome 10K Project, and eventually creating a better understanding of language problems in human beings.

Key Terms: Genetics
Ornithology

**CB-53**

## Epigenetic Modifications Associated with Active and Inactive Centromeres

Alyssa Ferris (North Carolina School of Science and Mathematics), Advisor: Amy Sheck (North Carolina School of Science and Mathematics)

Most chromosomes have a single centromere, but some chromosomes, called dicentrics, have two functional centromeres. This usually leads to cell death; however, in human dicentrics, one of the centromeres is turned off. To determine if the presence histone methylation correlated with centromeric inactivity, I measured the levels of euchromatic and heterochromatic methylation at active and inactive centromeres on the naturally dicentric human Chromosome 17. I used four hybrid mouse cell lines, derived from two distinct human cell lines that had a different active centromere (either centromere Z1 or Z1B) on each homologous chromosome. To quantify the levels of histone methylation, I used chromatin immunoprecipitation to pull down DNA that was tagged with specific groups and then measured the levels of histone methylation using semi-quantitative PCR. I found that the levels of heterochromatic methylation increased when centromere Z1 became inactive, but I did not find a similar trend at the other centromere (Z1B) or with euchromatic methylation. I also found that the levels of histone methylation were not constant across the cell lines, indicating that each had a unique epigenetic profile instead of a set level of histone methylation. This suggests that histone methylation is involved in centromere function, but that it is not the only component. The difference in responses between the two centromeres is probably due to structural differences that make Z1 more conducive to histone modifications. These results have long-term implications for cancer medications and gene therapy because of the potential to selectively turn off chromosomes.

Key Terms: Epigenetics
Dicentric chromosome
Inactive centromeres

**CB-54**

## *In Vivo* Imaging Of Mouse Thymus In Determination Of Differentiation Rates Involved In T-Cell Reconstitution

Kairan Xiao (North Carolina School of Science and Mathematics), Advisor: Benny Chen (Duke University Medical Center)

T-lymphocytes are an integral part of the immune system through cell-mediated immunity to pathogens. Any immunodeficiencies such as AIDS or Leukemia pose major threats to the host, causing relatively weak infections to cause damaging or even fatal effects. Therefore, it is important to investigate the processes involved in maturation of thymocytes for the purpose of investigating ways to accelerate immune reconstitution. The purpose of this research was to develop and execute an experimental design for a novel approach to imaging within the thymus (*in vivo)*. DsRed hematopoietic stem cells were injected into irradiated nude BALB/c mice which had previously been transplanted with a GFP C57BL/6 donor thymus. Using a dual-photon microscope, *in vivo* imaging scans successfully isolated candidate thymic settling progenitors within the thymus. Flow cytometry and a newly developed method of imaging confirmed the creation of CD4+ and CD8+ cells. Results indicated that using a green FLIVO apoptosis kit in conjunction with the DsRed cells allows for successful identification of apoptotic cells in *in vivo* imaging. Utilization of these results allows for an *in vivo* investigation in the rates of β-selection and Positive Selection. This research paves the way for future work investigating important signaling and structures within the processes.

Key Terms: Immunology
Lymphoid System
Positive and Negative Selection

**CB-55**

## Prions as a Novel Mechanism of Stress Response Through Yeast Colony Morphology

Hun Wong (North Carolina School of Science and Mathematics), Advisor: Amy Sheck (North Carolina School of Science and Mathematics)

Prions are self-propagating amyloid proteins that are most often associated with irreversible neurodegenerative diseases in mammals, but in *Saccharomyces cerevisiae* (yeast) recent findings have suggested that prions may serve an evolutionarily beneficial role in responding to stressful environments. This study attempts to discover a novel function of prions as a factor facilitating yeast complex colony morphology (CCM) and pseudohyphal development- two known nutritional stress responses of yeast. Twenty four strains were screened by growing them on media varying in nutritional stress (YPD, YPLD, and SLAD-1%, low, medium, high stress respectively) with and without 1mM GuHCl, a chemical known as an effective treatment to eliminate yeast prions. CCM and pseudohyphal growth were assayed as stress response indicators. Eight of the 24 strains tested for CCM responded to GuHCl with changes in overall complexity as well as morphotypes, and 5 of the 24 strains tested for pseudohyphal development displayed varying levels of pseudohyphae in response to GuHCl. These results suggest that the strains that responded to GuHCl have prions that play a novel role in stress management through CCM and pseudohyphal development.

Key Terms: S. Cerevisiae
Prion
Colony Morphology

**CB-56**

**Effect of Hyperthermia and Hypoxia on the Expression of Dysadherin, a Cancer Associated Cell-Membrane Glycoprotein Shown to Increase Metastasis**

Pranav Haravu (North Carolina School of Science and Mathematics), Advisors: Diane Fels (Duke University), Kathleen Aschraft (Duke University), Myra Halpin (North Carolina School of Science and Mathematics)

Though cancer treatments have significantly progressed, metastasized tumors still pose a significant challenge to modern therapeutic methods, resulting in poor prognoses and lower survival rates for patients with metastasized cancers. In this study we investigated the role of dysadherin in a possible mechanism for both hypoxia- and hyperthermia-induced metastasis. Dysadherin is a cell-membrane protein found highly expressed and glycosylated in cancer cells, but expressed only in a few normal cells. It down-regulates E-cadherin mediated cell-cell adhesion, facilitating metastasis. We treated Panc-1 and HCT116 cells with 43$^{\circ}C$ hyperthermia and .5% $O_2$ hypoxia. Western Blots, with $\beta -$ actin as a loading control, showed a significant increase in expression of glycosylated dysadherin in Panc-1 cells exposed to hypoxic and hyperthermic conditions. However, unglycosylated dysadherin expression was not affected, leading us to believe unglycosylated dysadherin does not play a significant role in metastasis. Therefore it suggests hypoxia- and hyperthermia-induced metastasis function by increasing the expression of glycosylated dysadherin, which in turn down-regulates E-cadherin and promotes metastasis. Inhibiting key steps within this mechanism could serve as a potential drug target, greatly reducing the metastatic potential of malignant tumors. To our knowledge, this is the first report indicating that hypoxia-induced metastasis and hyperthermia-induced metastasis may occur by increasing glycosylated dysadherin expression, and hence the potential benefits of this study are much greater than the data presented.

Key Terms: Dysadherin
Metastasis
Hypoxia

**CB-57**

## The RNA-Binding Protein HuR Binds and Stabilizes Pre-mRNA *in vivo*

Vipul Vachharajani (North Carolina School of Science and Mathematics), Kyle Mansfield (Duke University Medical Center), Matthew Friedersdorf (Duke University Medical Center), Advisor: Jack Keene (Duke University Medical Center)

Gene expression control through post-transcriptional regulation serves as a vital process in the normal function of cells. Factors such as RNA-binding proteins (RBPs) interact with target messenger RNA (mRNA) molecules, affecting their processing, stability, and cytoplasmic translation. Often, these proteins recruit, enhance, or inhibit RNA-processing machinery.
HuR is an RNA-binding protein which is important in normal cell function. Dysregulation of HuR can lead to neoplastic phenotypes and is implicated in carcinogenesis in colon and brain cancer. HuR acts in the cytoplasm to prevent degradation of mature mRNA molecules, but HuR's nuclear function is less well known. Recently, HuR targets which bind only intronic sequences in unspliced RNA have been proposed, which would reveal a HuR function which is distinct from the cytoplasmic one. We used RNA immunoprecipitation to confirm HuR binding to intronic only sequences of the proposed targets. We then used siRNA knockdown of HuR to show a functional effect of the observed binding on pre-mRNA transcript abundance. Our results show a high degree of functional HuR binding to intronic-only sequences in the NFATC3 gene. Our results suggest a complex nuclear function of HuR that may include splicing and splicing-concurrent processes.

Key Terms: Post-Transcriptional Regulation
RNA-binding Protein
RNA Splicing

**CB-58**

**The Effect of Dextrose Starvation on the Colony Morphology of *S. cerevisiae* Through Ammonia Signaling**

Mark Kirollos (North Carolina School of Science and Mathematics) Advisor: Dr. Amy Sheck (North Carolina School of Science and Mathematics)

*Saccharomyces cerevisiae* (bakers yeast) is often classified as a unicellular organism, however, this species displays complex behavior such as cellular differentiation and cell signaling often associated with multicellular organisms. Carbon limitation in media causes yeast colonies to form complex morphology, which is believed to be an adaptation for surviving stressful conditions. Yeast cells use extracellular ammonia production as one mechanism for synchronizing colony development in a complex pathway that communicates nutritional starvation to the individual yeast cells. By plating six strains of yeast with varying levels of dextrose and extracellular ammonia, the effects of the treatments on the strength of complex colony morphology and colony growth were compared. Ammonia exposure and dextrose limitation in the yeast did not always produce similar effects on colony morphology. Increasing extracellular ammonia levels actually decreased morphology strength in certain strains and promoted growth, contrary to prior published finding. The effect of dextrose and ammonia were found to be very strain specific, with different responses occurring even between strains of the same genetic background but of a different ploidy. These findings may help explain early multicellular traits such as chemical signaling in yeast.

Key Terms: Yeast
Ammonia Signaling
Complex Colony Morphology

**CB-59**

# Superoxide Reductase (SOR) Pathway Gene Expression Under Oxidative And Cold Stress In Hyperthermophilic Archaeon, *Pyrococcus Furiosus*: An Enzymatic Model For Amyotrophic Lateral Sclerosis (ALS)

Sainath Asokan (William G. Enloe High School), Anirudh Guduru (William G. Enloe High School), Karthik Ramasubramanian (William G. Enloe High School), Research Advisor: Amy Grunden (North Carolina State University)

Our research has focused on the experimental study of a superoxide-scavenging pathway in the archeaon *Pyrococcus furiosus* that normally lives in $O_2$-free, 90 $^{o}$C-hydrothermal vents but is frequently ejected into $O_2^-$containing, 4 $^{o}$C waters. We have specifically looked at the mRNA expression of superoxide reductase (SOR) and a related enzyme, rubrethyrin reductase (Rr), as a function of temperature and oxidative stress using quantitative Real-Time PCR (qRT-PCR) to understand SOR-dependent superoxide scavenging and detoxification. We have observed an increase in *SOR* expression upon exposure to oxidative stress, an increase in *Rr* expression upon exposure to $H_2O_2$ relative to expression upon exposure to ambient air, and an increase in expression of both *SOR* and *Rr* at 90 ºC relative to expression at 4 ºC. To monitor gene expression over a wider range of temperatures including physiologically relevant temperatures, we have also designed and fabricated a bioreactor for experimental validation of the above trends. Oxidative stresses are known to play a role in the onset and progression of neurological conditions such as Amyotrophic Lateral Sclerosis (ALS) due to a toxic gain of function in misfolded superoxide dismutase (SOD) enzymes. Our work suggests that the SOR pathway used by *P. furiosus* can potentially serve as an enzymatic model for designer therapeutics to replace mutated SOD in ALS and other neurological conditions like brain and spinal cord cancer.

Key Terms: Microbiology/Functional Genomics
Neurodegenerative Diseases
Bioengineering

**CB-60**

# Transcriptome Analysis to Identify Novel Components of the Gravitropic Signal Transduction Pathway

Avery Tucker (Ohio University), Zachary Abrams (Ohio University), Kaiyu Shen (Ohio University), Sarah Wyatt (Ohio University)

Gravity is a fundamental stimulus that affects plants growth and development. The gravitropic response is separated into three phases: perception, signal transduction and differential growth. The gravity persistent signal (GPS) treatment was used to isolate the mechanisms of gravitropic signal transduction from those of perception and response. After cold acclimation, Arabidopsis inflorescence stems were placed either upright (control) or on their sides (gravistimulated) at 4°C, and mRNA was collected at 2min, 4min, 10min, and 30min. Gene expression analysis was performed using an Agilent Arabidopsis gene expression array (4X44k) with dual color platform. 349 unique differentially expressed genes were distinguished: 8 genes at 2min, 96 genes at 4min, 190 genes at 10min, and 65 genes at 30min. Ontology terms were identified based on the most significantly enriched functional groups and pathways: response to exogenous stimulus, transcriptional activities and flavonoid pathways. The "top" five differentially expressed were selected for qRT-PCR analysis: WRKY18, WRKY26, WRKY33, BT2, and ATAIB. In addition, SALK lines with T-DNA insertions in these genes are being screened to assess any phenotype change during plant growth. These experiments will help determine the significance of these genes within the gravitropic signaling pathway. Partially supported by an Ohio University Student Enhancement Award to KS and an Ohio University Research Committee Award to SEW.

Key Terms: Gravitropic Signal Transduction
Gene Expression Analysis
T-DNA Insertions

**CB-61**

## The Effects of Energy Drinks on the Structure and Function of Epithelial Cells and Fibroblasts

Eric Shide (Saint Mary's College of California), Advisor: Vidya Chandrasekaran (Saint Mary's College of California).

Energy drinks and their ingredients were studied at the cellular level. Cellular effects of energy drinks were assessed on two cell types: Madin-Darby Canine Kidney (MDCK) cells and rat embryonic fibroblasts. To examine effects of energy drinks on cellular structure and function, cells were treated with Monster Energy and 5-hour Energy. It was discovered that both types of energy drinks negatively impacted cell structure and function in epithelial cells and fibroblasts.

The results of the project indicate that in both kidney cells and in fibroblasts, the function of the actin cytoskeleton is disrupted without affecting the microtubule cytoskeleton. However, the underlying reason for the disrupted function is different in the two cell types. In the kidney epithelial cells, the actin cytoskeleton is disrupted, whereas the fibroblast showed a normal actin cytoskeleton but aberrant filopodia/lamellopodia formation.

Key Term: Cellular Biology

**CB-62**

**Reactive Oxygen Species are Important for Promoting BMP-7 Induced Dendritic Growth in Rat Embryonic Sympathetic Neurons**

Charlotte Lea (Saint Mary's College of California), Advisor: Dr. Vidya Chandrasekaran (Saint Mary's College of California).

Neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease and the process of aging in humans are associated with changes in the neuronal morphology, specifically the retraction of dendrites. The purpose of this research study was to investigate the role of reactive oxygen species (ROS) in sympathetic neurons and to determine whether ROS are primarily harmful or beneficial to dendritic growth. ROS are types of free radicals found in cells, and they include molecules such as hydrogen peroxide, hydroxyl, and superoxide radicals. In large quantities, ROS can cause damage to DNA and kill cells, but recent research has shown that ROS production is necessary for non-cytotoxic and/or host defense functions. In this study, we first examined the effects of the antioxidants diphenylene iodinium (DPI) and nordihydroguaiaretic acid (NGA) on bone morphogenetic protein 7 (BMP-7) induced dendritic growth in cultures of sympathetic neurons from 21 day old rat embryos. In addition, since ROS are known to be produced during cellular respiration, we tested the amount and rate of oxygen consumption in neurons treated with BMP-7 using the Seahorse XF24 Analyzer. Our data suggest that ROS are produced in BMP-7 treated sympathetic neurons and are important to dendritic growth at low physiologic levels. Furthermore, different antioxidants can inhibit BMP-7 induced dendritic growth, indicating that though antioxidants are important for protective effects against excess ROS production, high levels of antioxidants may have undue damage to neurons in the form of decreased dendrite number and decreased dendritic arbor.

Key Terms: cell biology
dendritic growth
reactive oxygen species

**CB-63**

## Caveolin-Mediated Ozone-Induced Cardiac Toxicity and Lung Injury in Adult Healthy Rats

Shubham Manchanda (Texas A&M University-Corpus Christi), Magdalena Ramirez (Texas A&M University-Kingsville), Pranjal Manchanda (The University of Texas at Dallas), Vishal Sethi (The University of Texas-Pan American), Advisor: Dr. Rajat Sethi (Texas A&M Health Science Center, Irma Lerma Rangel College of Pharmacy).

Ozone is one of six pollutants included in the National Ambient Air Quality Standards set by USEPA. This study proposes to investigate change in the cardiac injury compared to lung function after exposure to chronic levels of $O_3$. We hypothesized differential changes in cardiovascular and pulmonary systems after chronic exposure to $O_3$ for long periods of time. Twenty age/weight matched male Sprague Dawley rats were randomly divided into two groups that were exposed to air or 0.8 ppm $O_3$ for 8 hours/day for 28 days. Cardiovascular parameters from both groups were measured in rats before and after exposure. Four rats were sacrificed, and their hearts and lungs were extracted. Western blot analysis was performed on lung and left ventricular heart tissue from air and $O_3$-exposed rats to quantify the differential levels of caveolin-1 in the membrane, p38MAPKα in the membrane and cytosol, and P-p38 in the cytosol. Decreased caveolin-1 in the membrane has been linked to enhanced death signaling due to decreased binding with p38MAPKα leading to increased translocation of death signal to cytosol. The significant findings are: a) 4 week $O_3$-exposed heart expressed decreased caveolin-1 in the membrane compared to lung, b) although cytoplasmic p38 MAPK alpha expression was increased in heart and lung exposed tissue, this increase was more in heart compared to lung, c) P-p38 activity was increased in heart compared to lung, suggesting decreased death signaling in lung. These novel findings indicate a regulatory role of caveolin-1 in chronic ozone-induced cardiac toxicity and lung injury.

Key Terms: Ozone
Caveolin
Cardiac Toxicity

**CB-64**

# Validation Of Protein Markers For Biocompatibility Of Endothelial Progenitor Cells-(EPC)-Coated Titanium Stents In Cardiovascular Implants

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Cardiovascular disease is currently the number one cause of death in the U.S.; the high continued incidence of major risk factors such as obesity, diabetes mellitus and age, emphasizes the need to develop new technologies that can be used to alleviate the symptoms of cardiovascular disease. To this end, we investigated three (3) proteins known to be associated with coagulation and inflammation, as biomarkers of the effects of autologous EPC lining on the biocompatibility and antithrombogenicity of blood-contacting titanium implants. Selected pigs were divided three groups: sham control (n=10), pigs receiving a bare Ti implant (n=10), and pigs receiving an autologous EPC-coated Ti implant (n=10). Peripheral blood was drawn from the pigs' ear immediately before and after the surgery, and 7 and 30 days post-surgery. Despite differences seen in the physical condition of implants upon explant, analysis of serum levels of C-reactive protein, Factor VIII, and Factor X by Western blot showed no significant differences between experimental groups. The preliminary data indicate that the serum levels of these proteins do not fall into the range to be suitable markers of the biocompatibility of EPC-lined Ti implants. These results agree with Quantitative Intact Proteomics results.

Key Terms: Protein Markers
Endothelial Progenitor Cells
Cardiovascular Implants

**CB-65**

## Recombination and Cryptic Heterokaryosis in Experimental Populations of *Aspergillus flavus*

Rodrigo A. Olarte (North Carolina State University), Bruce W. Horn (National Peanut Research Laboratory), James T. Monacell (North Carolina State University), Rakhi Singh (North Carolina State University), Advisor: Ignazio Carbone (North Carolina State University)

*Aspergillus flavus* infects both plants and animals, and is of toxicological importance due to its production of aflatoxins (AFs) and other mycotoxins. Mycotoxins can cause agricultural losses totaling upwards of $1.4 billion annually. Recent efforts to reduce AF concentrations have focused on the use of the biocontrols AF36 and Afla-Guard, both of which contain nonaflatoxigenic *A. flavus* strains as an active ingredient. Biocontrols are applied to fields, where they competitively exclude native aflatoxigenic strains. Although biocontrol is effective, the extent to which these strains recombine with native strains, and the overall effect on fungal populations is unknown. Here, we show direct genetic evidence of sexual recombination between *A. flavus* strains, and that the recombination breakpoints in the F1 correlate to those inferred from population studies of natural isolates. Furthermore, we demonstrate that a crossover within the AF cluster can revert a nonsense mutation, resulting in a regained toxic phenotype. Finally we observed non-mendelian inheritance of AF cluster alleles in crosses with partial AF cluster parents. These findings indicate the possibility of cryptic heterokaryons in *A. flavus* that may be important in modulating AF production in stressful environments.

Key Terms: Sexual Recombination
Toxin Heritability
Cryptic Heterokaryosis

**CB-66**

## M1/M2 Polarization After HSV-1 Corneal Infection

Adam C. Reichard (Wright State University), Advisor: Dr. Nancy J. Bigley (Wright State University), Co-Presenters: Benjamin Holmes (Wright State University), Norm Holcomb (Wright State University)

Two macrophage subpopulations have been identified. The M1, or classical, macrophage population is pro-inflammatory due to its tumor killing and host defense effects. The M2, or alternative, macrophage population is anti-inflammatory due to the release of anti-inflammatory cytokines, which leads to tissue remodeling. Our hypothesis is that when challenged with HSV-1 infection the M1 phenotype will predominate in the corneal epithelium leading to tissue injury. To examine this hypothesis it was necessary to determine the cytokine response of the M1 and M2 phenotype after HSV-1 infection. Murine macrophage cell lines considered M0 (unpolarized) were induced to the M1 or M2 phenotype before infection. When treated with IFN-gamma and LPS the macrophage cell lines undergo polarization to the M1 phenotype. In comparison with the unpolarized cells the M1 phenotype exhibited extensive vacuolization within the cytoplasm. Alternatively, when treated with IL-4 the macrophage cell lines undergo polarization to the M2 phenotype exhibiting less cytoplasmic vacuolization than the M0 phenotype. When the M0 macrophages (RAW 264.7) were infected with virus (2 MOI) cell death was obvious at 18 hours post infection and large cytoplasmic vacuoles were seen in viable cells. We verified phenotype using fluorescently tagged antibodies. RT-PCR was used to identify transcripts predominating in each phenotype (iNOS and CD86 for M1, and Arg I and CD206 for M2). We conclude that M1 macrophages control the replication of HSV-1 through production of antiviral molecules such as iNOS; however, corneal damage is likely attributed to the production of pro-inflammatory molecules produced by M1 macrophages.

Key Terms: Immunology
Innate Immunity
Cell Biology

**CH-01**

## Antibiofilm/Antibiotic Resensitization Activity Evaluation of 4,5-Disubstituted-2-Aminoimidazole-Triazole Conjugates

Zhaoming Su (North Carolina State University), Advisor: Christian Melander (North Carolina State University)

Antibiotic resistant pathogens have become an emerging crisis nowadays. Biofilms are considered one of the very important defense mechanisms in drug resistant in bacteria. We have recently synthesized a library of 4,5-disubstituted-2-aminoimidazole-triazole conjugates (2-AIT) and tested them for antibiofilm activity. This class of small molecules was found to inhibit biofilm formation by methicillin-resistant *Staphylococcus aureus* (MRSA) and *Acenitobacter baumannii* at low micromolar concentrations. Lead compounds were also verified to resensitize MRSA to traditional antibiotic oxacillin (resensitization activity) by 2 – 4 folds.

Key Terms: Biofilm
2-Aminoimidazole
Resensitization

**CH-02**

**Formazan Dyes as Potential Photosensitizers in PDT**

Alexandra B. Ormond (North Carolina State University), Advisor: Harold S. Freeman (North Carolina State University)

Formazan dyes have been used as antimicrobial, antiviral, and antibacterial agents, but have not been investigated as photosensitizers for photodynamic therapy (PDT). PDT utilizes a combination of photosensitizer, light, and molecular oxygen to treat cancers and skin diseases by generating reactive oxygen species (ROS) that interact with and destroy diseased tissue. Visible light is used to activate the photosensitizer, with light closer the red region preferred for deeper tissue penetration. Dyes of the porphyrin family exhibiting extensive conjugation are the dominant photosensitizers in PDT, but the difficulty in their preparation and low yields render them less than ideal synthetic targets. Formazan dyes are compounds with structurally similar chromogens that can be prepared with far fewer byproducts and in much higher yields than porphyrins.

Formazan dyes containing phenyl and heteroaryl groups in the periphery have been synthesized and complexed with metals previously employed in PDT photosensitizers. Metal-complexes provide rigidity to the formazan structure for ROS generatation and bathochromically shift absorption maxima. Non-metallized formazan dyes absorb near 500 nm, while metal-complexed dyes are red-shifted up to 100 nm. Additionally, non-metallized formazan dyes fluoresce in the 600 nm range with picosecond fluorescence lifetimes. Until now, fluorescence properties of formazan dyes have not been reported, but are the thrust of this investigation. The recently measured fluorescence properties of formazan dyes synthesized in the present study suggest that these dyes are potential sensitizers for PDT. Studies underway include testing for singlet oxygen generation efficiency.

Key Terms: Formazan Dyes
Photodynamic Therapy
Fluorescence

**CH-03**

**Cyclic Voltammetric Study Using Potassium Titration Of A Bridged Polyoxometalate.**

Dennis K.K Ampadu (Quinnipiac University), Advisor: Prof. James F. Kirby (Quinnipiac University)

The identity of counterions in solution with heteropolyanions is often now carefully considered because preliminary research has shown that they could affect their reactions as well as the products some form. It has also been noticed that under identical conditions, counterions in the same group could yield different products when in solution with particular heteropolyanions.

In this research, the redox potentials of cerium bridged polyoxometalate compounds ($K_{16}Ce(P_2W_{17}O_{61})_2 \cdot xH_2O$) formed as a result of the combination of potassium counterions in solution with a cerium bridged anion, $Ce(P_2W_{17}O_{61})_2^{16-}$ were measured by cyclic voltammetry. Several potassium ion concentrations were used in solution with this heteropolyanion, and the redox potential values were compared to those of earlier research on Thorium bridged anions by Dr. James Kirby and Dr. Louis Baker (deceased).

The redox potentials of the $[K^+]$:Ce ratios (0:1, 1:1, 4:1, 16:1) were compared for both bridged anions using MS Excel Spreadsheet and their trendlines showed equations to the third degree. It was also very interesting to note that for both Thorium and Cerium Wells-Dawson heteropoly-anions, the 4:1 ratio had the most negative redox potentials, -450mV for Thorium and -464.3 for Cerium.

Through this research it is adequately established that the concentrations of counterions in solution with heteropolyanions could affect their redox potentials. There was a relationship between the $K^+$ ion concentrations to bridged compounds such that the trendline equations for the selected concentrations were: $2.15x^3 - 16.55x^2 + 37.6x - 486.2$ and $17.5x^3 - 120x^2 + 207.5x – 465$ respectively.

Key Terms: Potassium Titration
Cyclic Voltammetry
Redox Potentials

**CH-04**

## Establishing Metal Binding as a Novel Antioxidant Mechanism: Comparative Studies of Sulfur and Selenium Antioxidants

Alyssa Rabon (Clemson University), Matt Zimmerman (Clemson University), Advisor: Julia Brumaghim (Clemson University)

Antioxidants can ameliorate oxidative DNA damage that has been linked to development of neurodegenerative diseases and cancer.[1, 2, 3] Thus, it is critical to understand how antioxidants prevent DNA damage and disease, and to identify the chemical characteristics necessary for increased activity. Sulfur- and selenium-containing antioxidants have been examined for their ability to treat or prevent neurodegeneration, cancer, and cardiovascular disease, which is attributed to their oxygen radical scavenging ability.[4, 5] The Brumaghim group investigates the ability of sulfur and selenium antioxidants to bind iron and copper, which generate DNA-damaging oxygen radicals. Metal binding would directly prevent radical formation rather than scavenging damaging radicals after their release. The ability of sulfur and selenium antioxidants to prevent iron- and copper-mediated DNA damage was tested using gel electrophoresis DNA damage assays. The analogous sulfur and selenium compounds 1,3-dimethylimidazole selone (dmise) and -thione (dmit), prevent 50% of copper-mediated damage ($IC_{50}$) at ~240 and 1550 ± 3 μM, respectively, and prevent iron-mediated damage with $IC_{50}$ values of 3.2 ± 0.9 and 89.1 ± 0.2 μM. Thus, the selenium-containing dmise is a more potent antioxidant than dmit. Similar DNA damage prevention studies were carried out with 1,3,5-triaza-7-phosphaadamantane selenide (PTASe) and -sulfide (PTAS), compounds structurally similar to dmise and dmit. PTASe and PTAS prevented iron-mediated damage with $IC_{50}$ values of <1000 and <350 μM, respectively. This reduced antioxidant potency implies that structure contributes to effective antioxidant activity. Understanding the mechanisms for sulfur and selenium prevention of DNA damage is required to fully utilize their antioxidant abilities.

Key Term: Bioinorganic Chemistry

**CH-05**

# Finding and Comparing the Composition of Almond and Black Seed Oil using Gas Chromatography-Mass Spectrometry

Jasmine Bellamy (Winston-Salem State University), Advisor: Dr.Siham Rahhal (Winston-Salem State University)

Within in this research study, natural almond and black seed oil is produced using soxhlet extractions to study the components of both oils. The chemical composition of almond oil and black seed oil was determined by Gas Chromatography-Mass Spectrometry (GC-MS). The basic procedure for a soxhlet extraction is using a solid sample, crushed almonds and black seeds, and placing it into a porous container and allowing a condensed solvent, ethyl acetate and hexane, as to continuous be extracted. Within soxhlet extractions the solvents, ethyl acetate and hexane were used to produce polar and non-polar compounds in the oils.

Also the composition of almond oil and black seed oil is compared towards each other and to other almond oils to conclude which is the better substance. Other research studies have shown that almond oil is used for treatment of the skin, but also for medical problems such as irritable bowel syndrome symptoms. Also, cardiovascular benefits have also been identified with almond oil elevating the levels of high-density lipoproteins (HDL). It's been know that black seed oil and extracts act as an antimicrobial, anti-inflammatory, and anti-cancer. The black seed oil is also known for containing vitamins A, B, B2, C and niacin. This study will demonstrate the quality components of almond oil and black seed oil and how they compared to other oils.

Key Terms: Medical Research
Human Nutrition
Analytical Chemistry

**CH-06**

# Elucidating The Role Of Copper Within Lysyl Oxidase Via Chelation Experiments

Michael Lynch (Emmanuel College), Hung Banh (Emmanuel College), Lauren Gagnon (Emmanuel College), Brittany Farias (Emmanuel College), Advisor: Dr. Faina Ryvkin (Emmanuel College)

Lysyl oxidase (EC 1. 4. 3.13), member of the amine oxidase family, is a copper-dependent extracellular enzyme that plays a critical role in cardiovascular function. Lysyl oxidase has an important function in the maintenance of extracellular matrix stability and could potentially participate in vascular remodeling associated with cardiovascular diseases. Tumor suppression activity of lysyl oxidase has also been recently documented. Among the copper amine oxidases, the physiologically important lysyl oxidase still remains a puzzle. Lysyl oxidase is difficult to obtain in large yields due to its low solubility in aqueous solutions except in the presence of high concentrations of urea. The native form of lysyl oxidase contains a covalently bound organic cofactor, lysine tyrosylquinone, and a tightly bound $Cu^{2+}$ ion in its active site; however the function of copper in the catalytic mechanism of lysyl still remains unanswered. This investigation was dedicated to resolving the existing dispute in the literature regarding the role of copper within lysyl oxidase. Lysyl oxidase samples were prepared by optimizing published procedures resulting in active enzyme samples that were used for further analysis. A series of chelating experiments have been conducted using two copper-containing amine oxidases: commercially avaliable diamine oxidase and purified samples of lysyl oxidase. Traditional copper chelating agents as well several other compounds identified by our molecular modeling experiments were tested. Enzymatic activity was monitored by a sensitive fluorescence assay, and copper content was determined using atomic absorbance techniques. The correlation of copper removal with enzyme activity will be discussed.

Key Terms: chelating agents
copper complexes
Metalloenzyme

**CH-07**

## Theoretical Calculations of Energy and Stability Based on Tryptophan Geometries

Brittany Batts (Winston-Salem State University), Advisor: John T. Yi (Winston-Salem State University)

Tryptophan (2-amino-3-(1H-indol-3-yl) propanoic acid) is one of the ten essential amino acids in the human body, well known for aiding in areas such as sleep and relaxation. In this research, the goal was to perform Quantum mechanical calculations using Hartree-Fock and Becke 3 LYP theory, in order to gain a better understanding of the stereochemistry of this amino acid. The relative energies of many different tryptophan isomers were used to compare stability based on energy as well as bond orientations. The orientation of the amine group based on the intra-molecular forces between nitrogen and hydrogen became an important area of focus and finding. We also detected the $C_{\alpha}$-$C_{\beta}$ bond rotation based on the position of the carboxyl group classifying an anti, pyrrole, or phenyl orientation, which would also contribute to the energy around the carboxyl group. The importance of a stable or ideal structure is what this research will further explain.

**CH-08**

# Probing Protein-Ligand Interactions Using The Stability of Proteins From Rates of Oxidation (SPROX) Method

Chris Lane (Jack Britt High School), Advisor: Dr. Michael Fitzgerald (Duke University)

Over 500,000 people died from heart disease last year in America, and millions more died or suffered around the world. This research will focus on probing a protein target of the antioxidant resveratrol. Resveratrol, a ligand, possesses anti-carcinogenic and longevity attributes that may be utilized to treat diseases, such as heart disease, Alzheimer's, and diabetes. To start off the research, the yeast colony Saccharomyces cerevisiae was grown. Additionally, protein purification and Bradford assay were utilized to develop and measure the concentration of the protein cytosolic aldehyde dehydrogenase, or ALD6. Then, the stability of proteins from rates of oxidation (SPROX) method was utilized, with/without resveratrol, to analyze the interactions between ALD6 and resveratrol. A matrix assisted laser desorption/ionization (MALDI) device was used to obtain spectra.

The major goal of the experiment was to possess enough protein and peptides by the end of the SPROX method. Spectra were developed to analyze the concentration of protein and peptides in the respective substances. A preliminary SPROX curve was created from the spectra using ribonuclease A (RNase A). The data refuted the goal, because there were not enough ALD6 and peptides within the ALD6 to conduct further studies. The experiment must be repeated, possibly with more protein, to further analyze the interactions. Ultimately, this research strives to utilize resveratrol's potential to interact with other proteins and alleviate the devastating and deleterious effects of heart disease.

Key Terms: Chemistry
Protein Purification
Proteomics

**CH-09**

# Chemical Vapor Depositon Growth of Graphene Using Cupric Oxide as the Catalyst

Kendall Dawkins (Simon G. Atkins Academic and Technology High School), Jay Simmons (Duke University)

In current electronics, indium tin oxide (ITO) is used as an electronical semiconductor in electronics such as iPhones, iPads, and any other electronics that uses touch screen technology. However, ITO is a very fragile material, naturally toxic, and costly to use at $800 per kilogram as of 2007. Graphene has been studied as a potential alternative to ITO. Unlike ITO, graphene exhibits no band gap making it a conductor and also allowing graphene to exhibit greater electrical conductivity. Also graphene is non-toxic, a strong material, and inexpensive to make. Cupric oxide will be used as the catalyst to speed up the process of making the graphene. In previous experiments copper was used, however due to copper contamination, graphene that was produced had many defects. It was hypothesized that if cupric oxide can be used as a catalyst to grow graphene then it can be used as an alternative in transparent electronic devices. Graphene was obtained by first making cupric oxide by heating copper foil, exposing the copper foil substrate to argon, hydrogen, and ethanol in that order and reheating copper foil substrate at a desired temperature. Finally Raman spectroscopy and a scanning electron microscope were used to examine if graphene was made. According to results from the Raman spectroscopy and scanning electron microscope, it was determined that graphene was made but with defects. In conclusion, the hypothesis was supported, but the graphene that was created cannot be used in electronics due to many defects exhibited in the graphene.

Key Terms: Chemistry
Engineering
Biochemistry

**CH-10**

## Using The Density Shifts of Streptavidinated Microbeads Upon Binding to Biotinylated Gold Nanoparticles to Develop a Novel Protein Quantification Method

Joshua Howell ( Simon G. Atkins Academic & Technology High School), Advisors: Benjamin Wiley (Duke University), Adria Wilson (Duke University)

Protein analysis is very important to society because with out it, amounts of proteins in different solutions will be unknown. Streptavidin has a natural affinity to biotin. By using this natural affinity and connecting it to a polystyrene microbead that is 7.4 micrometers in diameter and a gold nanoparticle that is 15 nanometers in diameter a bead gold complex will be formed. Completely covering a micro bead in gold nanoparticles will increase the density of it and by putting bead gold complexes in different density solutions and recording which solutions they float in, those bead gold complexes densities can be determined. The number of gold nanoparticles on its surface relates directly to the amount of protein on binding it together. In the future using antibodies instead of biotin and streptavidin, will develop a newer way of determining protein concentrations in a solution

Key Term: Chemistry

**CH-11**

## The Synthesis of Hydroperoxide Precursors Via Knoevenagel Condensation and Grignard Reactions

Kori McDonald (Hillside High School), Advisor: Jeff Johnson (University of North Carolina at Chapel Hill)

Endoperoxides are very important in cancer and malaria research. Their properties are said to posses anticancer and antimalarial activity. In order to synthesize the endoperoxides, a variety of derivatives from both Meldrum's and Barbituric acid need to be synthesized. Through this research it is essential to successfully produce a variety of the derivatives to answer the question, Are the substrates produced suitable for the hydroperoxidation reaction? The hydroperoxidation reaction is the next step in synthesizing the endoperoxides. Synthesizing the necessary derivatives is performed in a two step process. The first step, Knoevenagel condensation, is the process where either of the starting materials is mixed with an aldehyde. The product of this reaction is placed through the second step, the Michael addition of a Grignard reagent. Here the Knoevenagel product is mixed with the Grignard reagent and THF at 0°C. Reductive alkylation of Meldrum's acid was also performed in accordance with the first step. Meldrum's acid is added to a carbonyl and cooled to 0°C. The products of all the reactions are tested and analyzed using a proton NMR to identify the products purity. Successfully, a variety of the Knoevenagel products were produced in excellent yield. Thus, a variety of Grignard products were successful produced in excellent yield. Therefore, it was proven that the substrates produced are suitable for the important hydroperoxidation reaction.

Key Term: Organic Chemistry

**CH-12**

## Background Subtracted Fast Scan Cyclic Voltammetry for the Detection for Superoxide Anion

Eben Evbuomwan (Knightdale High School), Advisor: Dr. Leslie Sombers (North Carolina State University)

Reactive Oxygen Species (ROS) are oxygen containing molecules that are highly reactive. Characterization of ROS is difficult because these molecules have short half-lives and are highly reactive. Superoxide anion in particular, is an important ROS because it is a precursor to various other ROS. Using fast-scan cyclic voltammetry we are developing a method for the detection and quantification of superoxide anion. This technique is ideal for the detection of superoxide anion because it is capable of 100 ms temporal resolution and micron spatial resolution, both of which are pertinent in the detection of a rapidly fluctuating molecule, such as superoxide anion. Xanthine and xanthine oxidase were combined to generate superoxide anion. The cyclic voltammograms obtained after injecting xanthine and xanthine oxidase show that upon injection of the mixture, no superoxide was generated. It is apparent that the time it takes to mix the xanthine/xanthine oxidase solution and the time of injection surpass the lifetime of superoxide anion. A chitosan/xanthine oxidsase coated carbon fiber microelectrode will be implemented to optimize the generation and detection of superoxide anion using fast-scan cyclic voltammetry.

**CH-13**

## The Exploration of Phycobiliproteins and Their Role in Photosynthesis

Marcus Bullock (Riverside High School), Advisor: Andrew Moran (University of North Carolina, Chapel Hill)

***Purpose:*** To gain a better understanding of Phycobiliproteins through the research of light-harvesting antennae located in the light-harvesting apparatus of cyanobacteria and red algae. It was hypothesized that the structure of the apparatus should function like the funnel concept, meaning that the energy initially absorbed will be significantly reduced through a series of absorbance and fluorescence through multiple proteins by time it reaches the reaction center. These light-harvesting antennae also include light-harvesting pigments within their protein structure. How these pigments are orientated in relation to one another, effect how these pigments function.

***Methods:*** To conduct this experiment, the absorption spectrum and fluorescence spectrum of light-harvesting antennae samples (all located in the light-harvesting apparatus of cyanobacteria and red algae) R-Phycoererthrin, C-Phycocyanin, and Allopyhcocyanin and were taken using a Halogen Lamp (for the absorbance spectra) and a HeNe Laser (for the fluorescence spectra) and a spectrometer. Using MATLAB software, the effect of distance and dipole orientation between two pigments of allophycocyanin were experimented.

***Results:*** It was found that the light-harvesting antennae fluoresced a lower at a lower wavelength need for the next light-harvesting antennae to absorb. As the distance between the two pigments and dipole orientation increased, the pigment interaction decreased.

***Conclusion:*** The light-harvesting apparatus did function like the funnel concept, and as distance and dipole orientation increased, pigment interaction decreased

Key Terms: Chemistry
Environmental Science

**CH-14**

## Solvation Free Energy Simulations For Alternative FKBP12 Inhibitors: A Comparison And Mutation Study of FK506

Ja'kee Brown (East Bladen High School) Advisor: Dr. Weitao Yang (Duke University)

FK506 is an immunosuppressant that binds to FKBP12. This protein, when binded to FK506, is used to reduce transplant rejections. Because FK506 is an immunosuppressant a modified molecule is needed to replace FK506 when bonded to FKBP12. This will reduce transplant rejections without suppressing the immune system. Finding modified molecules of FK506 is essential to keeping a transplant recipient healthy after receiving a transplant. To conduct this research several different computer programs will be used. These programs will analyze FK506 where the major functional groups are and the amount of solvation free energy they give off. Calculating Molecular Mechanics/ Implicit Solvation the amount of solvation free energy was calculated. From this analysis it was determined that the functional groups containing oxygen could be changed to nitrogen. The modified molecules would also be soluble in water. The modified molecule that changed the functional groups containing oxygen and a distance less than four had the lowest amount of solvation free energy. It was concluded that the functional groups containing oxygen could be changed to nitrogen and maintain a similar structure. It was also concluded that the lower the amount of solvation free energy the more soluble the molecule is.

Key Term: theoretical chemistry

**CH-15**

**The Effect Of The Chemical Environment On The Function Of A Nanobiosensor**

Jakini Kauba (Middle Creek High School), Advisor: Melissa Pasquinelli (North Carolina State University)

With the use of biosensors, pharmaceutical development will be accelerated to the point that pharmaceuticals may be capable of generalizing and specializing depending upon the need of the patient. Specialization can be further afforded through the use of nanotechnology. An active area of research is in the development of nanobiosensors, which are biosensors on the nanoscale level that can detect molecules at extremely low concentrations and in miniscule dimensions through the use of biological molecules such as enzymes. Recently, a nanobiosensor was developed with carbon nanotubes (CNTs) and bombolitin, a polypeptide that was originally found in the venom of a bumblebee. These CNT-bombolitin nanobiosensors were shown to be highly selective when detecting nitroaromatic molecules. How this nanobiosensor can be so highly selective toward specific nitroaromatics, however, is not well understood.

The goal of this work is to investigate with molecular dynamics (MD) simulations how the chemical composition and conformation of Bombolitin III, when adsorbed onto the surface of the carbon nanotube, dictates the selectivity in detecting the nitroaromatics, cyclotrimethylenetrinitramine (RDX) and trinitrotoluene (TNT). The MD simulations revealed that the conformation of the Bombolitin III polypeptide is sensitive to its local environment, and this conformational motion is a key component to the specificity of this nanobiosensor. This knowledge will assist other researchers in developing more effective nanobiosensors that can be used in medicine, such as for specialized pharmaceuticals and nanoscale diagnostic devices.

Key Terms: Carbon Nanotubes
Nanoscale Level
Biosensor Microchip

**CH-16**

## Inhibitors of *Bordetella* Biofilms as a New Therapeutic Approach to Pertussis

Taylor Adair (William G Enloe High School), Advisor: Christian Melander (North Carolina State University)

Current pertussis vaccines prevent only the severe form of the whooping cough disease; however, they do not prevent bacterial carriage and the development of biofilms within the respiratory tract of vaccinated persons. The purpose of this research is to screen a variety of inhibitor compounds to determine their antibiofilm activity against *Bordetella bronchiseptica* biofilms. The results of these *B. bronchiseptica* inhibition studies can then be used as a model for the inhibition of *Bordetella pertussis* biofilms, which are directly associated with the pertussis disease.

Inhibition studies were conducted by completing a series of bacterial assays to screen a range of marine alkaloid derivative inhibitor compounds at 50µm and 100µm concentrations. $IC_{50}$ values were then determined for compounds expressing greater than 50% biofilm inhibition at 100µm concentrations and dose-response curves were generated.

Results of these studies showed that several compounds were active inhibitors towards *B. bronchiseptica* biofilms. It was observed that the compounds displaying the highest inhibiting activity were composed of a base 2-aminoimidazole (2-AI) structure with variances in the substituent group's alkyl chain and linker between the 2-AI and phenyl ring. Four of the eighty inhibitor compounds screened were active inhibitors of *B. bronchiseptica* biofilms exhibiting $IC_{50}$ values of >100µM; however, one of the four compounds was found to be operating under a toxic mechanism as opposed to natural antibiofilm properties.

Key Terms: Chemistry
Pertussis
Biofilms

**CH-17**

## Luminescence Quenching in Cd MOF for Enantioselective Sensing

Jeehae Nam (Hillside High School), Advisor: Dr. Wenbin Lin (University of North Carolina at Chapel Hill)

Metal Organic Frameworks (MOFs) have been greatly researched because of their highly porous frameworks that allow incoming molecules. They are synthesized with organic bridging ligands, and metal connecting points to form highly organized crystal structures. MOFs have numerous potential applications such as catalysis, drug delivery, and chemical sensing due to its chirality.

A series of luminescence quenching experiments have been conducted using different concentrations of (R)- and (S)- 2-amino-1-propanol, which quench our previously synthesized Cd MOF. Control experiments determined that no outside variables, such as photobleaching, were present when quenching studies were conducted. The intensities of the fluorescence were measured by a spectrofluorophotometer.

The intensities were then plotted using the Stern-Volmer relationship. The plots indicate that Cd MOF was ideal for enantioselectively detecting amino alcohol quenchers, with our ratio being 1.47 ($k_{SV}R/k_{SV}S$). However, the homogeneous ligand experiments did not show enantioselectivity, and higher concentrations of the quenchers had to be used to see a significant difference.

We believe that the Cd MOF shows an amplification affecting comparison with the homogeneous system and the quencher molecules prefer to be located in the porous channels of the MOF. The hypothesis, “If Cd MOFs are used for luminescence quenching, then it will be able to enantioselectively differentiate between two amino alcohol quenchers,” is supported.

Key Term: Metal Organic Frameworks

**CH-18**

## The Development Of Selective Receptors For The Various Methylation States Of Arginine And Lysine

Mariah Reese (University of North Carolina - Chapel Hill), Advisor: Joshua Beaver (University of North Carolina - Chapel Hill)

The purpose of our experiment is to find a selective receptor for the various methylation states of arginine and lysine using the method Dynamic Combinatorial Chemistry (DCC). DCC is the process where individual monomers are combined together to create potential receptors. When the library guest is added, the best receptor for that guest will be amplified. To start this process, we performed several procedures which included: Solid Phase Peptide Synthesis (SPPS) for the guests, purification using High-performance Liquid Chromatography (HPLC), monomer hydrolysis, pH test, and preparing the stock solutions for the DCC libraries. We analyzed the DCC libraries by using the instrument Liquid Chromatography (LC) / Mass Spectrometry (MS). The data collected showed that each monomer reacted together to create the different receptors, which is indicated by the numerous peaks on the UV spectrum from LC and MS spectra. When analyzing the data we found that there may be a potential receptor for arginine when $Pam1_2$-3,$5B_2$ was present. In conclusion, there were multiple receptors made that were also identified. Further studies will be conducted to determine the possible selectivity for the guests.

Key Term: Epigenetics

**CH-19**

## The Development of Peptide Based Prochelators For Use in Tumor Angiogenesis Inhibition

Kaylen Cutler (Whiteville High School), Advisor: Katherine Franz (Duke University)

The inhibition of tumor angiogenesis is a key step in the process of determining more efficient ways to discontinue the progression and spread of cancer. The indispensable role of Cu in growth factor production implies that tumor angiogenesis can be inhibited through copper chelation. Current copper chelators eliminate copper, but have a limited capability to distinguish between the toxic copper in tumors from that required to maintain homeostasis, in normal cells. Subsequently, using a procedure that would only permit a chelator to bind metals in a targeted site will be implemented in this experiment. An enzyme that is overexpressed in tumors will act on a peptide prochelator substrate. The enzymatic reaction will yield an active chelator that will bind Cu at that specific site. LCMS were performed to determine the purity of the prochelator and chelator. The prochelator and chelator were then both assayed against a calcein(Cu) complex. Job's Plot was then formulated to determine the stoichiometry of the chelator peptide(Cu) complex. The prochelator showed little interaction with copper indicating that copper binding by the prochelator would be insignificant in a biological system. The chelator showed a significant amount of interaction with Cu. In conclusion, the prochelator, after activation through enzymatic reaction, has the ability to seize copper from the extracellular environment of tumor cells and possibly inhibit tumor angiogenesis.

Key Term: Organic Chemistry

**CH-20**

## Quantifying Photosensitized Singlet Oxygen By Stalking Nitroxide Formation With EPR Spectroscopy

Ronald Sykes (Southern School of Engineering), Advisor: David Zigler (University of North Carolina at Chapel Hill)

***Purpose:*** The FDA has just recently approved the use of photodynamic therapy on cancer. This has helped cure many types of cancer (mainly skin cancer). However since it is still fairly new many things are unknown about it. Therefore it is necessary that we find the answers to the questions about how the process takes place.

***Methods:*** To conduct this experiment, chemical actinometry was performed in order to determine the photon flux (photons/second) of the light source, a standard calibration curve was formed using electron paramagnetic resonance (EPR), and photolysis found the quantum yield (product/photon) of nitroxide which allows for the quantification of singlet oxygen.

***Results:*** As a result, it was determined that the solutions were absorbing 100% of the light provided by the light source and the quantum yield of nitroxide was different than that stated in the literature.

***Conclusions:*** Due to the fact that one of the light sources used emitted too many photons for the solution to absorb a correct quantum yield could not be calculated which means more experiments will need to be performed before any conclusions could be made.

Key Terms: Chemistry
Photodynamic Therapy

**CH-21**

**Remote and Urban Air Quality: Surface Ozone in the Bay Area and White Mountains of California**

Christopher Beck (Saint Mary's College of California), Advisor: Joel Burley (Saint Mary's College of California)

Surface ozone concentrations are presented for seven sites: four from the White Mountains of California and three from the greater San Francisco Bay Area. The two highest elevation measuring sites in this study (White Mountain Summit = 4342 m, Barcroft Station = 3783 m) are believed to be the highest elevation ground-level ozone measurements ever taken in North America. Ozone data were collected over a four week sampling period and analyzed via statistical software. It was found that ozone concentrations in the remote White Mountains of California were consistently greater than those measured in the Bay Area, despite their distance from urban sources of primary pollutants. To explain this disparity, a variety of investigations are presented, including 72-hour HYSPLIT back-trajectories for an assessment of long-range transport, elevation trends, stratospheric intrusion, and fire impacts. Air quality was further investigated via passive sampling at the White Mountain sites; passive measurements for ammonia ($NH_3$), nitric acid ($HNO_3$), and sulfur dioxide ($SO_2$) indicate relatively good air quality.

Key Terms: Air quality
Surface zone
Portable ozone monitor

**CH-22**

## Co-encapsulation of dexamethasone-21-acetate and superparamagnetic iron oxide nanoparticles in anisotropic PRINT nanoparticles

Matthew Detter (University of North Carolina at Chapel Hill), Kevin Herlihy (University of North Carolina at Chapel Hill), John Fain (University of North Carolina at Chapel Hill), Advisor: Joseph DeSimone (University of North Carolina at Chapel Hill and North Carolina State University)

When compared to standard parenteral delivery, targeted therapeutic delivery has the potential for improved efficacy, decreased side effects, reduced systemic exposure (and associated toxicities), and diminished overall costs. This project is focused on the co-encapsulation of a superparamagnetic targeting agent and a steroidal hormone in a high aspect ratio polymeric nanoparticle using the Particle Replication In Non-wetting Templates (PRINT®) process. PRINT is a robust "top-down" micro- and nanoparticle fabrication technique, derived from technology used in the semiconductor industry, which enables strict control over particle parameters such as matrix composition, surface functionality, size, shape, and cargo encapsulation. Monodisperse 80 nm x 320 nm poly(lactic acid-co-glycolic acid) (PLGA) particles containing Superparamagnetic Iron Oxide Nanoparticles (SPIONs) and dexamethasone-21-acetate (DXM) were synthesized using the PRINT process. The $Fe_3O_4$ (magnetite) nanoparticles were stabilized using oleic acid/oleylamine and were spherical with an average diameter of 6.8 ± 1.1 nm. A co-encapsulation of 9.4 % (w/w) DXM, determined using high-performance liquid chromatography, and 12.5 % (w/w) magnetite, determined using inductively coupled mass spectrometry, was achieved. We demonstrate the ability to align these PRINT particles along their primary axis with an external magnetic field. We also demonstrate the ability to sterilize filtered particle suspension via passage through a 0.2 µm filter. There are several potential clinical applications for these particles. The magneto targeting and retention properties of these PRINT particles provide an attractive method for localized and sustained treatment of arthritis, asthma, and other inflammatory conditions.

Key Terms: nanoparticle
superparamagnetism
dexamethasone

**CH-23**

## Pyrene Excimer Kinetics Revisited

Andrew Hanlon (The Pennsylvania State University), Advisor: Bratoljub Milosavljevic (The Pennsylvania State University)

A singlet excited state of pyrene and other polycyclic fused aromatic hydrocarbons can react (in a diffusion-controlled reaction) with an unexcited state of the molecule to form an excited complex known as an excimer. Due to the relatively short lifetime of the excited state, high concentrations must be used to observe excimer formation. In previous studies, a nitrogen laser, which has an emission wavelength of 337 nm, was used as an excitation source. In sufficiently concentrated pyrene solutions (> 1mM), the absorbance is very high at 337 nm (> 100) causing a huge concentration gradient of excited pyrene molecules, which in turn leads to data that are difficult to interpret. Rather than introducing time dependent rate constant kinetics, we choose an excitation wavelength ($\lambda$ = 366 nm) at which the absorbance is low enough (A = 0.2) such that a homogeneous distribution results. In addition, we show that the excimer formation reaction is not reversible. In our experiments, a solution of pyrene in decane was used. Monte-Carlo analysis was applied to obtain the corresponding rate constants. Since the number of variables was reduced by two, the values obtained are more reliable. The new experimental approach and the data obtained can be used to further understand the biochemical applications of excimer formation.

Key Terms: Photochemistry
Excimer
Kinetics

**EB-01**

## Adaptive Significance of Sodium and Grazing Tolerance in Serengeti Grasses

Daniel Griffith (Wake Forest University), Advisor: T. Michael Anderson (Wake Forest University)

Adaptations are traits resulting from natural selection that provide a benefit to an organism in a particular, and often stressful, environment. Organisms have a limited amount of energy and resources to invest in any one adaptive characteristic. Therefore, significant adaptations come with costs in the form of reduced tolerance to other conditions or stressors. For many plants, a fundamental adaptation is the ability to tolerate loss of tissue to herbivores (i.e. defoliation). Consequently, one hypothesis is that plants strongly adapted to tolerate continual defoliation by animals should lack tolerance to extreme or stressful environmental conditions. This study will test the hypothesis that adaptations to one stress are associated with evolutionary tradeoffs to others stressors by looking at the special case of soil salinity stress (i.e. sodium) and herbivory in Serengeti grasses. High salinity is ecologically intriguing for a number of reasons, the most important being that grazing animals preferentially forage on grasses growing in saline soils in order to meet their sodium requirements, whereas too much sodium can be toxic to plants. This creates the evolutionary conundrum that plants must be successful in tolerating both herbivory and high soil salinity. The evolution and ecology of grasses living with these dual stressors was investigated in a greenhouse experiment.

Key Terms: evolutionary tradeoff
phylogenetics
community ecology

**EB-02**

## Evolution and Ethnobotany of Dragon's Blood's Tree

Pei-Luen Lu (University of Hawaii at Manoa), Advisor: Clifford W. Morden (University of Hawaii at Manoa)

Since ancient Greece time, the renowned traditional medicine, Dragon's blood, has been used in various cultures, such as Mediterranean, Chinese, Persian, Arab, ancient Greek, Roman, Indian, and African cultures for anti inflammatory treatment. In history, this case is not common. This is the first time to use molecular systematics to analyze the relationships of Dragon's blood' trees in a global scale, and to address the associations in ethnobotany. The classifications of Dragon's blood trees have been unstable due to the difficulty in characterizing each species morphologically. Phylogenetics is hence essential for deciphering the question. Literature reviews combined phylogenetics of all Dragon's blood's tree species using chloroplast DNA regions was explored. The resulting phylogeny was used to test hypothesis on the evolution of Dragon's blood's trees with the genus *Dracaena* and to examine the biogeography. Results show 1) The monophyly of *Dracaena* is confirmed; 2) *D. americana* and *D. cubensis* are the basal group; 3) The traditionally known Dragon's blood' trees are polymorphetic; 4) The distribution in diverse cultures of Dragon's blood has a correlation with wars; 5) The genetic pool of red resins decreases from the base to terminal of the phylogeny. A disjunction between the New and Old world occurred in Dragon's blood's trees' evolution and humans' history. Several dispersal events are required to explain their present-day distribution. These findings essentially contribute towards the connection of the plant evolution and humans' history, and the potential candidates for the new related medicinal development and pharmacological studies in Dragon's blood's trees.

Key Terms: Phylogenetics
Ethnbotany
Evolution

**EB-03**

## Spatial Patterns of Microbial Biomass and Community Structure in Stream Networks

Philips Akinwole (University of Alabama, Tuscaloosa), Louis Kaplan (Stroud Water Research Centre, PA), Advisor: Robert Findlay (University of Alabama, Tuscaloosa).

Sediment microbial communities form an important component of stream ecosystems yet the natural variations in stream microbial biomass and community structure across spatial scales ranging from biogeographic patterns to difference within and among riffles are not yet fully described. A field study was conducted to investigate factors controlling total microbial biomass and community structures of streambed sediments across two fluvial networks. We sampled stream sediments from 1st - through 3rd - order streams in the forested White Clay Creek watershed (Pennsylvania), and from $1^{st}$ – through $5^{th}$- order in the Neversink River watershed (New York) across 3 spatial scales (riffle, order, watershed). Microbial biomass and community structures were determined using phospholipid phosphate and phospholipid fatty acid (PLFA) analysis and were correlated to a variety of environmental parameters. Multiple regression analysis showed that watershed, percent carbon, surface area and percent water explained 58% of the variations in total microbial biomass. There were no systematic changes in microbial biomass with stream order. Most of the variability observed among riffles was attributable to sediment percent carbon, surface area and percent water, which appeared to vary with stream geomorphology. Principal component analysis (PCA) showed that microbial community structure displayed a distinct watershed-level biogeography, as well as variation along a headwater streams-large stream gradient. The importance of phototrophic microeukaryotes increased with increasing stream order suggesting that increasing light availability, as predicted by the River Continuum Concept, contributed to the observed pattern.

Key Terms: Stream Ecology
Microbial phospholipid fatty acids
Microbial Ecology

**EB-04**

**Below Ground Plant Defense: physical plant defenses in roots impact herbivore survival**

Kristine L. Callis (University of Florida), Amanda Pendleton (University of Florida) and Heather McAuslane (University of Florida)

Silica is a known herbivore defense in above ground plant tissue, however its effect on below ground herbivores is unknown. Using silica treated *Zea mays*, we assessed the impact of silica on banded cucumber beetle larvae (*Diabrotica balteata,* LeConte*)* survival and development. We predicted that the larvae feeding on silica-treated corn roots would slow development rates, due to a decrease in the per-bite-nutrient content. 50 larvae per rep were raised exclusively on corn roots that were treated with one of 3 silica treatments (1mM, 1.5mM and 2mM Si) or a control (0mM Si). 10 randomly selected larvae were weighed at each instar, as adults post-pupation and as adults at reproductive maturity. We also assessed survival at each stage transition – larva to pupa, pupa to juvenile adult and juvenile adult to mature adult. While we found no significant difference ($p=0.22$, $df=3$) in the mass of the larvae or the adults between silica treatments, but there was a significant effect ($p=0.02$, $df=9$, $f=2.79$) of silica on survival of larvae and adults. We conclude that while silica does not decrease larval growth rate, it may alter the amount of food necessary for survival. Since silica does increase mortality, the silica likely mortally damages larvae either internally or external. Further examination of larvae feeding on silica treated roots will help pinpoint the nutrient tradeoff for larvae feeding on silica roots and the mechanistic impact of silica on larval survival.

Key Terms: Below-ground herbivory
Plant-defense
Plant-insect interactions

**EB-05**

## Microsatellite Marker Development for the Blueberry Pathogen *Monilinia vaccinii-corymbosi*

Kathleen M. Burchhardt (North Carolina State University), Advisor: Marc A. Cubeta (North Carolina State University)

Fungal plant pathogens can impact economic viability and environmental sustainability in agricultural systems. *Monilinia vaccinii-corymbosi* (Mvc) is an important fungal pathogen that causes mummy berry disease on wild and commercial blueberry (*Vaccinium* spp.). Mummy berry disease causes yield loss by desiccation and premature drop-off of infected fruit. My overarching goal is to apply population genetic approaches to examine the spatial extent, genetic diversity and gene flow within and among populations of Mvc. The primary objective of this study was to develop informative microsatellite markers for Mvc for use in subsequent population genetic analyses. To address this objective, microsatellite loci were identified using 454 pyrosequencing to generate 135,661 reads with an average length of 355 bp. Microsatellite markers targeting 30 microsatellite loci were designed by screening sequence reads for microsatellite repeats suitable for primer design with the program MSATCOMMANDER. Genetic variability at 21 of the microsatellite loci was detected by performing fragment analysis on a total of 45 Mvc isolates; five isolates each from a field in Oregon, Washington, Michigan and two fields in North Carolina, and 20 isolates from a single field in North Carolina. Analysis of the multilocus genotypes of the 45 isolates indicated genetic variability among the sites, while within site genetic variability ranged from genotype uniformity to heterogeneity. Future research will focus on using the microsatellite markers to analyze a collection of 438 Mvc isolates from a total of 15 blueberry fields encompassing nine states across the United States to elucidate the population genetics of Mvc.

Key Terms: Plant Pathology
Population Genetics
Genetics

**EB-06**

## Mojokerto Revisited; Evidence for a Unique Pattern of Brain Growth in *Homo erectus*

Caitlin A. O'Connell (Boston University), Jeremy M. DeSilva (Boston University)

Brain development in *Homo erectus* is a subject of great interest. Some researchers have suggested that its brain development resembled that of nonhuman apes, while others argue for a more human-like growth pattern. In this study, we retested hypotheses regarding brain ontogeny in *H. erectus* using new methods (resampling), data from additional *H. erectus* crania and newly refined endocranial volumes for the Mojokerto calvaria. We assumed that the Mojokerto individual was between 0.5-1.5 years at death, and used brain sizes from similarly aged humans and chimpanzees. Our results reveal a considerable amount of overlap between chimpanzee and human brain development, with humans achieving 65% (±14%) and chimpanzees 81% (±12%) of brain growth by 6 months to 18 months of age. Mojokerto had reached 69%-73% of its adult volume when compared to all *H. erectus* crania (n=22). When compared to the most relevant specimens from Indonesian sites greater than 1.2 myr (n=9), Mojokerto had reached only 69% of its adult cranial capacity. Mojokerto thus falls within the range of both humans and chimpanzees, though slightly (but not significantly) closer to the average human pattern. These findings do not support the contention that *H. erectus* had rapid, ape-like brain growth, and have important implications for considering the evolution of human childhood and cognitive abilities. We suggest that *Homo erectus* would have had a unique developmental pattern that should be considered as an important step along the continuum leading to extreme infant altriciality and long childhood in modern humans.

Key Terms: biological anthropology
Homo erectus
brain growth

**EB-07**

**Distribution and Status of the Northern and Southern Short-tailed Shrews (*Blarina brevicauda* and *B. carolinensis*) in North Carolina**

Benjamin M. Hess (North Carolina Museum of Natural Sciences and North Carolina State University), Advisors: Roger A. Powell (North Carolina State University), Wm. David Webster (University of North Carolina, Wilmington)

Two species of the short-tailed shrews (genus *Blarina* Gray, 1838) exist in North Carolina. The northern (*Blarina brevicauda* (Say, 1823)) and the southern (*Blarina carolinensis* (Bachman, 1837)) short-tailed shrews can be distinguished in most cases mophometrically. Throughout North Carolina, these two shrew species are parapatric with very little overlap. However, the Middle Atlantic Coastal Plains and Southeastern Plains ecoregions show areas where both species may coexist. Morphometric data, consisting of 15 cranial and dental characters, were collected from 491 museum voucher specimens of *B. brevicauda* and *B. carolinensis* within the state of North Carolina. There was no measurable difference between sexes so the data was pooled to increase the sample size. Multivariate Principal Components and Maximum Likelihood Analysis were used to determine the factors contributing to the variation in measurements. The resulting plots show a clear separation of the two species, including the suggestion of a localized subspecies. Future genetic analysis will be utilized to confirm questionable overlap specimens. Based upon the locality information with the museum data, each specimen was geo-referenced and mapped to view the current distribution for the genus *Blarina* in North Carolina with its current taxonomic designation.

Key Terms: Zoology
Taxonomy
Statistics

**EB-08**

## The Geographic Distribution, Genetic, and Phenotypic Characterization of *Fomes fasciatus* and *Fomes fomentarius* in the United States

Meghan A. McCormick (North Carolina State University), Advisors: Marc A. Cubeta (North Carolina State University), Larry F. Grand (North Carolina State University)

The wood decay fungi *Fomes fasciatus* and *F. fomentarius* play essential roles in forest ecology and management throughout the United States. However, little is known about their spatial distribution as well as the phenotypic and genotypic diversity. We developed comprehensive United States distribution maps for *F. fasciatus* and *F. fomentarius* based on records from 26 mycological herbaria. The maps were used to sample and isolate *F. fasciatus* and *F. fomentarius* from spore-producing structures (basidiocarps) collected from 13 states within the US. Although both species are morphologically similar, the distribution of the species is disjunct, with *F. fomentarius* centralized in northern temperate forests and *F. fasciatus* in subtropical forests. We tested phenotypic differences between the species in temperature optima and range by measuring growth of two isolates per species on malt extract agar incubated for 9 d at temperatures ranging from 6 to 39 °C. The temperature optima of both species were 33 °C. *Fomes fasciatus* was found to grow at 39 °C. The genetic relatedness of the two species was examined using maximum parsimony analysis of the internal transcribed spacer region (ITS) of the ribosomal DNA (rDNA). Our results indicate that the two species are distinct lineages with <88% maximum identity at this locus. Further analyses of the ITS rDNA and RNA polymerase II gene (RPB2) are currently being conducted to examine intraspecific genetic diversity and determine whether intraspecific genetic diversity is correlated with fungal morphology, host, or US distribution.

Key Terms: Polyporeaceae
Wood decay fungi
Biogeography

**EB-09**

**Magnetic Compass Orientation in *Drosophila melanogaster***

Michael S. Painter (Virginia Tech), David H. Dommer (Mount Olive College), Matthew H. Gnirke (Virginia Tech), Dan Q. Tran (Virginia Tech, Brandon E. Moore (Virginia Tech), Advisor: John B. Phillips (Virginia Tech)

Birds, amphibians and flies have been shown to use a light-dependent magnetic compass (LDMC) involving a biochemical reaction that forms stable, magnetically sensitive radical pair products. Cryptochrome, a short-wavelength photoreceptor known to yield radical pair products, has been proposed as a likely candidate mediating the LDMC. Interestingly, magnetic compass orientation by adult *Drosophila melanogaster* was shown to exhibit wavelength-dependent shifts in the direction of response tested under short- and long- wavelength light, consistent with the absorption spectra of the fully reduced and radical forms of the cryptochrome flavin chromophore. Although this evidence supports cryptochrome's involvement in the LDMC, it suggests that the underlying mechanism may be more complex than originally proposed, possibly involving antagonistic spectral inputs that produce complementary patterns of response. Here we report spontaneous quadramodal compass orientation in larval *Drosophila melanogaster* tested under 365nm short-wavelength and 490nm long-wavelength light of equal intensity. Under short-wavelength light larvae exhibited quadramodal magnetic orientation along the $45^{o}$ axes (i.e. northeast, southeast, etc.). However, under long-wavelength light larvae exhibited quadramodal magnetic orientation along the cardinal compass axes (i.e. North, South, etc.) providing further support for a cryptochrome-mediated LDMC that receives antagonistic short- and long-wavelength inputs. Furthermore, we extend studies of magnetic compass orientation to show strain-dependent differences in patterns of response in additional larval strains. Future experiments that provide a more detailed characterization of the spectral sensitivity curve of larval magnetic compass orientation using a variety of *Drosophila melanogaster* strains will offer important insight to the biophysical mechanism(s) mediating the LDMC.

Key Terms: Magnetoreception
Orientation

**EB-10**

## Growth Dynamic Factors Explaining Yield Improvement in New vs. Old Soybean Cultivars

Charanjit Singh Kahlon (Louisiana State University, AgCenter), Advisor:James E. Board (Louisiana State University AgCenter)

Reasons for genetic yield improvement in soybean [Glycine max (L.) Merr.] during cultivar development are not clearly understood. Since greater yield in new vs. old cultivars is largely regulated by final vegetative total dry matter [VTDM(R7)] and/or production efficiencies for these yield components [(yield component no.)/ VTDM(R7) (no. $g^{-1}$)], our objective was to clarify the importance of these two factors for yield improvement in 18 public southern cultivars released between 1953 and 1999. The study was done near Baton Rouge, LA during 2007 and 2008, with a validation study in 2009. Yield increases were affected by increased production efficiencies for nodes, reproductive nodes, pods, and seeds ($R^2$=0.42-0.47), but not VTDM(R7). Increased yield component production efficiencies resulted in greater harvest index (HI) ($R^2$=0.55-0.73), which in turn, resulted in greater yield ($R^2$=0.42, $P<0.01$). We concluded that a major factor contributing to yield increases between old and new cultivars was increased yield component production efficiency.

Key Term: Plant Science

**EB-11**

# The Effectiveness Of Paired Suppressive Strains Of *Streptomyces* Species To Decrease Damage Caused By The Potato Scab Disease Pathogen; *Streptomyces scabies*

Michael Peters (Northern Michigan University), Advisor: Donna Becker (Northern Michigan University)

*Streptomyces* bacteria are common soil saprophytes, some are medically important, some are plant pathogens. *Streptomyces scabies* is an agriculturally significant pathogen which infects root/tuberous crops worldwide. Classical control methods for *S. scabies* include adding chemicals, irrigation, and practicing crop rotation. Biological control is an alternative control method which utilizes living organisms to decrease pathogenic populations and improve crop health. Prior biological control studies found that some non-pathogenic *Streptomyces* species (suppressives) which inhabit the soil may inhibit growth of pathogens by exuding antibiotics or by resource competition. This study consisted of two greenhouse trials which were performed using field soil which was artificially infested with the pathogen *S. scabies* strain 87, to test the ability of two suppressive strains (*Streptomyces* strains 10 and 93) to decrease scab disease on potato tubers and reduce pathogenic populations of soilborne *S. scabies*. Prior laboratory studies illustrated a synergistic effect by using paired suppressive bacteria to reduce success of *S. scabies in vitro*; however this greenhouse study did not show a significant difference in scab disease severity. Previous investigations of *Streptomyces* species as biological control agents noted a high degree of variability of disease reduction. This study also concluded that disease inhibition is variable; however, results from two treatments (strain 10 and 10 + 93) noted a significant reduction in pathogenic population levels in treated pots from one trial. It is conceivable that surviving suppressive bacteria could continue to lower populations of pathogens in the soil over time, until disease symptoms decrease and ultimately subside.

Key Terms: Streptomyces scabies
Biological Control
Agriculture

**EB-12**

## Changes In Double-crested Cormorant (*Phalacrocorax auritus*) Reproductive Success And Chick Bioenergetics After The Invasion Of The Round Goby (*Appollonia melanostomus*)

Margaret Van Guilder (Central Michigan University); Advisor: Nancy Seefelt, Ph.D. (Central Michigan University)

Bioenergetics is the study of energy intake and expenditure of an organism. For birds, energy enters the body as food and from there is allocated to several functions such as growth and reproduction. The fish community in Lake Michigan has changed over the past ten years. The Double-crested Cormorant (DCCO; a waterbird) diet has reflected this change from primarily alewife (energetically rich) to primarily round goby (energetically poor). This study was conducted to determine whether this change in diet would result in a change in reproductive output/success. Diet and growth rate data were collected from DCCO chicks in the Beaver Archipelago in 2010 to (1) model the caloric density of round goby near the Beaver Archipelago, (2) model the bioenergetics of chick prey consumption in the Beaver Archipelago and (3) model the potential reproductive success of the Beaver Archipelago colonies in 2010. Findings were then compared to earlier research prior to round goby invasion. Round goby was found to have a relatively low energy density compared to other dietary items. DCCO chicks were found to have consumed more fish per chick in 2010 than in 2000 of which round goby comprised the greatest proportion in 2010. The reproductive success of the DCCO colonies in 2010 was estimated to be about 250 chicks (much lower than in 2000). The model presented here suggests that DCCOs in the Beaver Archipelago consumed over 95% exotic invasive fish species in 2010 and could potentially act as a natural control for these invasive fishes.

Key Terms: Double-crested Cormorant
Bioenergetics
Waterbird Reproductive Success

**EB-13**

## Consumer-driven Nutrient Recycling Between a Stream-dwelling, Keystone Herbivore and its Periphyton Resources

Robert Mooney (University of Wisconsin- La Crosse), Advisor: Eric Strauss (University of Wisconsin- La Crosse), Advisor: Roger Haro (University of Wisconsin- La Crosse)

A larval caddisfly, *Glossosoma intermedium,* is a keystone herbivore that inhabits midwestern cold-water streams in high abundance. Larvae feed primarily on algae covering cobbles and strongly regulate algal biomass. *Glososssoma* larvae construct stone cases that offer an alternative surface for algal colonization. When the algal resources on the cobble reach low levels, *G. intermedium* grazes on the cases of conspecific larvae. We hypothesized the grazing system between *G. intermedium* and the algal resources on the cobbles and the cases represent "consumer-driven nutrient recycling (CNR)". Our study was conducted on three Driftless Area streams in western Wisconsin. Throughout autumn and winter 2010/2011, total nitrogen (N) and total phosphorus (P) concentrations were determined for stream water, *G. intermedium* larvae tissue, excretia, streambed algae, and the algae adhering to the cases. The N:P of the streambed algae at two of the study sites suggested P limitation (194:1, 38:1), however; the N:P of the case algae at the same two sites did not suggest P limitation (7:1, 11:1). Our results suggest that high P in *G. intermedium* excretia allows algae colonizing the cases to avoid P limitation. G*lossosoma intermedium* is an important part of Midwestern streams not only because it can regulate algal biomass by exerting heavy grazing pressure, but also because it can create a nutrient enriched surface for algal colonization on their cases. This alternative surface may, in turn, serve as an important supplemental algae resource for the entire grazing community.

Key Terms: Ecological Stoichiometry
Nutrient Recycling
Caddisfly

**EB-14**

## Nest Site Characteristics Of Four-Toed Salamanders (*Hemidactylium Scutatum*) In Natural And Constructed Wetlands

Susan King (Eastern Kentucky University), Advisor: Stephen Richter (Eastern Kentucky University)

If constructed wetlands do not mimic the condition of natural wetlands, we are losing critical amphibian habitat. To assess the condition of a created wetland the reproductive success of the fauna must be considered. Focal study species should have more restrictive habitat requirements, like the four-toed salamander (*Hemidactylium scutatum*). In Daniel Boone National Forest (DBNF) four-toed salamanders have been shown to utilize constructed wetlands, but it is unclear if embryonic survival is similar to that in natural wetlands. The objective of this research was to determine how nest site and wetland characteristics, and embryonic survival differ between wetland types. In the spring of 2011, I searched the shoreline of six natural and six constructed wetlands in DBNF, finding 207 nests. At each nest I measured aspect, slope, pH, temperature, soil moisture, percent ground cover, and distance to water. I also measured the canopy closure and amount of moss present at each wetland. I found four-toed salamanders nest more often in large clumps of moss and they utilize these moss clumps more often in natural wetlands. Eggs were laid on steeper slopes in natural wetlands (on moss-laden trees), and the pH of the soil was lower at nests in natural wetlands. Canopy closure was higher in natural wetlands. Results indicate the importance of maintaining canopy closure, trees within the wetland, and downed woody debris to promote the growth of large beds of moss. A second field season will focus on the temperature in the nest and hatching rates.

Key Terms: natural and constructed wetlands
Hemidactylium scutatum
nest site characteristics

**EB-15**

## Effects of tidal immersion and body mass on phosphorus cycling of *Geukensia demissa*

Jeffrey J. Illinik (Virginia Wesleyan College), Raluca E. Illinik (Christopher Newport University), Advisor: Maynard Schaus (Virginia Wesleyan College)

*Geukensia demissa* is an abundant filter feeder that may have important effects on nutrient cycling within East Coast salt marshes. This species is thought to interact mutualistically with salt marsh cordgrass (*S. alterniflora*), as nutrient cycling by mussels fertilizes the cordgrass, which provides attachment sites for mussels. We investigated phosphorus excretion and fecal deposition by *G. demissa* in the Lafayette River, Norfolk, VA, including how mussel mass and tidal immersion may impact rates of phosphorus cycling. Mussels were collected, cleaned, and placed in bags containing filtered estuarine water, which was later analyzed for $PO_4$ using the molybdenum blue technique. We observed a significant negative correlation between mussel dry mass and mass-specific phosphorus excretion and feces production. We also observed a significant decrease in phosphorus release and feces production with increased time since tidal immersion.

Key Terms: nutrient cycling
Geukensia demissa
cordgrass

**EB-16**

## Tardigrades of Mt. Desert Island, Maine

Courtney Tway (Unity College), Advisor: Emma Creaser (Unity College)

Found in moss, lichen, and various other substrates, tardigrade research is essential if we are to understand the complexities of forest meiofaunal communities. In this pilot study I focus on the tardigrade communities found in moss and lichen. This study aims to catalog the variety of tardigrade species found in Mt. Desert Island, Maine. Although there are over 900 species of tardigrades identified throughout the world, there is little data available for those of Maine. Thus far, I have identified 5 different taxa from samples taken at Mt. Desert Island. At least one genus has not previously been documented in Maine. Samples of moss and lichen were taken from various locations and then rehydrated. Tardigrades were located under a dissecting microscope, transferred to a slide and fixed with mounting medium. Tardigrades were identified using toe, buccal apparatus and whole body morphology. Species richness, evenness, abundance and heterogeneity were also calculated. Species accumulation curves were used to assess the observed species as a function of the sampling effort.

Key Terms: Tardigrades
meiofaunal communities
Maine

**EB-17**

## The Effect Of Nitrogen And Drought On Grassland Fungal Biomass

Vivian Lopez (University of California, Irvine), Advisor: Dr. Steven Allison (University of California, Irvine)

Fungi are important decomposers and depend on root-like structures called hyphae to obtain nutrients, particularly under environmental stress. As the climate changes, the amount of precipitation and nitrogen availability could affect the growth of hyphae and as an effect, rates of litter decomposition and carbon cycling in the environment. To determine how environmental change may affect hyphal biomass, we conducted a 3-month reciprocal transplant experiment at the Loma Ridge Grassland in Irvine, California. Under either reduced precipitation or added nitrogen conditions, we tested the effect of hyphal growth according to three factors: the local site (plot), litter origin, and microbial community origin. The plot factor represents the direct effect of water or nitrogen, whereas the other factors reflect indirect effects of the treatments on fungal hyphae. Following litter bag harvest, hyphae were extracted from the litter sample, prepared onto slides, and counted. We predicted that under reduced precipitation, there would be a decrease in hyphal biomass due to water stress on the fungi. Under added nitrogen, we predicted an increase in hyphal biomass due to reduced nutrient limitation of fungal growth. In support of our first hypothesis, we found a marginally significant decrease for reduced precipitation litter origin ($P=0.097$) and reduced precipitation microbial community origin ($P=0.069$), both of which are indirect effects of reduced precipitation on hyphal biomass. However, our hypothesis regarding the effect of added nitrogen was not supported by our data. These results suggest that indirect effects of drought could have an effect on decomposition and that hyphal biomass may be resistant to the direct effect of drought. They also suggest that nitrogen enrichment may have no effect on hyphal biomass and rates of decomposition.

Key Terms: climate change
hyphae
litter

**EB-18**

**Tardigrades of North America: Vertical Distribution in a White Pine Tree (*Pinus strobus*) in Kansas, USA**

Lagan Gallardo (Baker University), Advisor: William Miller (Baker University)

Modern canopy research has challenged the assumption of uniform Biodiversity in a tree. To date there is no data to support tardigrade usage of the canopy. Because tardigrades are distributed by the winds we hypothesized equal distribution of species throughout the tree. A vertical transect was conducted by climbing a 20 meter White Pine tree (*Pinus strobus*) on the campus of Baker University in 2011. Samples of tardigrade habitat (moss and lichens) were taken at four three meter intervals and 183 tardigrades were extracted and classified. The diversity and abundance of species was compared between the layers. We discovered significant variation from the model with higher levels of diversity and abundance at higher levels above the ground. Eight species were found on the tree. The four most common species were all predators and occurred only at the three upper levels with the greatest abundance occurring at the highest level. Only one species occurred rather uniformly at all four levels. The other three species were singletons and found only in the lower two levels. We suspected the envelope of the needles would reduce the probability of tardigrades arriving on the trunk at the higher levels. But the opposite seems to be true. There were more water bears higher in the tree. This could lead to a new three dimensional model for micro invertebrate distribution.

Key Terms: Tardigrades
Canopy
Ecology

**EB-19**

## Reintroducing The American Chestnut (*Castanea dentata*): A Comparative Analysis Of Pure And Hybrid Varieties

Jeffrey S. Hatzel (Ithaca College), Advisor: Jason Hamilton (Ithaca College)

In this study we are attempting to reintroduce American chestnut (*Castanea dentata*) into the forested habitats it once dominated. Within its native range American chestnut comprised upwards of 40% of the forest canopy before the accidental introduction of the chestnut blight (*Cryphonectria parasitica*) in 1904 (Rhoades 2006, Wang et al 2005). Within 60 years, American chestnut was functionally extinct, leaving a major gap in ecosystems it once dominated (Joesting et al 2008). Using seed provided by the American Chestnut Foundation (150 *C.dentata* and 200 *C. dentata/C. mollissima* hybrids [88%-91% pure]) two treatment groups were created. Group 1 was planted directly into an existing forest stand, while Group 2 was potted and put in a greenhouse. Group 1 was planted into two separate plots (A10 and A20), roughly 600m apart. Each seed was planted into a tree cage (5ft. high x 3ft. in diameter) that will protect the seedling for 5-8years. In mid-October 2011, A10 showed a germination rate and average height of 45% and 3.5", respectively for *C. dentata*. The germination rate and average height of hybrids in A10 was 42% and 5.8", respectively. In A20, *C. dentata* had a 26% germination rate, with an average height of 3.5". Hybrids in A20 also had a 26% germination rate and average height of 4.7". Group 2 was moved from the greenhouse to a cold frame in August to harden off. Plants will be overwintered in the cold frame, and transplanted outside in the spring of 2012. In this group, *C. dentata* had a germination rate of 97% and average height of 10.5" and hybrids had a germination rate of 91% and average height of 9.9".

Key Terms: Population Ecology
Environmental Science
Forest Ecology

**EB-20**

## The Life study of Fireflies Found around Pittsburgh, Pennsylvania: An Investigation of the Competitive Exclusion Principle

Sarah Szczypinski (Thiel College), Advisor: Michael Balas (Thiel College)

Competitive exclusion theory states that two species competing for the same resources cannot stably coexist; fireflies may exhibit such competitive behavior. The purpose of this study was to determine if the competitive exclusion theory was upheld by examination of firefly communities found around Pittsburgh, Pennsylvania. The study was done by collecting fireflies from both wood and field settings. Sixteen locations were sampled in the study. The first firefly was caught from the edge of the wood/field, then ten steps were taken after each catch. The captured fireflies were put into small sandwich bags and numbered. Sampling was concluded after firefly activity ceased for the evening. The most abundant species caught were *Photinus pyralis* and *Photinus marginellus.* Statistical analyses were performed in order to see if the competitive exclusion theory applied to these two species; however, there was no strong evidence to suggest this theory. A t-test showed that *P. pyralis* was equally common in both fields and woods; however, a Fishers exact test showed that *P. marginellus* was marginally more likely to be found in woods. It is suggested that *P. marginellus* is either exhibiting a habitat preference or a habitat restriction.

Key Terms: Competetive Exclusion Theory
Photinus pyralis
Photinus marginellus

**EB-21**

## A quantitative analysis of the foliar morphology of *Planchonella sandwicensis*

Lauren Stutts (Campbell University), J. Christopher Havran (Campbell University), Advisor: J. Christopher Havran (Campbell University)

*Planchonella sandwicensis* (Gray) Pierre is a morphologically variable tree endemic to the Hawaiian archipelago. Previously, *P. sandwicensis* has been divided into five species based on leaf and fruit morphology, but was later regrouped into a single taxon. Previous statistical analyses of *P. sandwicensis* have investigated morphological differences within the species, but none used multivariate statistical procedures. It has been suggested that environmental factors may be the basis for the broad differences seen in leaf size and shape throughout *P. sandwicensis.* In an attempt to better describe patterns of morphological variation in *P. sandwicensis*, we analyzed 299 herbarium specimens originally collected on Kaua`i, O`ahu, Moloka`i, Lana`i, Maui, and Hawai`i. We measured leaf width from the midvein to the leaf margin at intervals of fifteen degrees, recorded leaf length, fruit size, apex and base angles, presence of abaxial and adaxial trichomes, and type of leaf margin. Collection site data from herbarium labels were used to estimate rainfall zones from which specimens were originally collected. Canonical variants analysis does not allow us to distinguish between interisland populations of *P. sandwicensis*. Results of multivariate analysis of variance indicate significant differences between interisland populations. Post-hoc tests suggest that leaf length and width are significantly different between western and eastern Hawaiian Islands. Length and width are also significantly correlated with rainfall amounts. Increase in leaf length and width in accordance with increasing rainfall has been seen in other angiosperms. The variation in leaf morphology within *P. sandwiceneis* may be explained by environmental factors.

Key Terms: Evolutionary Biology
Island Biology
Morphometrics

**EB-22**

## Optimal Foraging of Whelks in the Intertidal Zone

Lara Voelker (Moorpark College). Advisors: Stephen Gosnell (University of California, Santa Barbara) and Steven Gaines (University of California, Santa Barbara)

Many biotic communities are characterized by foundational species that transition from a food source to habitat as they increase in size (e.g., trees, coral reefs). Given the importance of these species to community diversity, understanding how size mediates interactions between these species and their predators is an important step in understanding community dynamics. Mussel beds provide both a source of food and a refuge for many species in the intertidal zone. Although previous work has suggested other keystone intertidal predators (e.g., sea stars) may be limited in their ability to prey upon large mussels, the impact of size on whelk feeding has not been explored. We used optimal foraging theory to examine how the relationship between whelks (*Nucella emarginata*) and mussels (*Mytilus californianus*) changes with mussel size. Although larger mussels offer more consumable tissue per mm and whelks are able to consume a wide range of mussel sizes, field observations suggest whelks actively select their mussel prey. Growth studies in lab and field conditions revealed that whelks grow more quickly on smaller mussels. Together, these experiments suggest that although whelks can consume large mussels, they actively select prey to maximize their own growth as predicted by optimal foraging theory. However, future environmental change, such as ocean acidification, may weaken mussel shells, thus impacting this relationship and leading to community changes.

Key Terms: Marine Biology
Ecology
Intertidal

**EB-23**

## Effects of Seed Dispersal by Bison on Post-Dispersal Seed Predation

Emily Artz (Iowa State University), Advisor: W. Sue Fairbanks (Iowa State University)

Seed dispersal by animals is a key process in maintaining some ecosystems. In North American prairies, much potential seed dispersal was eliminated by the removal of bison (*Bison bison.)* Bison carry large numbers of seeds in their thick hair, which they shed in spring. I examined post-dispersal seed predation/removal of seeds in substrate and shed bison hair by birds, rodents, and insects. I hypothesized that seeds in bison hair would suffer less predation by rodents and insects due to increased handling time, but that birds would remove the hair itself for nesting material. I established 5 replicate plots in re-seeded areas of a reconstructed tallgrass prairie. Each plot contained four exclosures: one accessible only to insects, one to rodents, one to birds, and a control open to all seed predators. The exclosures contained two dishes: one with a known number of seeds in substrate, the other with the same number of seeds in 4-5 g of shed bison hair. I conducted two 7-day trials, 28 June-5 July and 8-14 August. More seeds overall were removed from the dishes in the second trial than in the first. In the second trial, more seeds were removed from the substrate than from bison hair by rodents, insects, and in the control. This may indicate that shed hair acts as a deterrent to seed removal when small mammals and insects may be foraging more actively, later in the summer, and efficiency is important. Removal of hair by birds may represent secondary seed dispersal.

Key Terms: Prairie ecology
Seed dispersal
Seed predation

**EB-24**

## The Identification of Arachnid Species in the Cockscomb Basin Wildlife Sanctuary

Lauren Kathryne Auer (University of Southern Mississippi, Hattiesburg), Advisor: Dr. Aimeé K. Thomas (Loyola University, New Orleans)

This study was conducted to engage in a field-based study of arachnids in the Cockscomb Basin Wildlife Sanctuary in Belize to determine the most frequently encountered arachnid species. Despite the known diversity of arachnids in the neotropical areas, there has been little considerable movement towards creating a collective means for identification of arachnids within Belize. For this study, four separate locations were surveyed within the Sanctuary: three trail sites and the main camp area. Each site was surveyed during two alternate time periods to account for diurnal and nocturnal species. While surveying the site, arachnids were visually identified along with microhabitat description to observe any habitat preference. Specimens were collected for subsequent identification and validation of the visual identifications performed on site. The preliminary data suggest that the most frequently encountered arachnids collectively among the surveyed sites included members of Araneae families: *Theraphosidae, Lycosidae, Salticidae,* and *Hersilidae*. In addition, species of the orders Scorpiones and Amblypygi were frequently encountered. Previous studies on ecotourism indicate positive trends between biodiversity education and conservation concern; therefore, the data will be incorporated to create a user friendly identification resource for the local tourguides and future visitors to the sanctuary. By creating and providing this resource to the Cockscomb Sanctuary it will contribute to the greater scope of environmental education by achieving increased awareness of the area's biodiversity.

Key Terms: Arachnids
Belize

**EB-25**

## Comparative Methods of Estimating Small-mammal Population Abundance

Erin Froetschel (University of Georgia), Terry Barrett (University of Georgia), Advisor: Dr. Gary Barrett (University of Georgia)

Investigation into the dynamics of small-mammal populations requires an effective method to estimate population abundance. Various mark-recapture devices have been traditionally contrived to capture small mammals, such as the HB Sherman live trap, nest box, and nest tube. This study investigates the effectiveness of each of these devices for estimating the abundance of the white-footed mouse, *Peromyscus leucopus*, commonly inhabiting the North Georgia Piedmont. Five transects were established within deciduous-forest habitat, each containing twelve stations (four stations per method). All devices were mounted 1.5 m aboveground on mature water oaks, *Quercus nigra,* of similar DBH with an average of 47.9 cm. Capture of *P. leucopus* was conducted from 1 October 2010 through 30 August 2011. Of 616 total captures, 80.7% were captured in live traps, 8.0% nest boxes, and 11.2% nest tubes. There was a seasonal trend in capture; nest boxes and nest tubes were occupied frequently during autumn and winter months, whereas the HB Sherman live traps were occupied consistently throughout the year.

Key Terms: Mammology
Population dynamics
Ecology

**EB-26**

**Metagenomics Of Colitis Associated With Infection By *Clostridium Difficile***

Jovanny Lucero (University of California Irvine), Ana Elena Perez-Cobas (Centro Superior De Investigacion En Salud Publica), Advisor: Maria Jose Gosalbes (Centro Superior De Investigacion En Salud Publica)

The human gut harbors $10^{13}$ to $10^{14}$ microorganisms, while outnumbering human cells by at least 10 times. Its genome consists of at least 100 times more genes than does the human genome. A common way of studying these microbes and their effects on the human body is by carrying out metagenomic analyses, sequencing the 16S rRNA gene, as it is highly conserved among different species of Bacteria and Archaea. A healthy gut microbiota has different functions, one of them is the colonization resistance against pathogens. One of these pathogens, *Clostridium difficile*, can flourish in an environment with an altered colonization resistance. After colonization *C. difficile* produces toxins that cause inflammation and diarrhea, leading to colitis. Various broad-spectrum antibiotics have been shown to cause *C. difficile*-associated diarrhea (CDAD).

In the current study we carried out a metagenomic analysis on fecal samples of two individuals that do not develop CDAD during antibiotic treatment, as well as two individuals with *C. difficile* infection. Preliminary results show that majority of constituents before antibiotic treatment belong to the *Bacteroidetes* and *Firmicutes* phyla; the predominance changes during antibiotic treatment to *Actinobacteria* and *Proteobacteria*. Furthermore, the diversity, richness, and evenness of the samples decrease with the use of antibiotics, which can alter the functionality of the biome. Future studies involving the use of the same and/or different antibiotics on *C. difficile* infected patients can help researchers understand the harmful or beneficial effects of these drugs on human health.

Supported by NIH-MHIRT Grant MD-01485

Key Terms: Metagenomics
Microbiota

**EB-27**

**Pollen-Pistil Compatibilities And Adaptive Divergence In The Genus *Cakile***

Kalli Bunch (Simon G. Atkins Academic & Technology High School), Advisors: Dr. Kathleen Donohue (Duke University), Charles Willis (Duke University)

The female reproductive structure of a plant (the pistil) is vital to the reproduction of plants, but can also prevent plants from different species from hybridizing. This poses a problem, because hybridization is important in the production and maintenance of crops. Pollen-pistil incompatibility occurs when the pistil prevents the paternal pollen from either germinating or reaching the ovule. This research tests to see if adaptive divergence is associated with pollen-pistil compatibility. For this experiment, we tested different subspecies of *Cakile*, which is a member of the *Brassicaceae* family. Populations were taken from 5 different climatic regions (two northern and three southern). One of the southern taxa, C. lanceolata, was used as a focal plant and was crossed with the two taxa from the north to test compatibility between species from different environments, and the two other southern taxa to test compatibility between species from similar environments. All crosses were analyzed for four different phases of pollen-pistil interactions: Adhesion, Germination, Pollen Tube Growth, and Total Compatibility. Based on these test, we concluded that adaptive divergence is not associated with the ability of two species to successfully hybridize. This suggests that crosses between adaptively divergent species within the Brassicaceae family should be successful due to the lack of hybridization barriers.

Key Terms: Biology
Plant Evolution
Evolutionary Biology

**EB-28**

## A Morphological Study of *Tovomita weddelliana* Planch. & Triana (*Clusiaceae*)

Michael Terbush (Ohio University), Ben Gahagen (Ohio University) and Harvey Ballard (Ohio University)

*Tovomita* is one of 28 genera in the St. John's-wort family, Clusiaceae, and one of 5 genera in the tribe Clusieae. The genus can be identified by long basal internodes of branches, 2 usually connate outer sepals that envelope the bud, one ovule per carpel, and stylodia nearly as long as the ovary. *Tovomita* ranges from tropical South America and the Antilles as far west as Nicaragua, and it is currently estimated to have around 25 species. The genus contains several species complexes, including the *Tovomita weddelliana* complex, with high variability; however, we suspect that the apparent variability of some broadly distributed "species" is due to the presence of many unrecognized narrowly ranging species with superficially similar morphologies. An example is the *Tovomita weddelliana* complex, unique in several ways, including leaves clustered near branch tips; (sub)sessile oblanceolate blades with distinctly pale or glaucous lower surface; ovate-suborbicular sepals; numerous stamens with linear-subulate filaments; and an oblong obtuse glabrous ovary with four to five locules. Morphological examination of herbarium specimens belonging to the complex has revealed several distinctive species previously lumped under the name. The current study, which emphasizes morphological evidence, has uncovered correlated patterns of variability in several characteristics including leaf phyllotaxy, leaf shape, petiole development and leaf decurrence, leaf scars, and lateral veins. To date, our investigation has distinguished nine morphologically divergent species including *T. weddelliana* sensu stricto. Imminent future research will use DNA data to examine molecular phylogenetic relationships among *Tovomita species*.

Key Terms: systematics
Tovomita weddelliana species complex

**EB-29**

## Effects of Environmental Complexity in Captivity on Foraging Behavior and Survival in *Microtus pennsylvanicus*

Amaranta Kozuch (University of Wisconsin-Oshkosh), Advisor: M. Elsbeth McPhee (University of Wisconsin-Oshkosh)

A popular tool used in conservation efforts is reintroduction, which involves removing individuals from the wild, housing them in captivity (typically for captive breeding or translocation purposes) and then releasing them into the wild again. Yet during captivity many behaviors may deteriorate, therefore animals may become unprepared to response to wild conditions resulting in failed reintroduction attempts. To better understand how environment affects critical behaviors, I am experimentally addressing this on foraging behavior of meadow voles (*Microtus pennsylvanicus*) in captivity. Animals captured from the wild were assigned to one of two environmental conditions: simple (environmental control) and complex (experimental). Behavioral testing was conducted on all individuals to measure foraging behavior using five variables: 1) number of dishes visited- containing food vs not containing food, 2) time spent eating, 3) latency to find 1$^{st}$ dish, 4) latency to find 1$^{st}$ food dish, and 5) latency to find 2$^{nd}$ food dish. Preliminary results show that both lines expressed similar foraging behavior except for number of visits to non-food dishes ($p=0.04$); individuals from the complex environment visited more non-food dishes than from the simple environment. All subjects were subsequently assigned and released simultaneously into one of 3 one-acre open outdoor enclosures. Monitoring of survival was conducted by trapping every week for three days over two months. Recapture data suggests a slightly greater number of complex individuals surviving than simple. This research is critical for enhancing the captive environment used during reintroduction and the success of re-establishing threatened and endangered species populations.

Key Terms: Animal Behavior
Conservation

**EN-01**

## Strain-release Assembly of Si Nanowires for Device Applications on Unconventional Substrates

John W. Durham III (North Carolina State University), Advisor: Yong Zhu (North Carolina State University)

Current electronic devices are fabricated on rigid, brittle materials, considerably limiting the range of applications, especially in biomedical or robotics fields where flexibility and/or conformability are significant factors. Fabrication of electronic devices on flexible or stretchable materials usually requires complex patterning and assembly methods because of their incompatibility with standard photolithography. Recently, our group demonstrated a simple method for assembling nanowires on a biocompatible elastomer, polydimethysiloxane (PDMS), by prestraining the PDMS, depositing nanowires, and releasing the strain to form well-aligned nanowire arrays. This study utilizes the versatility of the strain-release method to fabricate electronic devices on unconventional substrates such as transparent, stretchable and flexible materials. Silicon nanowire (SiNW) arrays were aligned on the PDMS surface, normal to the stretching direction to decrease strain in the wires via Poisson's ratio. Electrodes were deposited through a shadow mask by electron beam evaporation, resulting in a nanowire device that features constant resistance to approximately 40% axial strain. Aligned SiNW arrays on PDMS were also transferred to polyethylene terephthalate (PET) with adhesive coating, using the PDMS as a stamp to fabricate electronic devices on flexible, transparent plastic. The device showed strain sensor characteristics with wires aligned along the circumference of the bend radius. This study demonstrates stretchable and flexible electronic device applications for the simple, high fidelity strain-release assembly method. Furthermore, the secondary role of the PDMS as a stamp material consolidates the assembly and transfer processes, reducing fabrication steps and allowing for transfer to unconventional substrates.

Key Terms: Mechanical Engineering
Nanotechnology
Material Science

**EN-02**

## Microfabrication of Conductive Polymer Nanocomposite for Novel Sensor Applications

Chao-Xuan Liu (Louisiana State University), Advisor: Jin-Woo Choi (Louisiana State University)

As successful as silicon-based micro sensors have been in the commercial market, there is a glaring need for new sensing materials to overcome some inherent limitations of silicon. The detection of biomechanical strains in the biomedical field, for instance, mandates strain gauge to withstand large ranges of strain—over 20% in some cases. Also, the rigidity of semiconductor severely limits its sensing resolution in many applications.

This research developed a novel sensing material using conductive polymer nanocomposite (carbon nanotubes dispersed in polymer matrix) and solved a major technical challenge of patterning nanocomposite on the micron scale. Various microstructures of nanocomposite were realized through novel microcontact printing and screen printing processes. The proposed microfabrication protocols simplified over conventional lithography processes, reducing both time and cost. Manufactured patterns were then used as functional element for physical sensors.

The unique sensing capability of polymer nanocomposite is due to the combination of mechanical flexibility (elastomer) and electrical piezoresistivity (carbon nanotubes). For demonstration, prototype devices including large-strain strain sensor and ultra-sensitive pressure sensor were realized showing distinct advantages over existing technologies.

The strain sensor, for example, showed significant resistive response while sample withheld large range tensile strain of over 45%. Also, the pressure sensor indicated ultra-high sensitivity of differential pressure down to 10 Pa or less. Each prototype sensor showed distinctive advantages over conventional technologies. Upon further development and commercialization, this technology yields abundant sensor applications in various fields.

Key Terms: Electrical Engineering
Sensor
Polymer

**EN-03**

## Visualizations of Stress Distributions in Heart Valve Tissues

Siyao Huang (North Carolina State University), Hsiao-Ying Shadow Huang (North Carolina State University), Advisor: Hsiao-Ying Shadow Huang (North Carolina State University)

Heart valve tissues constantly experience different stress states during cardiac cycles. However, how tissue-level mechanical forces can translate into altered cellular stress states is unknown. In the current study, we provide an automated finite element analysis to visualize the overall stress distributions in heart valve tissues. Nonlinear and anisotropic material properties of heart valve tissues are adapted. Histological photomicrographs capturing collagen fibers microstructure and cell morphology are incorporated into the finite element analyses. The study shows that heterogeneously distributed collagen fibers are responsible for transmitting forces into cells. Cells adjacent to the collagen fibers experience lower stress states than those are not directly connecting to the collagen fibers, suggested that cells under higher stress stimuli tend to synthesize new collagen fibers. The finite element simulation result provides a mechanistic understanding of the experimental observations on cells secrete collagen fibers to provide strength and maintain tissue structure integrity. The current study provides new models for better understanding tissue-cell interactions in heart valves.

Key Terms: Heart valves
Stress distribution
Finite element simulation

**EN-04**

**Real-time Characterization of Hydrocarbon Fuels by NIR Absorption Spectroscopy**

Vilas Jangale (North Carolina State University), Advisor: Alexei Saveliev (North Carolina State University)

Growing energy consumption along with economic and environmental demands has resulted in opportunity fuels gaining increasing popularity in industrial and commercial applications. Opportunity fuels are unconventional energy sources that are primarily sold and purchased outside the mainstream energy market. The gaseous opportunity fuels are generally mixed in small quantities as blends with fossil fuels and combusted in turbines or engines for heat and power generation. With the development of fuel-flexible combustion systems, the mainstream fuels will be displaced by opportunity fuels resulting in reduced energy cost to the industry and lowered emissions. The primary challenge to using gaseous opportunity fuels is the transient variation in their composition and energy content due to several factors associated with their production process. Fuels having energy content outside of recommended specifications can reduce combustion efficiency and cause damage to turbines or engines. Thus, it would be highly desirable to measure the fuel properties in real-time and utilize this information as a feedback to an engine/turbine control module for process control purpose. Presently used methods, such as, gas chromatography and calorimetry are not capable of measuring the fuel properties in real-time. A method has been developed for measuring the properties of hydrocarbon fuels in real-time. The near infrared absorption spectra of fuels are correlated to their composition and heating value using statistical regression methods. The method is less expensive and has similar level of accuracy as gas chromatography. The accuracy and stability of the method have been validated at commercial landfill gas production sites.

Key Terms: Opportunity Fuels
Fuel Characterization
NIR Absorption Spectroscopy

**EN-05**

**Biologically Inspired Transforming Roving-Rolling Explorer (TRREx) Rover**

Lionel Edwin (North Carolina State University), Nathaniel Gallinger (North Carolina State University), Advisor: Andre Mazzoleni (North Carolina State University).

Over the years, we have sent numerous rovers to the Moon and Mars, but all of them have been limited in their mobility. For example, we have not yet been able to venture into craters or down ravines. With game changing developments over the past decade in robotic technologies, we are at a juncture in planetary exploration technology where we can transition from the conventional rocker bogie suspension rover and start employing more unconventional designs.

We have been constructing and evaluating one such design called the *Transforming Roving-Rolling Explorer (TRREx) Rover*. When searching for novel designs, we found that nature provides abundant inspiration. The armadillo curls up into a ball when threatened, and the golden wheel spider uses the inherent dynamic advantages of a sphere to roll down hills when escaping danger. This led to the idea of developing a rover that can traverse like a conventional 6-wheeled rover, but can also transform itself into a sphere when traveling down steep inclines or navigating rough terrain. Our poster will present our work to date, including the overall design of the rovers and the hardware development and prototype testing we have conducted. This work represents an important first step in developing a rover capable of traversing a variety of terrains that are impassible by NASA's current fleet of rover designs, and thus has the potential to revolutionize the way NASA conducts planetary exploration.

Key Terms: Aerospace
Rover
Robotics

**EN-06**

## High Temperature Biocatalyst Immobilization on Nanofibrous Supports by Reactive Electrospinning

Christina Tang (North Carolina State University, Advisor: Saad A. Khan (North Carolina State University)

Enzymes are highly efficient selective biocatalysts; hyperthermophilic enzymes are of particular interest due to their ability to function at elevated temperatures intrinsic to industrial processes. We immobilize a model hyperthermophilic enzyme, α-galactosidase from Thermotoga maritima, on electrospun nanofibrous supports for potential use in applications ranging from increasing nutritive value of animal feed to converting B-type to O-type blood, the universal blood type. Immobilization offers inherent advantages: increased enzyme stability, ease of separation so the enzyme can be reused, and lack of product contamination. However, immobilization can also impact the activity of the enzyme and the structure of the support material greatly affects the performance. Because fibers have high specific surface area, nanofibers are especially promising for enzyme immobilization. In electrospinning, a technique used to produce nanofibers, an electric field induces the formation of a liquid jet from a polymer solution. We have developed a single-step reactive electrospinning process where we electrospin aqueous solutions of polyvinyl alcohol and T. maritima α-galactosidase with glutaraldehyde, a chemical crosslinking agent, to generate water-insoluble, enzyme-loaded nanofibers. Using this reactive electrospinning eliminates post-electrospinning treatment, accelerating the process by 7-fold. The enzyme retains catalytic activity and its hyperthermophilic characteristics (optimal activity between 90 and 95°C). While the enzyme activity of the immobilized enzyme was about 5-fold lower than the free enzyme, the retained activity was significantly higher than following post-electrospinning treatment using two-step methods. Furthermore, apparent activity of the immobilized enzyme increases with decreasing enzyme loading, suggesting that glutaraldehyde deactivation affects the performance of the immobilized enzyme.

Key Terms: Chemical Engineering
Materials Science
Polymer fibers

**EN-07**

## Controlled Buckling of Nanostructures for Stretchable Electronics

Feng Xu (North Carolina State University), Advisor: Yong Zhu (North Carolina State University)

The creation of stretchable electronics is emerging as one of the most interesting research topics in materials science and technology. Devices that are stretchable, foldable, and deformable into complex curvilinear shapes can enable many new applications that would be impossible to achieve by conventional rigid electronics. In this study, Silicon (Si) nanowire (NW) coils and wavy carbon nanotube (CNT) ribbons were fabricated on elastomeric substrates by a controlled buckling process, which may find important applications for stretchable electronics and other stretchable technologies. Si NWs were first transferred onto prestrained and ultraviolet/ozone (UVO)-treated poly(dimethylsiloxane) (PDMS) substrates and buckled upon release of the prestrain. Two buckling modes (the in-plane wavy mode and the three-dimensional coiled mode) were found; a transition between them was achieved by controlling the UVO treatment of PDMS. The NW coils exhibited very large stretchability up to the failure strain of PDMS (~104% in our study). Single NW devices based on coiled NWs were demonstrated with a nearly constant electrical response in a large strain range. The wavy CNT ribbons were fabricated by a similar strategy, which show good transparency, excellent flexibility, and stable resistance with application of strains up to 100%. A simple circuit was constructed by connecting a light-emitting diode (LED) with two wavy CNT ribbons. When the ribbons were manually stretched, twisted and folded, the LED remained lit, demonstrating that the wavy CNT ribbons can work as stretchable conductors.

Key Terms: Nanotechnology
Stretchable Electronics
Buckling

**EN-08**

## An Integrated System for Energy Production and Nitrogen Removal from Swine Waste

Eric T. Staunton (University of North Carolina-Chapel Hill), Sarah R. Bunk (University of North Carolina-Chapel Hill), John P. McNeil (University of North Carolina-Chapel Hill), Glenn W. Walters (University of North Carolina-Chapel Hill), Stephen C. Whalen (University of North Carolina-Chapel Hill), Joseph Rudek (Environmental Defense Fund) and Michael D. Aitken (University of North Carolina-Chapel Hill)

Eastern North Carolina is home to over 10 million hogs in confined animal feeding operations (CAFOs). The waste produced from these is currently stored in uncovered lagoons and periodically sprayed onto fields to fertilize crops, which has led to impairment of water and air quality from the volatilization of ammonia. To mitigate these effects, there is a desire to couple anaerobic digestion of hog waste for power generation with biological nitrogen removal. We designed and operated a pilot-scale nitrification-denitrification system using full-scale anaerobically digested waste as process influent. This system operated at Butler Farms in Lillington, NC from July 2010 until May 2011. One objective of the study was to quantify the extent to which residual biodegradable oxygen demand (BOD) in the digested waste could contribute to denitrification. By the end of the project, >98% ammonia oxidation was achieved with an influent of 2,300 mg/L ammonia-nitrogen and an average of 68% total nitrogen removal was achieved with an average influent of 2,700 mg/L total nitrogen. The system converted 5% of the ammonia load into nitrous oxide, with 99% of the N2O production in the nitrification reactor. There was strong seasonal variation of COD/total N in the influent waste, reflecting responses of the full-scale anaerobic digester to changes in ambient temperature. During summer months, denitrification was limited by low influent BOD, whereas denitrification performance improved during winter months. Overall, it appears feasible that at least a 90% reduction of ammonium-nitrogen is possible in a full-scale system treating anaerobically digested hog waste.

Key Terms: Biological Nitrogen Removal
Swine Waste
Environmental Engineering

**EN-09**

## Static Friction between Silicon Nanowires and Elastomeric Substrates

Qingquan Qin (North Carolina State University), Advisor: Yong Zhu (North Carolina State University)

This paper reports direct measurements of static friction force and interfacial shear strength between silicon (Si) nanowires (NWs) and poly(dimethylsiloxane) (PDMS). A micromanipulator is used to manipulate and deform the NWs under a high-magnification optical microscope in real time. The static friction force is measured based on “the most-bent state” of the NWs. The static friction and interface shear strength are found to depend on the ultraviolet/ozone (UVO) treatment of PDMS. The shear strength starts at 0.30 MPa without UVO treatment, increases rapidly up to 10.57 MPa at 60 minutes of treatment and decreases for longer treatment. Water contact angle measurements suggest that the UVO-induced hydrophobic-to-hydrophilic conversion of PDMS surface is responsible for the increase in the static friction, while the hydrophobic recovery effect contributes to the decrease. The static friction between NWs and PDMS is of critical relevance to many device applications of NWs including NW-based flexible/stretchable electronics and NW assembly. Our results will enable quantitative interface design and control for such applications**.**

Key Terms: Stactic friction
Si Nanowires
Elastormeirc substrate

**EN-10**

## A Fatigue Analysis for Lithium-ion Batteries

Michael Stamps (North Carolina State University), Advisor: Hsiao-Ying Shadow Huang (North Carolina State University)

Lithium-ion batteries have become a widely known commodity for satisfying the world's mobile energy storage needs. These needs are becoming increasingly important, especially in the transportation industry, as concern for rising oil prices and environmental impact from fossil fuels are pushing for deployment of more electric vehicles or plug in hybrid-electric vehicles and renewable energy sources. Past research has shown that lithium-ion batteries lose capacitance over their life due to damage accumulation during the charge/discharge repetitive process and during times of high rate discharging. In the current study, we systematically investigate the relationships of the fatigue strength, the electrode particle size, the loading ratio, and the number of cycles in lithium-ion batteries. A time-varying load during lithium ion intercalation or extraction from the electrodes is considered. Crack sizes and material properties are obtained from available experimental observations and characterizations. The theory of linear elastic fracture mechanics and various fatigue crack growth models elucidate the relationships of the crack growth rate and the stress intensity factors incorporated into our fatigue analysis. The aim is to provide a better understanding on fracture and crack propagation-induced capacity loss in lithium-ion batteries. Use of this knowledge will help to provide new models and tools for clarifying the interplay of mechanics–property–electrochemistry and yield a greater level of mechanistic understanding with respect to lithium-ion battery materials.

Key Terms: Mechanical Engineering
Lithium ion Batteries
Fatigue Analysis

**EN-11**

## A Dislocation Based Stress Development in Lithium-ion Batteries

Yixu Wang (North Carolina State University), Hsiao-Ying Shadow Huang (North Carolina State University), Advisor: Hsiao-Ying Shadow Huang (North Carolina State University)

Lithium-ion batteries have been used for a wide range of applications, from power tools and portable electronics to recent plug-in hybrid electric vehicles and pure electric vehicles. However, current prototype Li-ion batteries have been reported to lose capacity or degrade rapidly under high discharging rate. In the present study, we report three different lithium intercalation-induced dislocation mechanisms explaining experimental observed cracks. We use the theory of elasticity to calculate dislocation stress fields. In most cases, dislocations are not perfectly parallel to one specific axis. Therefore, stress variations for arbitrary dislocation directions are investigated. In addition, multiple dislocations usually co-exist and interact each other in the crystal; therefore we use the superposition method to investigate stress fields and forces between multiple dislocations. The stress fields manifesting between dislocations are numerically calculated via Mathematica (Wolfram Research, Champaign, IL), and anisotropic material properties of electrodes are employed. The results provide links between stress fields and the observed structural failure in lithium-ion batteries. This study helps further the design of better lithium-ion batteries, and thus advances technology in energy storage systems for future modes of transportation.

Key Terms: Lithium Ion Battery
Stress Analysis
Fracture Mechanism

**EN-12**

# Ocean Compressed Air Energy Storage System with Thermal Energy Storage; Thermodynamic Design

Saniel Lim (North Carolina State University), Otmane Qarouach (North Carolina State University), Brendan Quinlan (North Carolina State University), Advisor: Andre Mazzoleni (North Carolina State University), Paul Ro (North Carolina State University)

Due to the increasing demand of renewable energy generation in recent years, compressed air energy storage (CAES) system is becoming a promising candidate for storing energy generated by renewable energy sources. CAES can be used to balance intermittent renewable energy and varying electricity demand. Two existing CAES plants, in Huntorf, Germany and in McIntosh, Alabama, have been already operated with high availability and reliability, and, with thermal energy storage and seabed air storage, CAES can be made a more efficient storage system.

This study focuses on a conceptual design of ocean compressed air energy storage (OCAES) in which the hydrostatic pressures in the deep ocean enable the compressed air to be kept at constant high pressures. In addition, thermal energy storage (TES) is considered to promote overall efficiency in which the heat extracted from compression process is used to reheat the compressed air before it goes into the turbine generator. By enabling a constant higher pressure (60bar) to be used than the pressure (45bar) that existing plants use, overall efficiency can be improved. TES makes possible to use the heat dissipated through intercoolers during compression and therefore fuel consumption is decreases by 50%.

This poster will present thermodynamic analyses for integrating OCAES with TES based on the investigation of two existing CAES and solar power plants. These analyses are being used to optimize various system parameters such as storage pressure, plant capacity, operation time, and fuel consumption.

Key Terms: Mechanical Engineering
Energy Storage
Compressed Air

**EN-13**

# Non-destructive Line Detection of Salted Egg Based on Image Processing and BP Neural Network

Zhongqiang Chen (North Carolina State University), Tao Zhu (Huazhong Agricultural University, China), Advisor: Qiaohua Wang (Huazhong Agricultural University, China)

This paper proposed a method to detect the quality of salted duck eggs based on image processing and artificial neural network. Fourier transform was employed after pre-processing for the images of eggs. It was found that the texture of phase spectrum images of four kinds eggs (“non-well pickled”, “well-pickled”, “over-pickled” and “spoilt” eggs), varied from clear and ordered to vague and disordered, while the corresponding entropies of images gradually decreased. Through the brightness statistics of images with wavelet reconstruction, it was found that in terms of brightness, the “well-pickled eggs” ranked the first, and the “spoilt eggs” being the last. Color, texture, and statistical moment parameters were selected as image parameters, and BP neural network was created with three-layer feedforward structure (10-18-4). Then the network was tested and the correct ratio of the model amounted to about 92%, certifying the feasibility of this method.

Key Terms: Salted egg
Non-destructive detection
Image processing

**EN-14**

**Elastic Imaging Assessment of Cryoablation Lesions in Heart Tissue**

Brittany Potter (Duke University), Secondary Author Stephanie Eyerly (Duke University), Advisor: Patrick Wolf (Duke University)

Cardiac cryoablation is an increasingly utilized treatment for atrial arrhythmias. To date, there is no method to directly image cryo-lesions within the myocardium. Direct visualization of delivered cryo-lesions would increase the success of the ablation procedure. Acoustic Radiation Force Impulse (ARFI) imaging is a two-dimensional relative elasticity imaging method that can image radiofrequency ablation lesions *in vivo* and *in vitro*. We investigated the ability of ARFI imaging and a quantitative elasticity imaging method, Shear Wave Elasticity Imaging (SWEI), to assess cryoablation lesions *in vivo.*

Cryo-lesions were created on the right ventricle of the epicardial tissue in an open chest, canine model. A Cry-AC tracker liquid nitrogen sprayer (Brymill Cryogenic Systems; Vernon, CT) with a 3mm probe attachment was used for cryo-lesion formation (4:20 contact time, approximately -30° C contact temperature). A VF10-5 linear transducer connected to an Anteres ultrasound scanner (Siemens Medical; Issaqua, WA) was suctioned to the epicardium over the cryo-lesion with a custom made vacuum device. B-mode, ARFI and SWEI images were obtained of the lesion.

ARFI imaging and SWEI images accurately differentiated cryo-lesion from healthy myocardial tissue. The cryo-ablated myocardium was visibly discolored and stiff to the touch, providing verification of lesion delivery. Implementing ARFI imaging and SWEI during cryoablation procedures could shorten the length of the procedure and increase the success of the initial procedure.

Key Terms: Cardiac Ablation
Cryo

**EN-15**

## Removal of Surface Active Contaminants from a Liquid-Liquid Interface

Dylan McCapes (Santa Barbara City College), Advisor: Gary Leal (University of California, Santa Barbara) and John Frostad (University of California, Santa Barbara)

A further understanding of coalescence is important for applications such as foam stability. Surface-active agents, or surfactants, complicate the study of coalescence phenomena. The purpose of this study is to design an apparatus to remove surfactants from a liquid-liquid interface so that coalescence can be understood without the added complications of surfactants. Surfactants are generally amphiphilic molecules. It is because of this amphiphilic nature that surfactants prefer to be at the interface of two liquids. This study takes advantage of this preferential adsorption to the interface, and the main focus of the apparatus is to isolate and remove interface while retaining as much liquid as possible. Before designing a surfactant removal apparatus an isotherm for the interfacial tension of water and polydimethylsiloxane (PDMS) as a function of the bulk concentration of the surfactant hexadecyl trimethyl ammonium bromide (HTAB) was constructed. This isotherm will be used when the device is tested so that graph for HTAB concentration as a function of either iterations or volume loss can be constructed by measuring the interfacial tension. A proof of concept experiment was also conducted to ensure that removal of interface results in the removal of surfactants. This experiment was conducted by simply removing interface with a syringe and measuring interfacial tension. The results of this experiment show that interface removal does indeed result in an increase in interfacial tension and hence a decrease in surfactant concentration. The apparatus is currently under construction and will be tested upon completion.

Key Terms: Chemical Engineering
Fluid Mechanics
Study of Interfaces

**EN-16**

## Quantum Well Intermixing for Hybrid Silicon Laser Integration

Anna Revolinsky (University of California, Santa Barbara), Advisor: Siddharth Jain (University of California, Santa Barbara), Professor John E. Bowers (University of California, Santa Barbara)

Fiber optics facilitate high speed, high bandwidth communications, but require expensive components such as lasers and photodetectors to operate. Research in photonics aims to lower the cost of the components of the fiber optic system by designing devices such as the hybrid silicon laser, which combines the optical abilities of photonics with inexpensive silicon-based CMOS manufacturing. On this laser, however, data is still only transmitted at one wavelength, leaving fiber optic communication uneconomical. Our research in quantum well intermixing aspires to make the hybrid silicon laser transmit data at multiple wavelengths, thus allowing the integration of several photonic devices onto a single chip. This multiples the data transmitted by a single device. Our work involved analyzing two specific quantum well intermixing procedures-ion implantation and dielectric capping. We received ion implanted samples from an outside vendor, anneal them at varying temperatures for a range of times, and then map the shift in the photoluminescence. The shift in the photoluminescence tells us the shift of the bandgap energy, which indicates the wavelength of light produced by that sample. We also deposited various dielectric caps onto unimplanted samples, and annealed and measured the photoluminescence change on those samples. We documented the trade-off between the implantation and dielectric capping techniques in order to select the ideal method for multiple bandgap integration.

Key Terms: Electrical Engineering
Photonics
Optical Communication

**EN-17**

## Assessment of Horse-Rider Kinematic Variables in Hippotherapy

Meredith Cole (Clemson University), Justin Arnosky (Clemson University), Beryl Walker (Clemson University), Simone Neuhoff (Clemson University), Advisors: Rick Blob (Clemson University), Kristine Vernon (Clemson University), John D. DesJardins (Clemson University)

Hippotherapy is a rehabilitation therapy that utilizes a horse as a moving platform for the treatment of physical or neurological conditions. The patient is placed on the horse's back and performs activities while the horse is led around an arena. The motion that the horse provides is a crucial part of the treatment, yet the biomechanical interaction between horse and rider in hippotherapy is largely unknown. Previous studies have found that conformational aspects effect the movement of the equine back. Horses can be evaluated by eye and classified according to their hock activity, freedom of shoulder and stride length. The rider is directly influenced by the motion in the horses back.

The purpose of this experiment was to evaluate the relationship between horse and rider kinematics during hippotherapy. A Biometrics motion system (SG150, Cwmfelinfach, Gwent, United Kingdom) was used to measure the spine (thoracic and lumbar) and hip (abduction and flexion) angles of the rider while the horse was lead on a straight path at the walk. A video capture motion analysis system (Casio Exilim Pro F1, Casio America, Dover, NJ) was used to capture the horse's motion at 300 frames per second. Results show that the horse produces cyclical motion in monitored joints corresponding to the stride phase. For one subject the mean (± 1 standard deviation) range of motion in the thoracic vertebra over 11 strides was 3.16±0.70 degrees. This study found that repeatable motion analysis data collection was possible for both horse and rider with this methodology.

Key Terms: Biomechanics
Bioengineering
Equine

**EN-18**

## Identification of the Optimal Flexion Axis in Total Knee Replacements Using a Robotic Manipulator

Timothy J. Warrick (Clemson University), Roy J. Rusly (Clemson University), Advisors: Laine Mears (Clemson University), John D. DesJardins (Clemson University)

A total knee replacement (TKR) is an engineered biomedical device that is surgically implanted to relieve pain, correct deformity and restore joint function. TKR alignment is critical to the function of the repaired knee, as misalignment can cause accelerated wear on the implant. However, reproducible alignment is challenging to attain due to variations in patient anatomy, surgical instrumentation and numerous TKR designs available. We are currently working to quantify the effect of femoral axis selection on resulting TKR femoral component kinematics using a robotic manipulator. The end-effector of a KUKA KR3 robot is securely attached to a Zimmer Natural Knee II, Size 3 Right femoral component. The femoral component is rotated about a selected flexion axis in the sagittal plane by running a KUKA command script. Proximal and distal motion of the femoral component is measured using a Novotechnik TRS 25 linear variable differential transducer (LVDT) and streamed into LabVIEW. Proximal and distal motion of the TKR is quantified as the implant rotates from 0° - 60° of flexion. A series of axes will be tested with the goal of identifying a flexion axis that produces the least proximal and distal motion.

The long-term goal of this study is to develop mathematical response surfaces for femoral component motion to optimize femoral axis design selection in complex TKR designs.

Key Terms: Total Knee Replacements
Bioengineering
Knee Flexion Axis

**EN-19**

## Molecular Dynamics Simulations of Carbon Nanotube-Polythiophene Interactions

Joseph Moo-Young (North Carolina State University), Advisor: Melissa A. Pasquinelli (North Carolina State University)

The goal of this work is to investigate the interactions between a series of polythiophenes and zig-zag carbon nanotubes (CNTs) with varying diameters using molecular dynamics simulations. We hypothesize that the interfacial interactions between the polythiophenes and CNTs will largely be a function of the chemistry of the polymer aliphatic substituents, as well as CNT diameter. These results provide the best combination of polymer and CNT diameter that produces desired material properties for unique application in better solar cell technologies. The correlation of these simulation results to experiments done by a collaborator will be discussed.

Key Terms: Molecular dynamics
Solar cell technologies
Carbon nanotubes

**EN-20**

## Preparation and Characterization of Optically-Active Metal Probes for Scanning Chemical Microscopy

Jae Cho (University of California, Santa Barbara), Isaac Riisness (University of California, Santa Barbara), Advisor: Michael J. Gordon (University of California, Santa Barbara)

Tip-enhanced Raman spectroscopy (TERS) has enabled spatially correlated topographic and chemical imaging of biomolecules, catalysts, photovoltaics, and materials on the nanoscale. As the name suggests, the tip is an important part of the TERS experiment; tip size sets the spatial resolution, whereas tip material (typically gold or silver) and shape determine how well far-field laser light couples to electron oscillations (plasmons) in the tip. These plasmons create a tightly confined field that enhances Raman scattering of molecules in the tip-surface gap, enabling sub-diffraction limited chemical identification. Tips are typically prepared via electrochemical etching of metal wires in strong acid or base solutions. The etching process is not well understood, and the production of sharp, plasmonically active tips remains a key challenge in the TERS field.

To address this issue, we use a highly sensitive tuning fork oscillator to study the electrochemical tip etching process. Specifically, we monitor the oscillator frequency and amplitude during electrochemical tip etching under varying wire immersion depth, etching solution concentration, and different etching parameters (e.g. voltage, current, time, etc.). In this presentation, we compare tuning fork dynamics during tip etching to overall tip morphology and the corresponding optical activity from TERS experiments in an effort to improve control of tip preparation.

Key Terms: chemical engineering
nanoscience
microscopes

**EN-21**

## Development of Cold Plasma Textile for Filtration and Decontamination Applications

Ivan A. Kuznetsov (William G. Enloe High School), Advisor: Alexei V. Saveliev (North Carolina State University)

The research focused on the development of a novel material, a plasma textile, which makes use of the unique antimicrobial and filtration properties of non-thermal plasma, and allows capturing and deactivating bacteria. The primary supposition of the study was that a micro-plasma array could be embedded in a textile fabric to induce a plasma sheath that filtered and deactivated all bacterial pathogens coming in contact with the fabric.

The work proceeded through a series of steps: (1) determining the optimal type of plasma discharge; (2) finding the ideal wire electrode materials, radii, and placement to achieve stable, uniformly-distributed non-thermal plasma; (3) modeling electric field surrounding electrodes to explain observed effects and estimate the impact of an insulating textile on the electrode system; (4) testing various polymers and developing a plasma textile based on electrode geometries found in experimentation; (5) measuring the filtration efficiencies of the plasmas using a condensation particle counter; (6) testing the textile's ability to deactivate bacteria.

The work confirmed the existence of sustainable, uniform plasma on the surface of the developed fabric that was capable of capturing over 98% of bacteria-sized particles and deactivating tested bacteria.

Key Terms: Engineering
Nanoscience
Filtration

**EN-22**

## Foundation Systems for North Carolina Ocean Energy Systems

Deepak Pappusetty (University of North Carolina at Charlotte), Advisor: Miguel Pando(University of North Carolina at Charlotte),Vincent Ogunro (University of North Carolina at Charlotte)

Recently in North Carolina (NC) a legislation was approved allocating recurring funds towards research on renewable ocean energy off the coast of NC. This poster presents a summary of the results available to date on an ongoing research project funded by the NC Ocean energy program to investigate the loading and design considerations on offshore energy device foundations under NC conditions.

Most design procedures for offshore foundations come from experience of the oil and gas (O&G) industry. Although useful, loading and design conditions for ocean energy devices can be very different than O&G platforms. One significant difference is on the nature of the loading for ocean energy devices that can be based on tides, waves or currents. Design of O&G offshore platforms often is controlled by a 100 year design storm, whereas ocean energy devices often are controlled by fatigue considerations resulting from exposure to countless loading cycles during their design life. This poster will present details on the loading characterization for offshore energy devices and will discuss the repercussions that this numerous loading cycles can have on the foundation design. This poster will relate primarily to the fixed foundations systems. The loading characterization involves challenges such as determination of time histories, evaluation of average loading magnitude, frequency, deformation, number of cycles per day and per design life. Furthermore, the loading characterization has temporal and spatial variability and is a function of the ocean environment at the depth and location of the proposed device, and also the geometry and foundation system.

Key Terms: Civil Engineering
Geotechnical
Offshore

**ES-01**

**Effects of Deepwater Horizon Oil Spill on the Growth, Reproduction, and Gene Expression of *Caenorhabditis elegans***

Yanqiong Zhang (East Carolina University), Baohong Zhang (East Carolina University), Advisor: Xiaoping Pan (East Carolina University)

In April 2010, the tragic oil spill happened in the Gulf of Mexico. The economic, environmental, and human health impacts of the Deepwater Horizon oil spill have been widely concerned by the public and scientists. One of the response actions was injecting tons of chemical dispersant into the flow of raw oil. In this study, we used *Caenorhabditis elegans (C.elegans)* as an animal model to test the toxicity of the raw oil and chemical dispersant. The *C. elegans* L1 and L4 larvae were dosed with raw oil and dispersant at five different concentrations. The growth, reproduction, and gene expressions were assessed. Results showed the offspring number was significantly affected by the oil-dispersant mixture and dispersant only. We also investigate the expressions of 30 selected egg-laying and stress related genes using real-time quantitative PCR and the affected genes will also be reported.

Key Terms: oil spill
toxicology
Caenorhabditis elegans

**ES-02**

**Metabolism of Isobutane by *Mycobacterium austroafricanum* JOB5**

Samanthi Kottegoda (North Carolina State University), Advisor: Michael Hyman (North Carolina State University)

Isobutane, the simplest branched alkane, is an important component of gasoline, liquefied petroleum gas and natural gas. Few isobutane-oxidizing organisms have been identified and little is known about the enzyme responsible for initiating isobutane oxidation. The only previous study of isobutane oxidation has suggested that propane and isobutane are oxidized by two different oxygenases.
We have characterized propane and isobutane oxidation by *Mycobacterium austroafricanum* JOB5 at both the physiological and molecular level. Cells grown on either alkane immediately oxidized both alkanes at high rates and these reactions were both inhibited by acetylene, a potent and specific inhibitor of alkane monooxygenases. Cells grown on either alkane also oxidized $1^{o}$ and $2^{o}$ alcohols at equivalent rates and with similar product profiles.
The proteins synthesized during induction of isobutane-oxidizing activity in fructose-grown cells was examined following *tert*-butyl alcohol accumulation as an indicator of isobutane-oxidizing activity. Two major polypeptides (53 kDa and 38 kDa) were present in cells grown on propane, isobutane, 1-propanol or 2-methyl-1-propanol. Neither polypeptide was present in fructose-grown cells. *De novo* synthesis of the 53 kDa polypeptide was also observed in fructose-grown cells during the induction of isobutane-oxidizing activity. Propane- and isobutane-grown cells were also compared with glucose- and fructose-grown cells using a whole cell shotgun proteomics approach. A membrane-associated particulate monooxygenase enzyme was identified that was differentially expressed at high levels in alkane-grown cells but not either glucose-or fructose-grown cells. The proteomic analysis demonstrated cells grown on propane and isobutane appeared to express the same alkane-oxidizing enzyme system.

Key Terms: Environmental Microbiology
Microbial Genomics and Metabolism

**ES-03**

## Establishing And Maintaining Enhanced Infiltration Through Shallow And Deep Tillage With Soil Amendments

Virginia K. Brown (North Carolina State University) , Richard A. McLaughlin (North Carolina State University), Joshua L. Heitman (North Carolina State University), (North Carolina State University), Barrett L. Kays (Landis, Inc.)

The process of constructing roads and building usually involves the removal of topsoil, grading, and traffic from heavy machinery and trucks handling construction supplies. The result is compacted subsoils with low fertility which hinder vegetation establishment, limit infiltration and are susceptible to erosion. The goal of this project is to quantify methods for restoring initial and long term perviousness of surface soils compacted by construction equipment by increasing storm water infiltration and accelerating vegetative growth. The study has three locations in North Carolina, the Coastal Plain, Piedmont, and Mountain regions. We are evaluating three treatments: a compacted soil, a compacted soil with shallow tillage (15cm), and a compacted soil with deep tillage (30cm), compost amendment, and two rate of liming. The objectives are to measure runoff quantity and quality, infiltration rate, biomass production, and rooting depth for each treatment. Soil compaction and resistance from penetrometer readings show little difference between the deep and shallow tillage treatments from the surface to 6 inches. Resistance was high from the surface to a 12 inch depth on the compacted treatment while the deep tillage treatment showed minimal resistance or increase with depth. Data from storm events and infiltration tests indicate that the tillage treatments substantially reduce runoff. Runoff water quantity and quality, infiltration capacity, and vegetative growth data will be presented.

Key Terms: Stormwater Management
Erosion Control
Infiltration

**ES-04**

## A Study of the Putative Protective Effect of Phenylmercaptoacetamide (PMA) to Arsenate Toxicity in *Caenorhabdites elegans*

Winchester Stuart (SUNY College at Old Westbury), Advisors: Fernando Nieto (SUNY College at Old Westbury) and Duncan Quarless (SUNY College at Old Westbury)

Arsenic contamination is a serious environmental problem affecting millions of people via contaminated drinking water extracted from underground aquifers in areas like Long Island. Some methods used for removing the contamination in soil involve the use of organisms capable of bio-accumulating the metal in its tissues using phytochelatins. Phenylmercaptoacetamide (PMA) is a chemical synthesized in our laboratory to mimic the nature of phyochelatins. Interaction between PMA and arsenate is investigated using the nematode *Caenorhabdites elegans* (*C. elegans*) as an indicator model. *C. elegans* is a nematode that lives in temperate soil environments. It is surmised that arsenate is using phosphate channels to enter the worm. To study effects of PMA on worms treated with arsenate, synchronized colonies of nematodes were exposed in liquid medium to concentrations of arsenate with and without PMA and incubated for twenty-four hours. Afterward, mortality rates were calculated for control and treatments. Worms exposed to arsenate at 100 mg/L, 50 mg/L and 10mg/L had percent mortality of 40.1%, 38.2% and 43.1% respectively. Worms exposed to arsenate and PMA at 100 mg/L +PMA, 50 mg/L + PMA and 10mg/L + PMA had mortality rates of 28.5%, 17.4% and 24.9% respectively. Worms exposed to concentrations of arsenate had a higher mortality compared to those exposed to both arsenic and PMA. The arsenate exposed worms that survived displayed decreased activity compared to worms exposed to arsenate and PMA. The next step is to do molecular analysis of nematode pathways to pinpoint mechanisms of interaction between arsenate and *C. elegans.*

Key Terms: Toxicology
Environmental

**ES-05**

## North Carolina Fungal Biodiversity by Development of an Online Database and Website

DeMonica M. Gentry (North Carolina State University), Advisors: Dr. Marc A. Cubeta (North Carolina State University), Dr. Larry F. Grand (North Carolina State University)

A user friendly, internet searchable database is currently being developed for access to information on fungal specimens housed in the Mycological Herbarium at North Carolina State University. As part of this project, the poroid wood decay fungi (polypores) were initially selected to develop a series of fungus profiles for use by scientists, educators, and the general public. Profile information included brief macroscopic and microscopic morphological features, type of wood decay, common hosts, and a North Carolina distribution map for each fungus. Currently, there are 35 profiles of wood decay fungi on the Mycological Herbarium website which can be accessed at

http://www.cals.ncsu.edu/plantpath/activities/labs-projects/myherb/

The project has expanded to develop additional profiles for specimens of powdery mildew fungi in the Mycological Herbarium. The content featured in the powdery mildew profiles will include morphological characteristics of each species and their common host plants. The profiles will serve as a valuable resource for identifying polypore and powdery mildew fungi in North Carolina and to better understand their diversity and geographic distribution.

Key Terms: plant pathology
plant biology
ecology

**ES-06**

## The Effects of the Captive Environment on Testosterone Levels in Wild Caught Meadow Voles (*Microtus pennsylvanicus*)

Korin Franklin (University of Wisconsin Oshkosh), Advisor: M. Elsbeth McPhee (University of Wisconsin Oshkosh)

The dramatic effects of captivity on wild-caught animals have been well-documented. These include behavioral and physiological changes such as inability to avoid predators, forage, or navigate in a complex wild environment. In addition, captive-held wild-caught animals are often difficult to breed because the captive environment is so different than the wild environment. To increase the success of captive breeding programs, the effects of captivity on hormone production need to be understood. This study specifically focuses on the effects of the captive environment on testosterone levels in wild-caught meadow voles *(Microtus pennsylvanicus)*. I compared the total testosterone levels in the urine of 11 wild-caught meadow voles that had been held in captivity for a period of time to the total testosterone levels of 17 newly-caught voles using a competitive ELISA kit. The urine samples were analyzed using a Wilcoxen test which showed testosterone levels to be significantly higher in the wild animals than in the captive animals ($p < 0.001$). This confirms that the captive environment does affect testosterone levels in wild-caught meadow voles. In conclusion, this study suggests that more research should be done to find out if similar mechanisms are at play with other species.

Key Terms: Animal Conservation
Captive Breeding
Biology

**ES-07**

## Toxicity Of Anionic and Nonionic Surfactants on *Geomyces* Growth

Amy Fischer (Arkansas State University), Advisors: Evan L. Pannkuk (Arkansas State University), Thomas Risch (Arkansas State University)

White-nose Syndrome (WNS) is a progressive bat-killing disease thought to be caused by the fungus *Geomyces destructans.* Bats with WNS experience interruptions of torpor and erratic behavior, which ultimately leads to starvation. Lipids are important molecules that affect fungal attachment and growth. Additionally, certain fatty acids have been shown to exhibit fungistatic and fungicidal properties. To screen for fatty acid effect on fungal growth, common lab surfactants are used to aid in lipid emulsification with aqueous microbial media. Surfactants possess a hydrophilic head that attaches to water and a hydrophobic tail that attaches to oil molecules, allowing for a more homogenous mixture. Surfactants can also slow down fungal growth and it is of paramount importance to pick the least toxic surfactant to use for emulsification. To test the toxicity of common lab surfactants, we grew *G. destructans* and *G. pannorum* on media containing Sodium Dodecyl Sulfate (SDS), Triton X-100, Tween20® and Tween 80® at 0.01%, 0.1%, and 1.0% concentrations. Cultures were grown for two weeks at room temperature. Fungal growth was quantified by total area, total perimeter, and total diameter of the colonies with a ColonyDoc-It™ Imaging Station. Fungal colonies were also vortexed and total spore counts were obtained. Triton X-100 exhibited the lowest toxicity at all tested concentrations as quantified by growth and production of spores. Tween 20® and SDS limited growth at 0.1% and 0.01% concentrations and severely inhibited growth at 1.0%. We conclude that Triton X-100 is the most suitable surfactant for lipid emulsifications with microbial media.

Key Terms: White-nose Syndrome
Surfactants
Fatty Acids

**ES-08**

## Assessing Air Pollution Near Roadways

James Taylor York (North Carolina State University), Carey Jackson (North Carolina State University), Olivia Bagley (North Carolina State University), Advisor: Bill Hunt(North Carolina State University)

The EPA currently has many air pollution monitors across the United States. Some of these are close to the road while others are further from the road. The purpose of our research is to see how air pollution varies according to distance from the road and the volume of traffic on the road. Are air pollution concentrations at "near-road" monitors changing at a different rate than monitors located elsewhere? Our goal for this project is to analyze records, both past and recent, to determine if our monitors are truly effective. For our purposes, we will focus on CO, $NO_2$, and $PM_{2.5}$. Five to ten case studies will be picked throughout different regions of the country, and exploratory statistical methods determined the relationship between set back distances, traffic counts and air pollution. Data was used to determine if monitors near-roads and monitors elsewhere had concentration levels changing at different rates for the last several years, certain days of the week, and hourly. This information will help develop better monitoring regulations and guidance for State and local air pollution control agencies.

Key Terms: air pollution
roadway

**ES-09**

## Effects of the Oil Dispersant Corexit® EC9500A on Bleaching of the Alcyonacean Soft Coral *Xenia elongata*

Michael Studivan (St. Mary's College of Maryland), Dr. Carys Mitchelmore (Chesapeake Biological Laboratory), Advisor: Dr. Walter Hatch (St. Mary's College of Maryland)

Oil dispersants have been used since the 1960s to improve oil spill cleanup efficiency, but little toxicology data has been published regarding the effects of some dispersants on coastal environments. Corexit® EC9500A is a commonly applied dispersant that was used extensively on the recent *Deepwater Horizon* blowout (April 2010). Despite the lack of solid toxicological data for coral reef species, there is limited evidence that Corexit® EC9500A can cause a bleaching response in corals. This study had two goals: (1) to determine the extent of bleaching after 24 and 72 hour exposures of sublethal concentrations (0-50ppm) of Corexit® EC9500A to the soft coral *Xenia elongata* and (2) to investigate the use of a percent bleaching calculation in acute exposure studies using zooxanthellae counts. For future chronic studies, we explored the possibility of spicule density and soluble protein concentration as zooxanthellae normalization techniques. Our zooxanthellae data suggested a strong relationship between exposure concentration and percent bleaching. Percent bleaching was an effective measure of coral health in acute (24 hour) exposures. However, zooxanthellae normalization with spicule density and soluble protein concentration in *Xenia elongata* was difficult because they may also be affected as a result of bleaching.

Key Terms: Oil Dispersant
Toxicology
Coral Reef

**ES-10**

## Allelopathic Growth Stimulation by *Glechoma Hederacea*

Adama Loos-Diallo (Warren Wilson College), Advisor: Michael Torres (Warren Wilson College)

*Glechoma hederacea* is an invasive weed that has been reported to allelopathically stimulate the growth of *Raphanus sativus* (radish). If such a result could be consistently repeated, *G. hederacea* could have applications useful to farmers in sustainable agriculture who wish to avoid using commercial fertilizer. To determine if the addition of *G. hederacea* leaf to soil increases radish growth, one hundred radishes were grown in each of three treatments: control, leaves of *G. hederacea* added to soil, and juglone (extract of walnut tree) as an internal control. After thirty days, the weights of the radishes with and without leaves were measured, and were analyzed with a nonparametric Kruskal-Wallis test. For the weight of the radishes with leaves, the variation among treatments was significant ($p<0.0001$), but the treatment with the largest mean weight was the control (3.118g), followed by the *G. hederacea* treatment (2.13g), then the juglone treatment (1.346g). For the weight of the radishes without leaves, the variation among treatments was significant ($p<0.0001$) although there was no significant difference between the *G. hederacea* and juglone treatments ($p<0.15$ after Bonferroni correction). The results from this research indicate that the use of *G. hederacea* leaves does not significantly increase the growth of radishes but, in fact, inhibits the growth of *R. sativus*; however, this experiment was performed under slightly different conditions than the report upon which it was based, and any phytochemicals supposed to be responsible for the reported effects are unknown. Further experiments may demonstrate positive growth stimulation by *G. hederacea.*

Key Terms: Allelopathy
Botany
growth stimulation

**ES-11**

## Orographic Precipitation Regimes in the Western North Carolina Mountains

Michael Goldsbury (University of North Carolina at Asheville), Daniel Martin (University of North Carolina at Asheville), Advisor: Douglas Miller (University of North Carolina at Asheville)

The mountains of Western North Carolina (WNC) are especially prone to destructive rainfall-related natural disasters due to local topography. Significant weather events, such as the remnants of Frances and Ivan passing through the area in 2004, have caused substantial damage via mudslides and river flooding. These events can also happen on a smaller time scale from short-lived but intense thunderstorms. Additionally, flash flooding can happen without warning as the areas receiving heavy rainfall are often at high elevations upstream with very few observations. A lack of observations outside of valleys can yield misleading results given the high variability of rainfall towards higher terrain. The Precipitation Measurement Mission of NASA is funding a collaborative research project between Duke University and the University of North Carolina at Asheville which seeks to study these rainfall patterns using a high density rain gauge network in Haywood County, NC. Once analyzed, results from this research can be used by forecasters to better understand and apply prediction methods for WNC mountainous flooding events. The forecasting community can find these data especially helpful as they issue potentially life-saving watches and warnings for the area.

Key Terms: Atmospheric Sciences
Rainfall
Meteorological Instrumentation

**ES-12**

**Use of Lipophilic Fertilizers and Biosurfactants to Enhance Oil Degradation by *B. Cereus***

Natalia von Windheim (North Carolina School of Science and Mathematics), Advisor: Amy Sheck (North Carolina School of Science and Mathematics)

Biostimulation, the boost of indigenous bacteria's growth by the addition of nutrients or other deficient requirements, has emerged as a viable solution for the cleaning of oil spills. Uric acid and lecithin (nitrogen and phosphorus sources, respectively) have shown promise as biostimulation agents of natural origin in aquatic environments. The goal of this work is to observe whether the beneficial qualities that these environmentally friendly nutrients have demonstrated in the aquatic environment will also be proven when they are employed in soil and further when they are paired with an oil-degrading indigenous bacterium (*B. cereus*). For this study, kerosene contaminated soil was used and an uric acid and lecithin treatment was compared to a control, with no additional nutrients, as well as to S-200, a commercially available biostimulation agent. In each case, the contaminated soil was amended with B. cereus bacteria and, for non-control samples, with appropriate additional nutrients. Soil samples were removed for evaluation after 11 days of stasis and after 22 days. In each case, dichloromethane and water were used as solvents to extract liquid from the soil and the organic phase was separated from the aqueous phase. Subsequently, the organic phase samples were prepared for gas chromatography to quantify the degradation of hydrocarbons in the kerosene. Upon analysis of the chromatography data, it is anticipated that the S-200 treatment will cause more degradation than the control treatment and that the uric acid and lecithin treatment will cause more degradation than both the S-200 treatment and the control.

Key Term: Biodegradation

**ES-13**

## Effect of Thiols on the Environmental Fate of Silver Nanoparticles

Avi Aggarwal (North Carolina School of Science and Math), Andreas Gondikas (Duke University), Advisor: Heileen Hsu-Kim (Duke University)

Silver nanoparticles (AgNPs) are used in consumer goods for their antimicrobial properties, yet little is known about their environmental impact. When released into aquatic systems, their fate is influenced by organic ligands that may adsorb to particle surfaces and modify reactivity, causing particles to aggregate or dissolve into potentially bioavailable forms of silver. The capability for all of these transformations makes nanomaterials unique contaminants in the environment, unlike other organic pollutants. The thiol (S-H) ligand is likely to play a key role in the transformations of AgNPs because of its affinity for silver. We assessed the effect of thiols on citrate-coated AgNPs using glutathione (GSH), a low molecular weight peptide produced by organisms during oxidative stress and exposure to toxic metals. Aggregation of AgNPs was measured through time-resolved dynamic light scattering (DLS). Silver dissolution over time was determined by filtering batch suspensions to separate dissolved from particulate silver and measured with inductively coupled plasma mass spectroscopy (ICP-MS). Also, GSH concentrations measured with high pressure liquid chromatography (HPLC) and zeta potential measured with DLS were used to monitor surface modifications on the AgNPs. Results show that glutathione sorbs on the surface of AgNPs, reduces growth rate, and improves AgNP stability in solution, and moreoverall, that these processes occur simultaneously. This has implications for persistence of silver in aquatic systems and less bioavailability to organisms.

Key Terms: Environmental engineering
Nanomaterials
Heavy metal complexation

**ES-14**

## Characterization of Cellulose Pellicles by *Acetobacter xylinum* After Genetic Modification

Bryan Sumner (Knightdale High School), Advisors: Joel Pawlak (North Carolina State University) and William Graham (North Carolina State University)

Acetobacter xylinum is a gram negative bacterium identified in 1886 by A.J. Brown for its ability to produce cellulose. Most recent studies have identified Acetobacter Xylinum as not only a model organism for cellulose biosynthesis, but also as an alternative method to produce biomaterials for medical and industrial applications. Early genetic research performed on Acetobacter Xylinum was successful in the isolation of the genes responsible for the production of cellulose. These studies suggest that the wild type model of cellulose production by Acetobacter Xylinum would be a poor substitute for the production of biomaterials and extremely cost prohibitive. A more comprehensive approach involving genetic manipulation and the use of self assembling scaffolding motifs will provide a more efficient and effective way of studying Acetobacter Xylinum cellulose production with the goal of identifying a cleaner and more environmental friendly way of producing biomaterials.

Key Term: Microbiology

**ES-15**

## The Effects of Photodynamic Inactivation and UV Light in Water Disinfection Treatments

Asha Bethea (Hillside High School), Advisor: Aaron Young (University of North Carolina at Chapel Hill)

*Abstract not available.*

Key Terms: Water Disinfection
Environmental Science
Photodynamic Inactivation

**ES-16**

## An Investigation into the Applicability of Supervised Injection to American Cities

Trevor Thomas (Duke University)

Supervised injection facilities (SIFs) are clinics that aim to moderate the negative results of public drug use by providing a location at which drug users can inject under the supervision of medical professionals and with a supply of sterile equipment. As a result of the controversy surrounding supervised injection, there is only one site in North America called Insite, located in Vancouver, B.C. Insite was opened in 2003 and has been the subject of a myriad of scientific evaluations since then, all of which support its effectiveness at remedying the drug addiction problems plaguing Vancouver's Downtown Eastside. Consequently, there exists a large volume of data about North America's only SIF and the injection drug epidemic that afflicts the area. This investigation uses Insite and the Downtown Eastside as a template to judge whether supervised injection would be a successful public health technique in several American cities that struggle with similar drug abuse problems. The results of this analysis show that the US cities of San Francisco, New York City, and Baltimore could benefit most from SIFs, using Insite as a template.

Key Terms: global health
medicine
public health

**GS-01**

**Historical Atmospheric Lead Deposition Records In An Ombrotrophic Peat Pocosin: A New Record Form North Carolina**

Jingyuan Sun (University of North Carolina at Chapel Hill), Larry K. Benninger (University of North Carolina at Chapel Hill), Advisor: Larry K. Benninger (University of North Carolina at Chapel Hill)

Over the last several centuries, increasing industrial activities have introduced pollutant metal elements into the atmosphere on a global-scale. These trace elements enter sedimentary environments such as ombrotrophic “rain-fed” peatlands via precipitation and dry deposition. Studies of lead records in European peatlands have suggested that estimated lead flux not only relates to the historical anthropogenic activities in different times (i.e. the Industrial Revolution), but also acts as an indicator of local industrial activities involving leaded gasoline on shorter time scales. Records from Asia and North America represent quite different lead deposition profiles compared with the European ones for the same time periods. Peat samples were collected from a pocosin in the Croatan National Forest, located in the Coastal Plain of North Carolina. Bulk density and the activities of radioactive nuclides ($^{137}$Cs, $^{226}$Ra, $^{228}$Ra and $^{228}$Th) have been analyzed. Eventually, selected trace elements’ (Pb, Sr, Nd, V, Cu and Zn) accumulation rates and concentration profiles will be determined by ICP-MS. Also, lead isotope composition ($^{206}$Pb/$^{207}$Pb), typically used as a signal to trace local industrial histories such as the frequency of coal mining and burning, will be obtained from Thermal Ionization Mass Spectrometry (TIMS). $^{210}$Pb dating and weapons-fallout radionuclides will be measured by gamma counter and Alpha Spectrometry, which is used to establish the recent (last ~100 years) chronology of peat deposition. Based on this chronology, a historical record of metal elements deposition and Pb isotopic composition will be produced. This new record from southeastern North America will add another interesting perspective to previous peatlands studies.

Key Terms: Atmosphere
Geochemistry
Ombrotrophic Peat

**GS-02**

# Integrating Remote Sensing and GIS for Flash Flood Analysis in Jeddah, Saudi Arabia

N. Seth Rose (University of North Carolina Wilmington), Eman Ghoneim (University of North Carolina Wilmington)

Flash floods are a deadly and costly event that can be exacerbated in arid environments. On November 25, 2009, the city of Jeddah, Saudi Arabia, received more than 90mm of rainfall in a short period of time causing massive flooding, extreme destruction of property, and an indiscriminate loss of life. In December 2010, another severe flood event wreaked havoc on Jeddah. Such extreme events have been a catalyst into furthering the understanding of flash flood events and how to properly manage their sudden and destructive nature.

Jeddah is surrounded by eleven wadis that empty directly into the city. A hydrologic model driven by information on the topographic and drainage characteristics (SRTM data), precipitation (TRMM data), and land cover/use plus soil properties (satellite images and geological maps) was generated for the area. Utilizing HEC-HMS, hydrographs were produced to illustrate the response of the wadis to rainfall and aided in locating high risk areas.

Wadis have specific morphometric parameters which can explain the variations in risk. Analysis shows that there are several wadis that have high-risk outlets which can result in high velocity floodwater entering the city. These floodwaters can exacerbate the already poor environmental condition of the city.

Using remotely sensed imagery for pre and post rainstorm event shows that the standing water and destruction after the event validates the results produced by the research methodology.

Key Terms: Geographical Information Systems
Hydrological Engineering
Remote Sensing

**GS-03**

**Using Pb-210 As A Chemical Proxy For Particle Flux And Bioturbation Intensity Off The West Antarctica Peninsula**

Richard Taylor (North Carolina State University), Advisor: David J. DeMaster (North Carolina State University)

The distribution of the naturally occurring radioisotope, Pb-210, has been used on the West Antarctic continental shelf to establish the relative rates of particle flux to the seabed and biological sediment mixing on decadal timescales. Core samples of sediment were obtained from 5 stations along a N-S transect between 63°S and 68°S. The 5 stations exhibit a gradient in ocean temperature and sea ice cover, such that temporal variations in oceanographic conditions responding in part to global climate changes can be assessed from the distributions of radiochemical proxies. The Pb-210 data suggest that there is a 4 fold decrease in particle flux between 63°S and 68°S on a decadal timescale. In contrast, C-14 data suggest that sediment flux along this transect on a 1000-year timescale is 11 times greater to the north than at the southern stations. The enhanced particle flux at the southern stations on decadal timescales is consistent with increased sediment flux to the seabed in response to reduced sea-ice formation (as a result of decadal warming in high latitudes). On decadal timescales no apparent trend in biological sediment mixing intensity was observed in the Pb-210 data.

Key Terms: Geochemistry
Climatology
Radioisotopes

**IR-01**

## Geometric Morphometric Assessment of Pelvic Sexual Dimorphism in Pan, Gorilla, and Homo sapiens

Ronda R Graves (Stony Brook University), Advisor: Brigitte Demes (Stony Brook University)

Pelvic sexual dimorphism is closely linked to obstetric requirements in modern humans. Female pelvic morphology evolved to accommodate the delivery of neonates with head circumferences approximating the dimensions of the pelvic inlet, while human males and African apes of both sexes faced no such requirement. Early literature reported sexual dimorphism in the pelves of chimpanzees, but many recent studies refuted these initial claims. This study addresses these contradictions, using qualitative character states and three-dimensional landmark data to record and describe the shape of pelvic morphology specifically linked to obstetrics (the focus of most previous studies) and morphology that is presumably unrelated. Geometric morphometric techniques are used to assess a large sample of African ape and modern human pelves. Principal components analyses effectively separate chimpanzees and humans by sex, but gorilla specimens overlap in shape space. Canonical variates analyses successfully assign all specimens to the correct sex category for each species. Pairwise analyses of regression coefficient vector angles suggest significantly different patterns of variation between humans and chimpanzees and between humans and gorillas, but not between chimpanzees and gorillas. Character states for five qualitative traits used in forensic studies to sex human pelves are considered in African ape pelves. Analysis of these character states fail to separate male and female apes. Many of the sexually dimorphic characters identified in African ape pelves appear to be unrelated to parturition, requiring further examination in the context of phylogenetic history and functional morphology to elucidate the underlying explanations for their presence.

Key Terms: Physical Anthropology
Anatomy
Primatology

**IR-02**

## Toxicological Effects Of Nicotine In Breast Cancer Cells MCF7 In The Perspective Of MicroRNAs

Dongliang Chen (East Carolina University), Advisor: Baohong Zhang (East Carolina University).

Nicotine, the major alkaloid present in tobacco, can reach the pharmacologic concentrations of 90 to 1000nM in the bloodstream of smokers and was found to promote the progression of human breast and lung cancers, although it was once thought to cause addiction only. However, the exact molecules and signaling network(s) involved in nicotine exposure remain largely unknown. My research used human breast cancer cell line MCF-7 as a model to study the toxicological effects of L-nicotine and the molecular mechanism of L-nicotine treatment. Our result shows that this environmental toxicant can inhibit cell growth at a high concentration (1mM) and regulate the expression of 78 microRNAs. Dysregulation of five microRNAs under nicotine treatment was also confirmed by real-time quantitative PCR. Among these microRNAs, two members of the same microRNA family (miR-1274a & miR-1274b) were up-regulated by nicotine treatment in dose-response and time-response pattern. Among the 236 predicted targets of miR-1274a and 128 predicted targets of miR-1274b, there are transcriptional factors and tumor necrosis factors, implying that miR-1274 family members may be an important players in the network that responds to toxicity of L-nicotine. This work constitutes the first study in the toxicological effects of nicotine in the perspective of microRNAs.

Key Terms: toxicology
nicotine
microRNAs

**IR-03**

## Synthesis and Characterization of Elastin-Like Polypeptide-Polyelectrolyte Conjugates for Tissue Engineering Applications

Paul Turner (University of Mississippi), Adivisor: Amol Janorkar (University of Mississippi), Sponsor: George Moll (University of Mississippi)

Obesity and liver metabolic disorders are growing concerns across the United States, contributing to fatal pathologies such as stroke, atherosclerosis, and progressive liver failure. Attempts to construct *in vitro* models simulating metabolic dysfunction have failed due to brief survival of explanted adipose and hepatic cells and lack of physiologically-relevant behavior believed related to lack of appropriate cellular organization. In the current study, elastin-like polypeptide (ELP) was used as a substrate material due to its biocompatibility, tailored physiochemical properties, and susceptibility to chemical modification. Modifying charge on ELP molecules via conjugated polyelectrolytes was found to induce cultured pre-adipose and hepatic cells to form three-dimensional spheroids similar to histological organization found *in vivo*. We hypothesized primary cells arranged into three-dimensional spheroids will show enhanced activity and survival versus those grown on conventional two-dimensional tissue culture polystyrene or collagen substrates. Polyethyleneimine (PEI), a polymer that adopts positive charge at physiological pH, was covalently bound to ELP by carbodiimide coupling reactions and characterized using quantitative fluoraldehyde assay (OPA), atomic force microcopy (AFM), and Fourier-Transform Infrared Spectroscopy (FT-IR). The reaction mechanism was optimized to favor maximum molecular conjugation of ELP to PEI. Tissue culture polystyrene plates were coated with ELP-PEI's and then seeded with rat hepatoma (H35) cells whose morphological response and organization were assessed with optical techniques. Rat hepatoma (H35) cells organized into spheroids within 12 hours and maintained architecture while growing to almost 90 um diameter within 5 days. Our results opened the way to future studies of function and spheroid growth.

Key Terms: Tissue Engineering
Biomedical Tissue Culture
Hepatic Spheroid Tissue Culture

**IR-04**

## Branching Processes and Mean Reversion in Financial Market

Sheng-Jhih Wu (North Carolina State University), Advisor: Min Kang (North Carolina State University)

Branching processes are ubiquitous into our daily life. Incorporating randomness in the propagation, branching process is a natural mathematical model depicting population evolution in which individuals reproduce according to a common probabilistic law. The problems concerning the generation size in the branching system are of essential importance as they characterize the dynamics of this random system chronologically. It is of special interest to explore the remote future of the branching system. This study investigates the asymptotic behavior of the rare event on how much the ratio of successive generation sizes deviates from the mean.

On the other hand, the asymptotic behavior of the ratio described above is useful in the study of financial products and their return. A previous study showed that stock price could be modeled by a Poisson randomly indexed branching process in such a way that the random generation size could be interpreted as stock price. This model successfully captures certain key features such as the discrete stock price fluctuation, the possibility of bankruptcy of the firms and the inverse relationship between the variance of return and the initial stock price. The result of the large-time behavior obtained in this study shows that the probability that the rates of return deviating from the estimated average rate decays exponentially fast. Therefore, it provides the evidence of a well-known phenomenon predicted by many financial experts, namely "mean reversion" in financial market.

Key Terms: Mathematics
Finance

**IR-05**

## Controlling Interconnected Silver Network Structure in Sol-Gel Nanocomposite via Shrinkage-induced Stress

Chi-Kai Chiu (North Carolina State University), Tsan-Yao Chen (North Carolina State University), Yong-Jae Choi (North Carolina State University), Tsan-Lang Lin (National Tsing Hua University), Advisor: Tzy-Jiun M. Luo (North Carolina State University)

Interconnected silver nanostructures at the surface and interior of nanocomposite sol-gel materials have been synthesized by heat-treating sol-gel nanocomposite containing 10~14 wt% silver ion and minimum of 34 wt% polyvinylpyrrolidone and polyethyleneglycol. These hybrid materials were initially transparent after drying, became dark-glassy when exposed to light, and then turned into silver metallic color upon heat-treated at 160˚C. The silver interconnected nanostructure was found to nucleate at the internal defect surfaces and developed into interconnected structure. This interior silver-covered area was shown to be related to shrinkage-induced stress induced by different temperature and vacuum drying treatments. We found the interior silver-covered area and its interconnectivity measured as bulk resistivity both increases with the surface stress, whose value was estimated by Vickers hardness measurement. The formation of silver crystal structure within nanocomposite was confirmed by XRD and EDX. AFM and SEM images show that the formation of silver network is due to the unique structure of polymer-blended silica matrix. The ability to utilize shrinkage-induced stress of sol-gel materials to control interconnectivity of metals within nanocomposite may prove that solution method is an easy and scalable approach to create porous materials for micro-electronics and fuel cell applications.

Key Terms: Materials Science and Engineering
Nanocomposite
Sol-Gel

**IR-06**

## Polar Synchronization: A Mechanism For The Complexity Of Climate Variability During The Last Ice Age

Yue Zhang (University of North Carolina at Chapel Hill), Advisor: Jose A. Rial (University of North Carolina at Chapel Hill)

The term synchronization is used here to describe the nonlinear frequency and phase locking that occurs when two or more coupled oscillators adjust their (initially different) rhythms to a common frequency and constant relative phase. In complex biological and ecological systems synchronization is a widespread phenomena, and some of the most intriguing areas of research in neuroscience include the study of synchrony among far away regions of the brain, and its behavioral meaning. Available evidence suggests that synchronization is also a common process in the earth's climate, but research on detecting its presence and documenting its consequences is still at a very early stage. Though synchronization has mainly been studied in relatively low-dimensional discrete systems or networks, the possibility of similar dynamics occurring in extended spatiotemporal systems such as the earth's climate could open an important new interdisciplinary area of research. The climate system is complex, whatever our definition of complexity may be, but if that complexity can be reduced in some measure by detecting and recognizing long-range symmetries caused by synchronization, our understanding of climate dynamics would greatly benefit. If applied to the history of climate, as proposed here, detection of synchronization among paleoclimate time series can likewise benefit climate science by explaining hitherto poorly understood processes.

Key Terms: Complex System
Synchronization
Abrupt Climate Change

**IR-07**

## A Comparison of the Gastrointestinal Microbiota Associated with Primate and Carnivore Species

Erin McKenney (North Carolina State University), Melissa Ashwell (North Carolina State University), Joanna Lambert (University of Texas at San Antonio), Advisor: Vivek Fellner (North Carolina State University)

Bacteria in the gastrointestinal tract contribute to host health by digesting fiber and other inaccessible food components. This project aimed to quantify the microbial populations and fermentation profiles of three primates and one carnivore which display different feeding strategies across the omnivorous spectrum. Fecal samples were collected from 3 gorillas (folivores), 12 chimpanzees (frugivores), 17 Hamadryas baboons (omnivores), and 10 binturongs (carnivores that have evolved to eat mostly fruit). Each species was fed a different, fixed, standardized diet for fourteen days prior to collection. Fresh fecal samples were pooled within species and blended with buffer; inoculums were added to 1g of appropriate ground dietary substrate, sealed and incubated at 37°C. Methane concentration and short chain fatty acids (SCFA) were measured after 24 hours, and all fermentation products were analyzed using the Proc Mixed procedure in SAS. Microbial DNA was extracted from individual fecal samples frozen at -70°C, and combined into standardized pools for each host species. A region of the bacterial *cpn60* gene was sequenced to identify microbial species by comparison with the GenBank database, and biodiversity indices were calculated to compare microbial population composition across host species. Phylogenetic trees were compiled using the PHYlogeny Inference Package. Significant differences in SCFA ($p<0.0001$) and methane ($p<0.001$) concentration were observed across species. Molecular analysis suggests that microbial biodiversity increases with dietary fiber and the complexity of nutritional niches *in situ*. This link between patterns of energy usage and host-specific endosymbionts agrees with previous studies of humans, non-human primates, and other hindgut fermenters.

Key Terms: gastrointestinal microbiota
fermentation
diversity

**IR-08**

**Identification of Host Factors to Block Vascular Leakage when Exposed to SEB using siRNA Approach**

Oladimeji Abegunrin (Howard University), Allison Hoke (USACHER, Frederick,MD)
Advisors: Dr. Aarti Gautam (USACHER, Frederick, MD), , Dr. Rasha Hammamieh (USACHER, Frederick, MD), Dr. Marti Jett (USACHER, Frederick, MD), Agnes A. Day (Howard University, Washington D.C.)

*Staphylococcocal* enterotoxin B is a toxin produce by the bacterium *Staphylococcus aureus* which induces an intense and rapid release of cytokines such as interferon-γ, interleukin-6, and tumor necrosis factor-α as well as histamine and leukotriene release from mast cells. The induced "cytokine storm" results in damage, vascular leakage, to the endothelium which acts as a barrier controlling leukocyte trafficking and the passage of materials into and out of the bloodstream. In the current experiment the human lung microvascular endothelial cell (HMVEC-L) transfected with siRNA were treated with peripheral blood mononuclear cells (PBMCs) infected with SEB at 4hours incubation and overnight incubation. Initially, viability of PBMC at a concentration of $1 \times 10^4$ and $1 \times 10^5$ cells/well after infection with varying concentrations of SEB (0, 1, 10, 100, 1000, 2000, and 4000 ng/ml) was performed. The results showed less than or exactly 20% cytotoxicity of SEB to PBMC ($1 \times 10^4$ cells/well) regardless of SEB concentration after an overnight incubation. PBMC without SEB treatment had very minimal, less than 20% cytotoxic effect on HMVEC-L at a 1:1 ratio of PBMC to HMVEC-L cell concentration. Vascular permeability of HMVEC-L cell monolayer after treatment with PBMC ($1 \times 10^4$ cells/well) shows a gradual increase at all concentrations of SEB. These results suggest that PBMC at concentration of $1 \times 10^4$ cells/ml treated with SEB induces vascular permeability in HMVEC-L cells at a concentration of $1 \times 10^4$ cells/well *in vitro*. One way ANOVA analysis of the results further indicates that the means are significantly different with a p-value $<0.0001$. Transfection of HMVEC-L cells with selective siRNA involved in vascular permeability and analysis by real-time PCR shows significant knockdown of these genes. This further indicates that siRNA is a novel approach, with significant possibilities as a therapeutic treatment against vascular leakage induced by SEB.

Key Terms: Microbiology
Immunology
Cellular and Molecular Biology

**IR-09**

## Statistical Analysis of Microarray Gene Expression Data from a Mouse Model of Toxoplasmosis

Shrikant Pawar (Western Kentucky University), Research Advisor: Cheryl D. Davis and Claire A. Rinehart (Western Kentucky University)

Toxoplasmosis, caused by the protozoan parasite, *Toxoplasma gondii* is a major cause of morbidity and mortality in patients with AIDS and an important cause of miscarriage, stillbirth and congenital disease in newborns. Previous studies have provided evidence that dietary supplementation with vitamin E and selenium is harmful during experimental toxoplasmosis in mice, whereas a diet deficient in vitamin E and selenium results in decreased numbers of tissue cysts in the brain and dramatically reduced brain pathology. The overall goal of the present study was to determine the impact of dietary supplementation with antioxidants on gene expression in the brains of non-infected mice and in mice infected with *T. gondii* using microarray analysis. RNA was isolated from the brains of C57BL/6 mice, and an Agilent Oligo Whole Mouse Genome Microarray (Agilent Technologies, Inc.) was performed. A total of 48 chips were normalized by Z ratios and the Data Driven Harr Fisch Normalization methods. Differentially expressed genes were identified by applying thresholds to identify significant values and the results were compared between the normalization methods. These differentially expressed genes and their respective fold change ratios were used in Ingenuity Pathway Analysis (IPA) software to analyze the pathways involved with these genes.
These identified pathways associated with differentially expressed genes are very important in determining the impact of dietary supplementation with antioxidants on gene expression in the brains of mice infected with *T. gondii* and specific alterations of those pathways can help us to reduce the harmful effects of the same in future.
Support from the National Center for Research Resources NIH Grant Number 2 P20 RR-16481 and from the WKU Bioinformatics and Information Science Center is gratefully acknowledged.

Key Terms: Bio informatics
Immunology
Cell and Molecular Biology

**IR-10**

**Survey of Drug Take-Back and Disposal Programs in the U.S.**

Donald Lefeber (American College of Acupuncture and Oriental Medic), Advisor: Mathew C. Mireles (Community Medical Foundation for Patient Safety**)** and Joshua Chang (Northwestern University)

**Objectives:** The *Annual Survey for Drug Take-Back Programs* gathered data on location, type of collection and destruction methods, classification system, and purposes of existing drug take-back programs in the U.S. to identify and measure the progress of drug take-back initiative.

**Methods:** In 2008 and 2009-2010, a one-page survey requesting information about drug take-back activities was sent electronically to organizations collecting and disposing unused and expired medicines (UEMs) in 2009 and 2010. Organizations were contacted through selected listservs: pharmwaste, substance abuse, patient safety, etc.

**Results:** 66 organizations responded to the 2008-2009 survey and 492 to the 2010 survey, a 645% increase. Thirty states have 492 take-back programs in operation. Collection schedule of the programs included: Ongoing/Continuous (76%), Others (10%), One-Time Event (7%), Yearly (4%), Monthly (2%), Quarterly (1%). Collection method included: Drop-off at Pharmacy (53%), Police Station (19%), Event(s) (17%), Others (8%), Direct Mail Back (3%). Primary Destruction Method for UEMS were: Incineration Only (98%), Landfill (1%), Incineration and Landfill (1%). UEMs were classified as: Hazardous Household Waste (40%), Non-hazardous Household Waste (33%), Don't Know (12%), Medical Waste (7%), Others (5%), Solid Waste (3%). The purpose of the programs was for Environmental Protection (18%), followed by Community Service (17%), Home Safety (17%), Public Safety (17%), Crime Prevention (15%), Patient Safety (14%), and Others (2%).

**Conclusions:** Responses from the *Annual Surveys* provided critical data on community-based drug take-back programs designed to effectively and safely deal with the steady accumulation of UEMs at home. Promoting public safety and patient safety is imperative.

Key Term: Patient Safety

**IR-11**

## Validation of a Pre-Clinical Mouse Model for Renal Cell Carcinoma

Sharanya Sivanand (University of Texas at Dallas), Blanka Kucejova, Samuel Peña-Llopis, Payal Kapur, Hong Zhao, Xian-Jin Xie, Noelle Williams, James Brugarolas (University of Texas Southwestern Medical Center)

While surgery is the primary mode of treatment for renal cell carcinoma (RCC), overall survival for patients with metastatic disease is very low. Primarily due to lack of efficacy, most drugs entering clinical trials for cancer treatment fail to receive FDA approval. Current model systems, generated using cell lines, may compromise the tumor biology due to extensive in vitro culturing. A pre-clinical model that mimics the genetic complexity of RCC can be valuable to test new drugs. To address this, 136 unadulterated patient tumors were implanted orthotopically in mice, generating tumorgrafts. H&E and genetic studies compared tumors derived from tumorgrafts with corresponding patients. Clinically used drugs, sirolimus, sunitinib, and erlotinib were evaluated in 9 tumorgrafts at pre-determined concentrations based on PK studies, and pathway inhibition was assessed by immunohistochemistry. 16 established stable lines showed retention of tumor morphology and architecture. Analysis of 94 tumors showed correlation between tumor nuclear grade, tumor extension, lymph node involvement and engraftment. Treated cohorts showed reduction in overall tumor volume. Tumorgrafts retained most mutations found in the primary tumors and the vast majority of chromosomal amplifications and deletions. Gene expression profiles of the tumors and tumorgrafts of each patient clustered together after subtraction of the tumorgraft component, indicating tumor heterogeneity and retention of gene expression despite serial passaging. The value of the proposed model lies in using fresh tumor fragments to mimic the biology of RCC. Retention of the histological and genetic characteristics of the tumor provides a relevant platform to test drugs.

Key Terms: Renal cell carcinoma
pre-clinical model
tumorgraft

**IR-12**

## Control Methodology In Organic Residue Analysis Using FT-IR Spectroscopy

D. Kyle McCandless (East Carolina University, Dr. Laura Mazow (East Carolina University), Dr. Anthony Kennedy (East Carolina University, Susanne Grieve (East Carolina University, Kim Tillapaugh (East Carolina University)

In this poster, the author raises concerns about the impact of contamination in organic residue analysis projects of archaeological materials. Concerns with contamination and subsequent methodological controls are rarely mentioned in the archaeological literature, but could have profound effects on the results that are obtained in research involving residue analysis. Through an organic residue analysis project at East Carolina University, a set of control experiments were developed, with the goal of determining the impact of contamination introduced by the sample methodologies used during the original project. These experiments attempt to isolate and identify the sources of potential contamination in the sample methodologies, while building a database that will be used for comparative analysis of data from collected samples. Preliminary results suggest that almost all of the sampling materials (i.e. swabs, solvents, and storage containers) have introduced analytically significant contaminants into the control samples. The results of the control experiments further suggest that previously collected samples will include some amount of contamination from sampling methodologies, and storage and shipping materials which may impact data analysis. The results of these experiments should allow the project to develop a successful sample collection methodology by ruling out unsatisfactory materials and determine a collection methodology that introduces the least amount of contaminant residues into samples. This case study serves as a means of addressing the greater issue of contamination in residue analysis projects, particularly those using Infrared (IR) spectroscopy, a method that is becoming increasingly common in archaeology for the analysis of organic residues.

Key Terms: Organic Residue Analysis
Spectrometry/Spectroscopy
Archaeology

**IR-13**

## Evaluating Spatial Distribution of Oscillatory Potentials in Normal Rat Eye for Functional Assessment of Deformity

Maryam Hanif (University of Illinois-Chicago; Neural Engineering Vision Laboratory)
Advisor: John Hetling (University of Illinois-Chicago; Neural Engineering Vision Laboratory)

Lighthouse International has reported there are more than 161 million people in the world who have visual impairment. Not only eye trauma, but many illnesses and diseases affect the eye; which if not diagnosed and treated soon, can lead to permanent blindness. Therefore, it is crucial that a visualization system be capable of detecting these defects; even more useful would be the system's ability to provide early stage detection of any defects in the eye. The Neural Engineering Vision Laboratory at the University of Illinois has developed a new diagnostic tool, the multi-electrode electroretinogram (meERG), to provide a map of retinal health.

The rising edge of the b-wave on the ERG signal shows high frequency wavelets, called Oscillatory Potentials (OPs), which have been used to study different retinal disorders. meERG used in this research was made of PMMA and adapted to the rat eye, with 25 electrodes spatially distributed. The ERG waveforms were spatially plotted and analyzed using Microsoft Excel. The purpose of this study is to compare and analyze ERG signals averaged spatially and temporally. Variation in the OP signal based on location and time allows detection and functional assessment of deformity at the specific area of the retina. Furthermore, since the exact origin of OPs is not completely understood, comparing the acquired data with histology studies would provide further understanding of the mechanism of generation of these signals.

Key Terms: ERG (electroretinogram)
OP (Oscilatory Potentials)
Signal Processing

**IR-14**

## A Physico-chemical Perspective of Dendritic Polymers for Environmental Remediation

Priyanka Bhattacharya (Clemson University), Pengyu Chen (Clemson University), Advisor: Pu-Chun Ke (Clemson University)

Our research offers a fundamental understanding of the physico-chemical properties of highly branched dendritic polymers and their capability in detecting environmental chemical species, namely, transition metal ions, polyaromatic hydrocarbon phenanthrene, membrane foulants like humic acid, and environmentally discharged nanoparticles.
Specifically, we characterized the dynamics and stoichiometry of phenanthrene (Phe) binding with poly(amidoamine) (PAMAM) dendrimers, using the technique of fluorescence resonance energy transfer. Using a novel physical scheme based on the surface plasmon resonance of a gold nanowire substrate we demonstrated submicromolar level detection of copper. An experimental study on the physical chemistry of a tri-functional *tris*-dendrimer for a remarkable hosting and detection capacity at the nanomolar level towards various chemical species, and a molecular dynamics simulation on the binding capacity of poly(amidoamine) (PAMAM) dendrimers for humic substances will be discussed. In addition, the thermodynamics of binding between environmentally discharged nanoparticles and dendrimers will be addressed.
Through an intermingling of physics, chemistry, biology and mathematics, our research aims at providing innovative solutions for improving the state-of-the-art of water filtration and environmental remediation, including the recovery of the Gulf region from the oil spills, as well as exciting dendritic applications in the fields of supramolecular chemistry, soft matter, chemical engineering, and nanomedicine.

Key Terms: Physics
Chemistry
Environmental Remediation

**IR-15**

## *Salmonella* and Human Foodways in North Carolina

Edward Bennett (University of North Carolina, Chapel Hill), Advisors: Fatimah Jackson (University of North Carolina, Chapel Hill) Richard Marciano (University of North Carolina, Chapel Hill)

Food consumption patterns and agricultural practices have changed dramatically over the last century. Prior research demonstrates anthropogenic activity influences the evolution of pathogenicity among *Salmonella* serovars, and predicts an inverse relationship between socioeconomic status (SES) and incidence. Modern agricultural practices facilitate the evolution of virulence factors through the creation of novel host environments and an increase in available routes for transmission. This research is a validation study of the CDC's estimation for case-incidence of *Salmonella* in low SES populations of North Carolina.

Initial data from the North Carolina DHHS active surveillance system suggest strong seasonal periodicity with an upward trend in incidence and a positive relationship between SES and incidence of *Salmonella*. Bayesian spatiotemporal analysis determining the overlay of covariates with incidence by county will help determine noise contributing to this trend. In addition, we will be using respondent driven sampling to collect transmission ethnographies of individuals affected by *Salmonella* and determining how improvements to instrumentation may contribute to an upward trend.

In the morass of confusion generated by the politics of food, food knowledge, including safe handling and preparation, has declined precipitously in low SES communities. *Salmonella* has low associated mortality. However, low SES populations are underserved and frequently lack access to medical care. This lack of access increases the potential for loss of productivity, increasing and entrenching poverty, and amplifying the risk of transmission.

Key Terms: Salmonella
Epidemiology
Anthropology

**IR-16**

# The Effect of Silica on Plant Hormones in Well Watered and Osmotically Stressed Cucumber Plants

Alyson Bradshaw (University of Florida), Advisor: Kristine Callis (University of Florida)

Drought stress decreases growth and productivity of a plant and can ultimately lead to mortality. Additionally, plant hormones, such as ABA, zeatin, auxin, and gibberellins change when plants are under osmotic stress. Previous works have shown that silica acts as a defense against drought stress by aiding in the retention of water and by increasing the rigidity of the plant. However, the rigidity alone does not account for all the benefit afforded to the plant by silica. Therefore, we looked at the effect of silica on plant hormones under drought stress to see if silica would reverse the effects of drought stress on plant hormone levels by decreasing the amount of ABA, increasing the amount of IAA, and increasing the amount of zeatin and gibberellins. Cucumber plants (*Cucumis sativus*) were grown in pots under different osmotic conditions and were also treated with or without silica. Treatment groups included: silica treated plants (2 mM) with normal water levels, silica treated plants (2 mM) under drought stress, untreated plants with normal water levels, and untreated plants under drought stress. The hormone levels of each different treatment were then assessed using vapor phase extraction, and compared to the controls.

Key Terms: Plant Hormones
Drought Stress
Silica

**IR-17**

## How a nearby phospholipid headgroup affects anion recognition

Ashley N. Wercholuk (East Carolina University), Ber Xiong (East Carolina University), Danielle M. Jessen (East Carolina University); Advisors: William E. Allen and Andrew L. Sargent (East Carolina University)

Defective transport of small anions like chloride and bicarbonate across cell membranes lies at the root of several diseases. In cystic fibrosis, for example, thick mucus in the lungs arises from poor flow of $HCO_3^-$ out of the epithelia. Synthetic systems that can promote diffusion of anions may therefore have potential as drugs. Some artificial transporters operate by shielding the ions within a nonpolar "coat," yielding complexes that can passively penetrate the hydrophobic bilayer core. Others allow anions to hop among electrophilic sites in a large membrane-spanning assembly. Regardless of the mechanism of transport, all such systems must recognize their target anions near the aqueous interface, which is an environment rich in charged phosphate and alkylammonium units from the lipid headgroups.

This project measures how such phosphocholine (PC) headgroups affect the strength and selectivity of anion recognition. Fluorescent phospholipid analogues containing an anion-binding urea group were prepared. In one of the systems the urea lies just four bonds away from the PC, while in the other, it is far removed. Fluorescence titrations in dichloromethane solution show that the presence of a *distant* PC enhances binding strength ($K_{assoc}$) with $Cl^-$ and $NO_3^-$ by a factor of 20 or more, while $K_{assoc}$ values for $HCO_3^-$ and $H_2PO_4^-$ increase much less dramatically. A *nearby* headgroup renders the equilibrium constants too high to determine accurately. DFT calculations suggest that tight interactions occur in cases where both an anion and its countercation can associate with a lipid analogue.

Key Terms: Molecular Recognition
Membrane Transport
Organic Synthesis

**IR-18**

## Activation of Kinesin-1 Through RanBP2 Domain Coordinates Cystosolic Localization

Jason C. Del Rio (University of California, Irvine), Michelle Mattson (University of California, Irvine), Suvranta Tripathy (University of California, Irvine), Steven P. Gross (University of California, Irvine)

The microtubule based motor, kinesin, is essential for cellular transport and organization. However, exactly how kinesin function is regulated is still relatively unexplored. Ran Binding Protein 2 (RanBP2), a regulator of the Ran-GTPase cycle, is an integral component of nuclear transport. Recently, it has been shown to bind to kinesin's tail domain and increase kinesin's ATPase activity. This brings into question whether the increase in ATPase activity is functionally important? That is, does it reflect increased single-motor velocity, more active motors, or an increase in futile hydrolysis? To address this, I plan a two-pronged set of experiments. I have started to manufacture the kinesin-binding segment of Bovine RanBP2 in *e. coli*. Once expressed, I will test its effect on kinesin function *in vitro*, using both recombinant tail-less and full-length purified kinesin. I will determine whether RanBP2 alters single-molecule force production, velocity, and travel distances using an optical trap. Furthermore, through microtubule affinity experiments, I will verify whether more kinesin motors are active in the presence of RanBP2. Lastly, to evaluate the role of Ran BP2 in regulating transport *in vivo*, I will carry out RNAi experiments to decrease RanBP2 dosage and quantify what effects this has on intracellular cargo motion. Combined, these experiments will both help understand regulation of transport and alteration of kinesin function. Further, because RanBP2 is critical for cell cycle regulation, understanding how microtubule-mediated transport is altered may shed light on the functional coordination of these two important processes.

Key Terms: Kinesin Regulation
Microtubule Based transport
Biochemistry

**IR-19**

## Economic Feasibility of Solar Water Pump

Akua S. Akuffo (NC A&T State University) and Chris Duncan (NC A&T State University), Advisors: Osei Yeboah and Frank Yeboah (NC A&T State University)

Agriculture is a production-oriented sector and energy is an important input. Various energy sources including petroleum-based fuels and electricity are used to power crop dryers and irrigation equipment. While many irrigation systems are gravity flow systems requiring little energy, other irrigation systems operate using energy. In the 2003 USDA Farm and Ranch Irrigation survey, it cost $953 million to irrigate 24.1 million acres at an average cost of $39.50 per acre using electricity.

These high costs can be reduced with solar pumps. Initial cost is high; however, it offers the best solution for irrigation in terms of long-term cost. An economic feasibility analysis similar to Cox et al, (2006), is conducted to compare the viability of solar-powered water pumps over electric, using data from a representative farm in North Carolina. The power of the electric pump is 1.5Kilowatts with pumping hours/month of 150/30 days, resulting in total energy used of 225KWhr. With electricity rate of 5cents/KWhr, monthly electricity consumption expenses estimated to be $11.25. Using a 20-year life span for the solar with initial cost of $2,000.00 (Lighthouse Solar, 2011) and a private interest rate of 5% (Business Assessment, NC Dept. of Revenue, 2011), and no maintenance cost- since there are no storage batteries, the net present value (NVP) of ($2,000.00) for solar pump was determined. NVP of ($2,135.55) for electric pump was also determined with initial cost of $1,179.00 (L.L.Bean, 2011) for a life span of 10 years with ($959.56) annual expenditure. For easy comparison, a new electric pump is installed year 11 with same initial cost, life span and annual expenditure. A total NVP of ($4,277.07) was determined. The results indicate that the savings on solar pump is twice that of the electric pump.

Key Terms: Economics
Engineering

**IR-20**

## Do Heat Waves Impact Ground Level Ozone Levels and Increase the Threat to Public Health?

Holly Sweeney (North Carolina State University), Tracey D'Angelo (North Carolina State University), Lorelei Zumbrunnen (North Carolina State University), Advisor: Bill Hunt (North Carolina State University)

Heat waves are currently defined as extended periods of unusually hot weather. It is known that these periods of time can affect us in many ways, such as worsened drought conditions, decreased animal production, increased hospital admissions, and increased energy use (e.g. air conditioning). It is also known that ground level ozone exposure can lead to respiratory problems and high levels can damage vegetation and ecosystems. The relationship between heat waves and ground level ozone is currently not well known. Our client from the North Carolina State Climate Office has asked us to examine heat wave occurrences in North Carolina for the past 40 years, specifically studying their intensity, frequency, and length. We will then examine the relationship between these heat waves and ground level ozone levels during the same time period, focusing on the months of April through September, North Carolina's ozone season. We will analyze climate and ground level ozone data from seven stations across North Carolina covering the coastal, piedmont, and mountain regions. Our analysis will provide information to make more informed decisions about public health resulting from heat waves and ground level ozone concentrations.

Key Terms: heatwaves
ozone
public health

**IR-21**

## Tracing Origins Through Sequence Matching

Elliot Elias (SUNY Plattsburgh), Advisors: Nancy Elwess (SUNY Plattsburgh), Salvador Gutierrez (SUNY Plattsburgh)

The motive behind this project was to construct a versatile and unique program that would allow the user to identify a sub-sequence within larger sequences in a database. The importance of the program is for the identification and classification of DNA sequences. A statistical analysis of the variations of the sub-sequence would help identify possible links between the different human races found in geographical sections of our world.

To approach this problem, the Needleman-Wunsch and Smith-Waterman algorithms were used for scoring. Selections of sequences were based on achieving a reasonable score that identified that the sub-sequence was matched correctly. String matching was the main tool used for this project, with alignment scoring applied for selection.

Using this approach, 141 variations of the control sequence were identified. Most of the sequences contained the control sequence, thus verifying the statistical accuracy of the project. The remaining were one to two point mutations. Without knowing the identity of the human sequence, the designed program allowed for identification of possible races indicating the origin point of the sequence based on the mutation identified and previous data.

The results of the analyses could certainly help to identify the racial background of a DNA sequence as well as possible migration patterns of humans throughout history. Ancient remains may be identified by mutations in their DNA. With the right amount of data and the proper information on the sequences to be queried, it may be possible to answer questions that in the past have been unanswerable.

Key Terms: Bioinformatics
Sequence Matching
Genetics

**IR-22**

## Coevolution of a Pentatricopeptide Repeat (PPR) Protein and the Editing Site Target

Azieb Ermias (University of California, Irvine), Karolyn Giang, Dr. Michael Hayes, Dr. R. Michael Mulligan (University of California, Irvine)

RNA editing is a post- transcriptional modification that employs the use of pentatricopeptide repeats (PPR) proteins to correct mutations on the mRNA by making a C-to-U conversion. PPR genes are known to be involved in many RNA processing reactions in plant mitochondria and chloroplasts including RNA cleavage and RNA editing. In this study, the coevolution of an editing site target and the editing PPR protein required for editing was examined in the Brassicales. The *otp80* gene is a PPR gene that is responsible for editing chloroplast *rpl23* transcripts. The presence of *rpl23* editing sites was determined by sequence analysis of PCR fragments from chloroplast genomic DNA and complementary DNA (obtained from reverse transcriptase and PCR reactions) from plant species. Comparison of the DNA sequence and the percent of C-to-U conversion were used to determine the extent of editing. In addition, *otp80* gene sequences were determined by amplification of the nuclear gene sequence by PCR. These results demonstrated that variation in editing site conversion exists between the plant species from the Brassicales typically with 60% to 80% conversion. In addition, several species exhibit editing site loss through substitution of an edited C with a genomic T. PPR genes have a characteristic repeat structure, and analysis of *otp80* gene sequences demonstrated that some species showed distinctive changes in the protein. These results indicate that a major structural change in PPR proteins occurred in the evolution of some branches of the Brassicales; however these taxa retained the ability to edit the target site.

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**IR-23**

## An approach to validating mRNA targets of brain-specific microRNAs

Heidi Klumpe (North Carolina State University), Alex Chung (University of Texas at Austin), Aaditya Nagaraj (University of Texas Southwestern), Niculin Herz (University of Texas Southwestern), Advisor: Joachim Herz (University of Texas Southwestern)

MicroRNAs are ~20 nucleotide non-protein-coding sequences often contained in the introns of host genes. Processed miRNA binds to the 3'-untranslated region of an mRNA transcript; this leads to the increased instability of the transcript, which results in a decrease in gene expression. Unlike siRNA, imperfect complementarity characterizes miRNA binding to mRNA; miRNA can thus influence smaller and more precise changes in tissue- or time-specific protein levels as well as contributing to disease when they become unregulated. We hypothesized that certain brain-specific miRNAs (218, 744, and 744*) could be components of pathways playing a role in the regulation of learning, memory, and brain disease. Using *in silico* prediction tools, miRNAs were selected which are expressed alongside their brain-specific host genes and which target components of the Reelin signaling pathway. In the human brain, this pathway has importance in directing neuronal migration during development as well as influencing synaptic plasticity in adulthood. A pMiR-Report plasmid was cloned to contain the various proposed target sequences, downstream of a *luciferase* gene, and then co-transfected in HEK293 cells with a mimic or vector containing the miRNA sequence. Subsequent luciferase assays can quantify the down-regulation of the target gene as a result of miRNAs binding to their target genes. This project validated this approach as a tool for verifying *in vitro* a predicted relationship between a miRNA and its target gene.

Key Terms: Molecular Genetics
Biotechnology
miRNA

**IR-24**

## DNA Analysis in a Nanofluidic Device

Elizaveta Davies (Santa Barbara City College), Travis Del Bonis-O'Donnell (University of California Santa Barbara), Advisor: Dr. Sumita Pennathur (University of California Santa Barbara)

There has been an increasing interest in developing “lab-on-a-chip” devices, which would allow for DNA analysis in the order of minutes instead of hours, in addition to decreasing sample size and the reagent consumption, therefore dramatically reducing cost.
The purpose of our investigation is to inform future experiments involving the analysis and detection of DNA and single nucleotide polymorphisms (SNP). We start by determining the resolution at which DNA and SNPs can be separated and detected using nanofluidic devices, and determine optimal conditions for successful experiments. Industry standard DNA ladder solutions are electrokinetically manipulated by applied electric fields within an etched fused silica nanochannel. The movement of fluorescently labeled DNA molecules ranging from 25-300 base pairs is tracked and measured by recording intensity profiles using an EMCDD camera and microscope. These results are used to quantitatively characterize the separation capacity of nanofluidic devices.
Preliminary results show that fluorescently labeled DNA has tendency to accumulate in the channel and coat the channel walls, and that electroosmotic flow dominates over the electrophoretic movement of DNA in the nanochannels. To alleviate these obstacles and improve performance, we will repeat our experiments using channels coated with hydrophilic neutral silane.

Key Terms: Biomolecules
Physics of fluids
Mechanical Engineering

**IR-25**

## The Role of De Novo Sphingolipid Synthesis in Upregulation of the GCV Genes in *Saccharomyces cerevisiae*

Ben Emery (Grove City College), Advisor: David Montefusco (Medical University of South Carolina), Yusuf Hannun (Medical University of South Carolina)

Sphingolipids have been shown to regulate a number of important cellular processes. It was previously observed that heat stress stimulates both *de novo* sphingolipid synthesis and upregulation of genes encoding the glycine cleavage protein (*GCV*) complex. Previous microarray data also shows that in the presence of *myriocin,* a drug that specifically inhibits *de novo* sphingolipid synthesis, heat stress-induced *GCV* upregulation is blocked, implying that intact sphingolipid synthesis is required for upregulation of the *GCV* genes. It is also known that the *GCV* genes are strongly upregulated by glycine. This set of observations prompted the hypothesis that glycine-stimulated upregulation of the *GCV* genes is mediated by sphingolipids. To address this hypothesis, *myriocin,* which inhibits sphingolipid biosynthesis, was used while treating with glycine to determine if *GCV* upregulation would be blocked in the absence of sphingolipid synthesis. Glycine dose response experiments revealed that *myriocin* blocked upregulation at low glycine levels, confirming that *GCV* upregulation is sphingolipid-dependent. Because the *GCV* complex plays an important role in the formation of specific one-carbon metabolic precursors, this regulatory "bridge" between the sphingolipid and amino acid metabolic pathways may play a critical role in maintaining a balance of those metabolic pathways. More significantly, the direct relationship between sphingolipids and the glycine cleavage complex may be evidence for an entirely unexplored class of glycine-based sphingolipids in yeast.

Key Terms: Sphingolipids
Amino Acid
Molecular Biology

**IR-26**

## Non-Medical Use of Stimulant Medication Among College Students: An Optional Randomized Response Technique

Jennifer Figueroa (University of North Carolina at Greensboro), Anna Tuck (University of North Carolina at Greensboro), Advisors: Sat Gupta (University of North Carolina at Greensboro) and Mary Crowe (University of North Carolina at Greensboro)

This study tests the efficacy of a statistical method called randomized response technique (RRT), which has been found to be effective in reducing response bias in studies involving questions that are sensitive in nature. The sensitive question of interest for us was the non-medical use of stimulant medication. The main focus of our project was on improving the original unrelated question model by Greenberg by allowing the respondent to answer the stimulant misuse question truthfully if that question was considered non-sensitive, or answer the question using the unrelated question model if the question was deemed sensitive.

Surveys were administered to a random sample of 550 undergraduate college students at the University of North Carolina at Greensboro. The check-box confidential survey was given to 150 participants, the face-to-face question survey was given to 150 participants, and the Optional RRT survey was given to 250 participants. The efficacy of the proposed Optional RRT method was checked by comparing the results of the RRT survey with the methods of the check-box confidential response, and the face-to-face question method.

Key Term: randomized response technique

**IR-27**

## Algae Enhanced Nutrient Removal From Municipal Wastewater Treatment Plants

Sarah Bauer (Rowan University), Andrea McFarland (Rowan University), Advisor: Dr. Kauser Jahan (Rowan University)

With global shortages of fossil fuels, a major focus has developed on sustainable biofuel production derived from algal species. Research was conducted to study microalgae growth and lipid production for biofuel using untreated municipal wastewater rich in nitrogen and phosphorous: major nutrients that stimulate plankton growth. These nutrients contaminate wastewater and must be removed by municipal wastewater treatment plants through expensive chemical/biological treatments before being recycled into the environment. Growing microalgae in wastewater serves the dual roles of nutrient reduction and biofuel production. The microalgae grown in the untreated wastewater medium, chosen for their high lipid content, were *Scenedesmus dimorphus* and *Chlorella vulgaris*. Wastewater samples were collected from Atlantic County Utilities Authority (ACUA), Landis Sewerage Authority (LSA), Gloucester County Utilities Authority (GCUA), and the Sewage and Treatment Plant of Harrison Township. Nutrient removal was monitored, and percentage lipid yields were calculated for each municipal plant and algal species. ACUA produced an average of 20.28% lipid yield. LSA and GCUA showed an average of 11.83% and 12.57% lipid yield, respectively. The Sewage and Treatment Plant of Harrison Township yielded an average of 9.27% lipid content. Lipid yields of 20-50% are common for microalgae of these species. Microalgae growth and lipid yield met expectations, averaging 13.49% lipid yield. The two algal species removed an average of 87% total phosphorus and 84% total nitrogen from the untreated wastewater. The experiment shows a potential for biofuel production through microalgae growth in municipal wastewater treatment plants, as well as an efficient alternative for nutrient removal.

Key Terms: Nutrient Removal
Wastewater
Lipid Yield

**IR-28**

**Determining Mitochondrial Lineages of Ancient Maya through aDNA Analysis**

Edmund Adjapong (SUNY Plattsburgh), Advisor: Nancy Elwess (SUNY Plattsburgh) and Sandy Latourelle (SUNY Plattsburgh)

The primary objective of this research is to examine ancient DNA extracted from Maya skeletons that were previously unearthed from Tipu, Belize. The goal of this research project is to determine the migration routes of ancient Maya using haplogroups, which are unique mitochondrial lineages. This is done by extracting ancient DNA from the teeth of Maya skeletons that were unearthed by Dr. Mark Cohen. There are approximately five hundred and eighty eight skeletons that were unearthed and collected. These skeletons are the largest collection of Mayan remains from one burial site and are currently housed at SUNY Plattsburgh for continued study. The four primary migration routes of Native Americans (A, B, C, and D) are being studied, this research will contribute to the study of haplogroups of ancient Maya people to date. A very specific DNA extraction protocol has been followed with the use of specific primers. The mitochondrial DNA is then amplified using Polymerase Chain Reaction (PCR) and then digested by specific enzymes that previous studies have shown test for specific haplogroups. DNA fragment sizes are then determined through the use of agrose gel electrophoresis. Bases on the DNA fragment size it is possible to determine which of the four (A, B, C or D) haplogroups that individual skeletons belong to. Researchers have determined the haplogroups group for twenty-three different samples and are continuing. This research will contribute more knowledge and understanding of the migration of people in Central America and Belize.

Key Terms: Genetics
Mitochondrial DNA
Haplogroups

**IR-29**

## A Systematic Literature Review and Survey of Spinal Muscular Atrophy Research and Awareness

Kerri Roberts (University of North Carolina at Wilmington), Advisors: Dr. Kris Walters,(University of North Carolina at Wilmington), Dr. Susan Roberts, (University of North Carolina at Wilmington)

Spinal Muscular Atrophy (SMA) is a collection of genetic, neuromuscular diseases with onset in early childhood that result in deficiency of nerve cells in the spinal cord, causing progressive muscle degeneration and weakness that, in most cases, lead to death.
The objective of this systematic literature review is to evaluate the prevalence of research activity in this area to determine if there is a lack of research and to identify the current awareness of SMA in the human population. To address the research objective, the review of the literature and an online survey about common knowledge of SMA will be conducted. The survey will target North American adults of different ethnicities, demographics, age, race, and gender. The following databases were searched: EBSCOhost, AHEC Digital Library, PubMed, and Medline. Extensive literature searches revealed that approximately 4 out of every 100,000 people are diagnosed with SMA, the disease affects one in 6,000 to 10,000 infants, and an estimated one in every 35 to 40 people are carriers. This pan ethnic neuromuscular disorder is designated as the most common genetic cause of infant mortality, the second leading cause of neuromuscular disease, and the second most common lethal, autosomal recessive disease in Caucasians after cystic fibrosis; yet, there is no known efficacious drug treatment and the disease is not one that is commonly known, like Muscular Dystrophy.
The systematic literature review indicates a dire need for more trials and research for SMA. The parent survey is under development and will be implemented November, 2011.

Key Terms: Neuromuscular Diseases
Genetics
Molecular Biology

**IR-30**

## The Incorporation of Cardiac Stem Cell Therapy to Induce Angiogenesis at Infarct Regions of the Heart

Pamela Tiet (University of California, Berkeley), Advisors: Derek Dashti (University of California, Berkeley), Kevin Healy (University of California, Berkeley)

Congestive heart failure is prevalent in the US, affecting 64.4 million Americans each year. In order to address this need, a novel method, involving regenerative medicine and biomaterials, is being researched in order to alleviate and restore the infarct region of the heart. Cardiac progenitor stem cells, which are integrated within a synthetic thermo-responsive hydrogel polymer network, can be transplanted into the infarcted myocardium for therapeutic cardiac tissue regeneration. Due to its source of specific growth factors and mechanical properties, the synthetic polymer allows the cardiac progenitor stem cells to proliferate and differentiate into cardiac tissue. The cardiac progenitor cells are initially tested on Matrigel, ECM derived from a mouse sarcoma, before testing on the hydrogel proceeds. Moreover, specific endothelial progenitor cells will be studied in a similar manner to use as an appropriate comparison. Ultimately, these growth factors and the mechanical properties of the polymer network help to induce angiogenesis (formation of blood vessels). With the incorporation of growth factors and peptides within the polymer network, this will increase cell proliferation and adhesion, leading to robust vessel formation. Angiogenesis is pertinent in cardiac wound-healing. Therefore, the ability of the cardiac progenitor cells to proliferate and form vessels within the synthetic polymer needs to be assessed. The direction of this research will be aimed at assessing and quantifying the appropriate amount of growth factors for robust proliferation and vascular tube formation of cardiac progenitor stem cells in order to achieve tissue regeneration.

Key Terms: Stem Cell
Material Science
Cell & Tissue Engineering

**IR-31**

**Automatic Transcriptome Analysis & Quest for Signaling Molecules in Ctenophore, *Pleurobrachia bachei***

David Girardo (Worcester Polytechnic Institute), Andrea Kohn (Whitney Laboratory), Mathew Citarella (Whitney Laboratory), Advisor: Leonid Moroz (Whitney Laboratory, University of Florida)

Ctenophores are one of the most basally branched lineages of Metazoan. Their nervous system's unique structure and function make them useful for understanding the evolution of nervous systems. We hypothesize that signaling peptides can be the earliest neurotransmitters and their origin precedes the recruitment of classical transmitters in neural circuits. As the first step in our analysis, we developed an automated transcriptome analysis pipeline fully integrated with a signaling peptide prediction system. Using the analysis pipeline, we generated a *de novo* list of potential signaling peptide genes in *Pleurobrachia bachei*. Manual analysis of the list verified promising results, including signaling peptide candidate 'GVEDin'

Key Terms: Bioinformatics
Genomics
Neuroscience

**IR-32**

## An Inhibitory Model for Neuronal Symmetry Breaking

Lisa Zheng (North Carolina School of Science and Mathematics), Advisor: Zachary Wissner-Gross (Harvard University)

As neurons develop, several immature processes, or neurites, grow out of the cell body and break symmetry by competing to become the neuron's single axon. To explain how this symmetry breaking occurs, two contrasting ideas have been proposed: depletion and inhibition. Depletion involves neurite competition for a collective pool of growth proteins, while inhibition includes additional inhibitory signals. Several computational models have been proposed for depletion, but so far, no inhibitory models have been developed. Here, we propose the first inhibitory models by adding negative feedback to a previously published depletion model. Numerically, we find that inhibition based on both concentration and length accelerate axon formation and induce axon formation over a larger range of parameters. However, only concentration-based inhibition allows shorter neurites to regenerate. Analytically, we find that the strength of our model's positive feedback must exceed a value related to the neurite count in order for symmetry breaking to occur. Our work expands the current understanding of axon specification and growth mechanisms that are important for nervous system development and relevant for treatments of Alzheimer's disease and nerve injury.

Key Terms: Neurobiology
Symmetry Breaking
Computational Model

**IR-33**

## Isolation Of The CO1 Gene Of *Rana clamitans melanota* Using Experimental Mouth Swab Protocol

Lauren Vaccaro (Plattsburgh Senior High School), Advisor: Nancy Elwess (State University of New York at Plattsburgh), Sandra Latourelle (State University of New York at Plattsburgh)

*Rana clamitans melanota* is a commonly-found true frog of the Lake Champlain Basin. Like many frogs worldwide, various populations within the region are in decline due to modernization and the Greenhouse effect. These populations, found in isolated locations, have yet to be cataloged through DNA-barcoding and their CO1 mitochondrial gene. In this experiment, over fifty samples of genetic material were collected from individual frogs using a new, more humane protocol than traditional toe-cutting. Using this method, individual frogs had their mouths swabbed. Using a Rana CO1 gene-specific primer, sample DNA was observed using gel electrophoresis. Certain bands of DNA found inside these gels were removed from the gel, frozen, and purified. This resulted in ten samples that had observable indications of the location of the CO1 gene at ~650 bp. From these, however, only three samples showed detectable luminescence by a bioanalyzer. Many samples contained low concentrations of genetic material, and were therefore undetectable. While these samples are applicable to sequencing, the rate of usable samples to non-usable samples calls the new protocol used in sample collection into serious question. While it was possible to apply a typical mouth-swabbing protocol to *R. C. melanota* individuals and gain applicable results, the protocol needs refinement to ensure that it can be used to collect higher concentrations of DNA.

Key Terms: Frogs
Protocols
Populations

**IR-34**

## Engineering a Genetic Toggle Switch Controller Using Synthetic Zinc Finger Transcription Factors

Aakash Indurkhya (North Carolina School of Science and Mathematics), Peter Fan (North Carolina School of Science and Mathematics), Advisors: Dr. Myra Halpin (North Carolina School of Science and Mathematics), Dr. Jingdong Tian (Duke University)

The activation or repressions of key genes, controlled by gene regulatory networks, often cause genetic diseases during stem cell differentiation and DNA replication. Synthetic biology holds promise for advances in gene therapy through the engineering of novel gene regulatory networks. Using synthetic zinc finger transcription factors, we increased functionality of an established network topology, the genetic toggle switch, by adding an interfacing component, called the "controller," and splitting the network onto two plasmids. The toggle switch operates using negative feedback of regulatory genes and can be induced to form two stable states. The bacterial-two-hybrid assay, a standard method in zinc finger characterization, was tested and found to be too long and tedious for use in fast paced and high throughput synthetic biology. Hence, we proposed a modified experimental protocol and presented a computational BLASTn screening and protein-DNA docking characterization method that efficiently selected nine, from several hundred, viable zinc finger transcription factors. We used TinkerCell, a CAD network modeling software, to construct a stochastic model for the toggle switch controller and found that all defining characteristics of the genetic toggle switch were maintained with reduced transcriptional noise. We have begun a library of synthetic repressor-promoter pairs for common use by the synthetic biology community. The use of synthetic zinc finger transcription factors establishes synthetically generated biological parts as the key to next generation gene regulatory networks. The full development of the toggle switch controller will serve as a major step towards personalized medicine and gene therapy.

Key Terms: Synthetic Biology
Electrical Engineering
Genetics

**IR-35**

## Using Blocking Peptides to Control and Analyze the Mechanical Properties of Single Fibrin Fibers

Pranav Maddi (North Carolina School for Science and Mathematics), Michael Falvo (University of North Carolina at Chapel Hill), Timothy O'Brien (University of North Carolina at Chapel Hill), Oleg Gorkun (University of North Carolina at Chapel Hill), Jonathan Bennett (North Carolina School for Science and Mathematics)

Fibrin is the main structural protein involved in blood clotting. Fibrin study traditionally focuses on entire clots, whereas we employ new AFM-based nanoManipulation techniques to study single fibrin fibers. The unstructured alpha-C regions and the alpha-helices within the coiled-coil regions of fibrin's monomers are known to extend when fibrin stretches, though it is not known exactly how they contribute to fibrin's mechanical properties. We isolated these regions using 4-residue peptides that interfere with the knob-hole interactions that connect the coiled-coil regions and a 12-residue peptide that interferes with the alpha-C interactions. We found that the alpha-C interactions and the knob-hole interactions were equally important for the assembly of fibrin, since the EC50 of fibrin assembly inhibition was the same for both peptides. The fibers were equally extensible for all treatments though the breaking strain of the peptide treated fibers decreased. The reversibility of the fibers' extension reduced when the knob-hole interactions are interfered with, and the worm-like chain behavior of the fibers decreased when the alpha-C interactions are interfered with. Our data suggest that the coiled-coils are responsible for the majority of fibrin's extension at low strains, and that the alpha-C regions account for the majority of fibrin's high strain, strain-stiffening behavior. These findings advance the fibrin extension model and may lead to better treatment and prevention of deep-vein thrombosis. We demonstrate that blocking peptides provide a viable method of altering the mechanical properties of fibrin fibers, which could lead to methods for making full clots with pre-programmable properties.

Key Terms: Biophyics
Protein Fibers
Fibrin

**IR-36**

## Effect of Wall Material on Ocarina Sound Quality

José Medrano (North Carolina School of Science and Mathematics), Advisor: Jonathan Bennett (North Carolina School of Science and Mathematics)

We used a microphone and human listeners to compare the sounds produced by identically shaped ocarinas, an early woodwind, made from aluminum, polycarbonate and stone. We used Fourier analysis to compare the fundamental and overtone frequencies of these ocarinas for 18 different notes as measured by a microphone. The frequencies for all three ocarinas varied randomly around the accepted values, with no discernible differences among any of the three materials.

In order to test this result and the hypothesis that any perceived differences in sound are due to cognitive biases, we had 12 volunteers attempt to differentiate between the sounds when they could not see the instrument being played. We played 15 note recordings to each listener and had them choose the ocarina the sound came from. They were correct on average 4.5 times of 15, nearly consistent with random chance (5/15). We also had the listeners rank 15 pairs of notes according to how similar they perceived them to be. We found that listeners were equally likely to rank notes from the same ocarina as dissimilar as they were to rank notes from different ocarinas as dissimilar.

We have found that not only are the variations in sound from each ocarina random, the differences between them are not audible to humans when they cannot see the source. This implies ocarinas made from more expensive materials are not superior and sound no different than those made from cheaper materials.

Key Terms: Acoustics
Psychoacoustics
Musical Instruments

**IR-37**

## Computer-Aided Method for Targeted Inhibition of LuxIR-Dependent Quorum Sensing

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In a process known as quorum sensing, Gram-negative infections rely on the activation of LuxR-homolog receptors by small-molecule autoinducers to regulate pathogenicity. Quorum sensing inhibition (QSI) in such bacteria inhibits virulence factors such as swarming motility and biofilm production. A computational model was developed for the rational design of inhibitors of the LasR receptor for the *P. aeruginosa* autoinducer, 3-oxo-$C_{12}$-HSL. The crystallographic structure of LasR was validated using an all-atom contact analysis performed on the *MolProbity* web server. Molecular dynamics software (*Molegro Virtual Docker*), employing a differential evolutionary algorithm, was used to assess the binding affinities of synthetic and natural compounds in LasR. A preliminary docking of six known inhibitors identified calmidazolium as possessing the highest LasR binding affinity. These results are consistent with previous experimental studies, supporting our computational model. A second docking study of 11 flavonols within LasR generated highest binding affinities in luteolin. A comparative analysis of residue binding in the docking results of LasR autoinducer, calmidazolium, and luteolin identified critical hydrogen bonding between active site residues and carbonyl, primary amine, valerolactone, and phenol moieties. This functional pattern represents a chemical pattern for autoinducer antagonism, a key step in the rational drug design of quorum sensing inhibitors.

Key Terms: quorum sensing inhibition
molecular docking
rational drug design

**IR-38**

## Computational and Experimental Study of the Absorption Spectra of Nickel and Zinc Tetraphenylporphyrins

Jonathan Chan (William G. Enloe High School), Jessica Smeltz (North Carolina State University), Dr. Takashi Tsuchiya (North Carolina State University), Advisors: Dr. Elena Jakubikova (North Carolina State University) and Dr. Elon Ison (North Carolina State University)

Dye-sensitized solar cells (DSSCs) are a promising way to convert visible light into electricity without the fragility and costs of silicon solar cells. The most efficient DSSCs to date use Ru(II)-polypyridines as dye-sensitizers. Ruthenium is, however, rare and expensive; search for dyes based on cheaper and more abundant metals is therefore an important area of basic research. We use density functional theory (DFT) and UV/Vis absorption spectroscopy to investigate the absorption spectra of nickel, zinc, and free-base (Fb) porphines and tetraphenylporphyrins (TPPs) which could be employed as dye-sensitizers in DSSCs. Q and Soret bands are identified in calculated and measured absorption spectra for all molecules investigated. According to TDDFT calculations, Q-bands can be described as HOMO to LUMO and HOMO to LUMO+1 excitations, while Soret bands arise due to the HOMO-1 to LUMO and HOMO-1 to LUMO+1 transitions. The wavelength of Q-band peaks is influenced by the addition of a central metal (Zn or Ni) to TPPs, which shifts the bands to lower wavelengths: from 575 and 538 nm for free-base TPP, to 543 nm for Zn TPP and 524 nm for Ni TPP. Addition of a central metal does not influence the wavelength of Soret bands, but increases their intensity. Q and Soret bands of TPPs shift to lower wavelengths in comparison to the absorption bands of porphines. The error between measured and calculated absorption wavelengths of TPPs is less than 0.25 eV, suggesting that TDDFT can serve as a powerful tool for computational modeling of dyes for DSSCs.

Key Terms: Energy Production
Quantum Chemistry
Analytical Chemistry

**IR-39**

## Use of Spray Adhesives for the Manufacture of 3-D Capillary Origami Microstructures

Mia de los Reyes (North Carolina School of Science and Mathematics), Advisor: Jonathan Bennett (North Carolina School of Science and Mathematics)

In the past, the field of microengineering has been limited to largely two-dimensional wafer techniques, such as etching and lithography. The method of “capillary origami”—using the surface tension of an evaporating water droplet to fold a flexible membrane into a three-dimensional polyhedron—has shown promise as a way to create fully 3-D microstructures. However, the membrane re-opens past a critical evaporation point, and previous attempts to prevent this re-opening have proven to be expensive and time-consuming. We therefore investigated the use of various spray adhesives in keeping these origami microstructures closed. Three characteristics were measured: efficiency, tackiness, and strength of the adhesive. Measurements of these parameters point to 3M™ Super 77™ Spray Adhesive as an optimal adhesive for spraying microstructures. Furthermore, we designed a new method to calculate adhesive strength by using an analytical balance to measure force applied by a micrometer to a microstructure. We also developed procedures to create uniformly-sized microstructures and to accelerate the folding process. These novel procedures, combined with the measurements that indicate 3M™ Super 77™ as an optimum adhesive, suggest a potential method for the mass-production of truly 3-D microstructures.

Key Terms: Microengineering
Microstructures
Capillary Origami

**IR-40**

## The Effect of Vector-Host Coupling on Vector-Borne Disease Dynamics: Consequences of Vector's Oviposition Dependence on Host-Related Habitats

Daihyun Kwon (University of North Carolina Greensboro), Edwitch Dely (University of North Carolina Greensboro), Advisor: Gideon Wasserberg (University of North Carolina Greensboro), Clifford Smyth (University of North Carolina Greensboro)

Modeling vector-borne diseases, in particular, pathogens transmitted by blood-sucking arthropods, presents the challenge of determining which factors influence the invasion or persistence of the disease agent in a susceptible host population. Particularly, the significant role of the host is often neglected when modeling vector-borne disease dynamics. Vectors need host as a source of blood-meal for egg-production as well as a source of habitat. Our study focused on the effect of disease dynamics due to the vector's dependence on its host (hereafter termed vector-host coupling). Specifically, we investigated the epidemiological consequences of the vector's demographic dependence on the host based on availability of host's habitat as breeding sites. We used an object-oriented programming approach in MATLAB to simulate three vector-host coupling scenarios; uncoupled, loosely-coupled, and coupled. The uncoupled scenario is a hypothetical system where contact between vector and host is random. The loosely-coupled scenario models vectors that depend on the host mainly for obtaining blood-meals (e.g., mosquitoes).The coupled scenario models vectors that depend on the host as source of habitat (e.g., ticks, fleas, mites, etc.). We also performed meta-analysis to validate predictions of our model with respect to patterns published in scientific journals. In contrast to conventional models that expect inverse relations, we observed a positive relationship between host abundance and infection prevalence for both the loosely-coupled and coupled systems. In the latter, however, a decrease in infection prevalence was observed at higher host abundance. The meta-analysis reported a positive association in most cases between host number and disease prevalence.

Key Terms: Disease Ecology
Mathematics

**IR-41**

## Nanostructured Silica Functionalized Cell Culture Substrates

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In this paper, we report the fabrication of cell culture substrates using a novel nanoimprint lithography based approach. First, a nanoimprint mold or template is formed on the surface of a fused silica wafer using high numerical aperture focusing femtosecond laser patterning. A cellulose acetate negative replica of the nanostructured template is then extracted, via nanoimprint lithography, by solvent casting cellulose acetate onto the template surface and allowing it to dry. The cellulose acetate replica of the nanostructured template thus obtained is then coated with silica by reacting silicon tetrachloride with water in a two-step chemical vapor deposition process. Due to the presence of silanol groups on the surface of silica, these silica nanostructures can be easily functionalized by covalently bonding with a variety of active biochemical molecules, which can be further conjugated with other biological species. Silica nanostructures prepared by this technique have been envisioned as cell culture substrates for cell differentiation studies, and are currently being explored for mouse embryo fibroblasts (NIH 3T3).

Key Terms: Materials Science
Biomedical Engineering
Nanotechnology

**IR-42**

## Utilizing the Shape Memory Effect to Enable Flexible Electronics

Abhishek Raj (The University of Texas at Dallas), Wenzhe Cao (Princeton University), Advisors: Sigurd Wagner (Princeton University), Walter Voit (The University of Texas at Dallas)

Stretchable and flexible electronics have been proposed for a variety of devices and sensing systems in which stiff silicon substrates are not practical. Instead, polymer substrates in these devices and systems can recover strains up to 800%, but typical electrode and circuit materials (gold, chrome, titanium, semiconductors) fail at strains well below 50%. This work seeks to demonstrate electrodes with improved strain capacity to enable new applications in neural biotechnologies. This is achieved by pre-straining polyacrylate shape memory polymer (SMP) substrates (up to 50%) at a temperature above their glass transition ($T_g$) and cooling them to fix a temporary shape. Then an E-beam evaporation process deposits a 3nm Ti adhesion layer and a 30nm Au electrode on the pre-strained SMP. Alternatively, the SMP substrate can be used as a carrier to temporarily pre-strain other materials such as poly(dimethylsiloxane) (PDMS) before electrode deposition. The SMP is then heated above $T_g$ enabling strain recovery while compressing and wrinkling the gold electrodes. Electrical resistance measurements for the electrodes are measured before and after release of the pre-strained substrates. Results demonstrate a drop in resistivity of an order of magnitude for the 1.4 mm × 9 mm electrodes for the pre-strained PDMS electrodes using an SMP carrier. Compression of microcracks due to the electrode buckling, as illustrated by SEM and AFM analyses, improves unstrained electrodes and also enables higher strain electrodes for emerging stretchable and flexible electronic devices such as multi-electrode arrays, cortical brain probes and cochlear implants.

Key Terms: Electrical Engineering
Materials Science
Polymer Chemistry

**IR-43**

## Effects Of Ractopamine On 4E-BP1 Phosphorylation

Diego Jaime (California State Polytechnic University, Pomona), Advisor: Robert J Talmadge (California State Polytechnic University, Pomona)

**Introduction:** Paylean® (Elanco Corporation), a common feed additive used to increase muscle mass in swine, contains ractopamine as the active drug and is a beta-adrenergic agonist whose cellular mechanism of action is unknown. The eukaryotic translation initiation factor 4E-binding protein (4E-BP1), a translation repressor protein, inhibits translation by binding to the eukaryotic translation initiation factor 4E (eIF4E). Phosphorylation of 4E-BP1 disrupts this binding leading to increased translation. 4E-BP1 is regulated by the cell signaling protein mTOR. Because ractopamine results in increased muscle mass and protein accretion, we hypothesized that ractopamine would increase the phosphorylation state of 4E-BP1 allowing for enhanced protein synthesis via enhanced translation. Specifically, this study assessed the phosphorylation state of 4E-BP1 following ractopamine treatment of pigs.

**Methods:** The treatment group (n = 10) was fed standard feed supplemented with 9 grams of ractopamine per ton of feed ad libitum for 28 days. The control group (n =10) was fed a standard feed without ractopamine. White semitendinosus muscles were removed and frozen in liquid nitrogen. Western blots were performed using a 4E-BP1 specific antibody. Bands corresponding to phosphorylated and non-phosphorylated 4E-BP1 were quantified.

**Results:** Phosphorylation of 4E-BP1 was elevated by 33% in Paylean® treated pigs compared to controls.

**Conclusion:** The data show that ractopamine, in part, induces muscle growth via activation of translation through 4E-BP1 derepression of eIF4e.

Key Terms: Ractopamine
4E-BP1
Skeletal Muscle

**IR-44**

## An Integrated Approach To Rural Infectious Disease Management: A Preliminary Study

Jacqueline Bailey (Meredith College), Advisors: John Mecham (Meredith College), Larry Grimes (Meredith College), Doudou D. Faye (Africa Bound Corporation/Senegal Neem Foundation).

More than one-sixth of our world's population, the majority of which lives in impoverished areas, is afflicted with one or more World Health Organization (WHO) recognized "Neglected Tropical Diseases" (NTDs). As such, local populations must rely on immediate natural resources for effective vector control.
This study investigates the vector suppression capacities of phytochemicals from *Azadirachta indica A. Juss* (the neem tree), introduced to sub-Saharan Africa in the twentieth century. Traditional knowledge gleaned in the Indian subcontinent, where the tree is indigenous, provides this study's conceptual framework. Many metabolically active constituents have been isolated from the tree, particularly azadirachtin and gedunin. This study compares the effectiveness of these purified compounds to that of the raw materials (fresh leaves, seeds, fruit, bark) from which they are extracted. Materials are being tested on intermediary vectors of two major NTDs: *Biomphalaria glabrata*, vector of *Schistosoma mansoni* (Schistosomiasis), and *Aedes albopictus*, transmitter of the flavivirus that induces Dengue/Severe Dengue fever. Previous reports investigated the molluscicidal/larvicidal capabilities of neem extracts; this study focuses on exposing vectors to plant-part infused water from egg to adulthood. Preliminary results demonstrate the potential to affect the growth, feeding, and oviposition behaviors of both vectors. Literature also shows that parasites of these organisms are highly sensitive to the constituents of *A. indica*. These results suggest that vector exposure to the plant could induce carrier state resistance. This work may provide a strategy for use of a less ecologically-disruptive form of NTD control through vector neutralization, rather than vector elimination.

Key Terms: Natural Resource
Neglected Tropical Diseases
Integrated Vector Management

**MC-01**

## Multifactor dimensionality reduction as a filter based approach for genome wide association studies

Noffisat Oki (North Carolina State University) Advisor: Alison Motsinger-Reif (North Carolina State University)

Advances in genotyping technology now provide a vast amount of genetic data that is proving to be useful in the quest for a better understanding of human genetic diseases through the study of genetic variation. This has led to the development of approaches such as genome wide association studies (GWAS) designed specifically for interrogating variants across the genome for association with disease, typically by testing single-locus, univariate associations. More recently it has been accepted that epistatic (interaction) effects may also be great contributors to these genetic effects, and GWAS methods are now being applied to find epistatic effects. The challenge for these methods still remain in prioritization and interpretation of results, and it has also become standard for initial findings to be independently investigated in replication cohorts or functional studies. In the current study we present and evaluate the use of Multifactor Dimensionality Reduction (MDR) as such a filter, with simulated data and a wide range of effect sizes. Additionally, we compare the performance of the MDR filter to a similar filter approach using logistic regression (LR), the more traditional approach used in GWAS analysis, as well as Evaporative Cooling (EC)-another prominent machine learning filtering method. The results of our simulation study show that MDR is an effective method for such prioritization, and that it can detect main effects, and interactions with or without marginal effects. It also significantly outperforms logistic regression for various two-locus epistatic models, while it has equivalent results as Evaporative Cooling for the epistatic models.

Key Terms: Genome wide association studies
Epistasis
Multifactor dimensionality reduction

**MC-02**

## Soliton Cellular Automaton Associated With $G_2^{(1)}$ Crystal Base

Kailash C. Misra (North Carolina State University), Advisors: Masato Okado (Osaka University), Evan A. Wilson (North Carolina State University)

In this presentation we give the combinatorial $R$ matrix for all elements of $B_l \times B_1$ where $B_l$ denotes the $G_2^{(1)}$-perfect crystal of level $l$, and the soliton cellular automaton constructed from it. The solitons of length $l$ are identified with elements of the $A_1^{(1)}$-crystal $B_{3l}$. The scattering rule for the soliton cellular automaton associated with the $G_2^{(1)}$ crystal base is identified with the combinatorial $R$ matrix for $A_1^{(1)}$ crystals.

Key Terms: Quantum Algebra
Mathematical Physics

**MC-03**

## Validation of RST-Based Feature Selection Approach to Network Intrusion Detection

Tejaswi Panchagnula (University of North Carolina at Greensboro), Advisor: Shan Suthaharan (University of North Carolina at Greensboro)

In Network Intrusion Detection systems, labeled datasets have been used to validate the machine learning based intrusion detection techniques. These datasets are generally huge and depend on many network features which provide computational disadvantages and inaccuracies in intrusion detection. Therefore, it is important to eliminate non-contributing features to facilitate speed and accuracy to the evaluation of machine learning techniques. Our goal in this research is to analyze the intrusion datasets and investigate the relevance of the features to a specific attack. If a feature does not contribute to any of the network attacks we eliminate it from the dataset automatically.

We use Rough Set Theory (RST) to select relevance features and Chebyshev's inequality in multidimensional scatter-plot to automate the process. We compare pairwise-features to simplify the solution. In a previous research the RST based, automated approach was validated using a well-known KDD'99 dataset. However, the KDD '99 dataset was found to contain many redundant records which causes the learning algorithms to be biased towards more frequent records and thus prevents the algorithm from learning less frequent records which are usually more harmful. Also, the dataset suffers from false positives, which combined with the redundant data leads to high computing time of algorithms. In this research, we use NSL-KDD dataset, an improved version of KDD'99 dataset to validate the proposed RST based approach.

The findings will help the advancement of intrusion detection research using KDD'99-based datasets and lead to better understanding of network features and their influences to attacks.

Key Terms: Computer Science
Intrusion Detection
Rough Set Theory

**MC-04**

## Lego Mindstorm NXT Controller with Peer-to-Peer Video Streaming in Android

Derek Harrington (St. Norbert College), Christopher Gusman (St. Norbert College),
Advisor: Ravikant Agarwal (St. Norbert College)

With Android technology advancing rapidly, using Android devices in wireless robotics communication is a relatively new area of study where it is possible to harness the built-in features of the Android platform and combine them with capabilities of wireless-enabled robots like a Lego Mindstorm NXT to create advanced applications. By utilizing features already available in an Android powered device, the camera for example, it is possible to enhance the navigation of robots.

An Android application, named Stream-O-Bot was developed to demonstrate this integration by controlling a Lego Mindstorm NXT robot. An Android device was mounted on the robot, capturing live video using the camera on the device. The video footage was then streamed back to another Android device being used as the controller. A new methodology to stream video peer-to-peer was also created and successfully implemented in this application. A user can use this application to drive the robot, while simultaneously receiving a live video feed of the robots surroundings.

Stream-O-Bot application (published in Android Market) provides a relatively inexpensive means to make robots (Lego Mindstorm NXT) go places that humans don't want to or physically can't go. Through this application, it was demonstrated that Android is a portable, relatively inexpensive, useful enhancement to robotics programming. An Android powered device is a viable asset in the field of robotics and can be successfully used in advanced wireless remote control navigation of robots.

Key Terms: Robotics
Andoid Application
Peer-to-peer Streaming Video

**MC-05**

## OpenSesame: A Multi-Level Authentication App for Android 2.2+

Sergii Bilokhatniuk (St. Norbert College), Advisor: Ravikant Agarwal (St. Norbert College)

This research examines security capabilities of Android platform based on GNU/Linux and components developed by Google. The focus of this research is multi-level user authentication mechanisms, display/keyboard locking methods and analysis of various device security scenarios. Research specifically analyzes Android 2.2 API, highlighting advantages and challenges that came in transition from Android 2.1. Even though Android platform is in rapid development, discussed material is still relevant because Android release 2.2 was a milestone, establishing its maturity and suitability as a secure platform.

The result of this research was twofold. Restrictions introduced in Android 2.2 for startup time of applications depending on their context, and how the keyboard can be controlled or intercepted rendered the conventional design approaches for the screen locker/login applications for Android 2.2+ not feasible. On the other hand, device administration API presented a new avenue for security management, either through existing Exchange ActiveSync services or developing new apps to enforce device security policies in centralized, consistent and manageable manner.

OpenSesame application (published in Android Market) is a proof of concept for Android 2.2+ device administration API's potential. OpenSesame enforces policies of password protected login for keyboard/screen lock. It requires user to enter a trusted phone number for emergency password recovery. If application detects more than five consecutive incorrect login attempts, it resets the password to a random alphanumeric string and sends the new password to the trusted phone via sms. OpenSesame is in early release, a development planned to add new password recovery methods and improved interface.

Key Terms: Android
Authentication
Security

**MC-06**

**Modernizing Legacy Systems: One Step at a Time!**

Christopher Gusman (St. Norbert College), Derek Harrington (St. Norbert College), Sergii Bilokhatniuk (St. Norbert College), Advisor: Ravikant Agarwal (St. Norbert College)

With the current rate of advancement in technology, software designed thirty years ago sounds like an ancient artifact. However, there are many software applications that were designed decades ago, but remain in service as they support crucial systems. The software may often be replaced by new and more functional products, but lack of comparability with old data sources makes transition very hard and sometimes even impossible.

The objective of this project was to transition an existing legacy system into a functional modern application. This project stepped into the “ancient” remains of software written in BASIC programming language and a flat-file driven database. This database kept records of fish diet in Wisconsin lakes by a Biology researcher and his team for thirty years. A few years ago, the original hardware retired, leaving only screenshots of what the text driven interface used to look like.

The project involved understanding the original data structures and rebuilding the data model from the ground up, consulting with the researchers and comparing the snapshot of the original records to the flat-file database. The data sources were analyzed and a database compatible with the original records was designed and implemented. A new software written in C# allowed secure access to the database, providing interface to input new research data and generate reports.

The data of thirty years research is an invaluable scientific resource. It was crucial to design an updated system not only to support ongoing research, but capable of incorporating previous data without loss.

Key Terms: Databases
Legacy Systems

**MC-07**

## Impact of Wayfinding Aids within a Virtual 3D Patient Safety Simulation

Aliceann Wachter (Clemson University), Advisors: Dr. Sabarish Babu (Clemson University), Dr. Larry Hodges (Clemson University)

Hospital acquired infections affect about two million annually, according to the Centers for Disease Control. The need for programs on patient safety and hygiene has increased greatly. In this project with the University of Iowa hospital, a virtual interactive medical simulation was created to educate medical practitioners in safety hazards, which were modeled and rendered in the virtual hospital. A post-game walkthrough was created to provide feedback. Also, a wayfinding aid was implemented.

Objects typical to hospital wards, like syringes, were modeled and placed within the virtual rooms to pose safety hazards. Objects fell into one of three categories: important items far from patient, trip hazards, or medical hazards. The objects were randomly placed into rooms and programmed to highlight yellow when tagged. The trainee's position was logged each frame and used to replay the simulation. In this feedback session, the safety hazards were highlighted green, if identified correctly, or highlighted red, if not selected, to evaluate the user's performance.

To enhance spatial awareness in the virtual ward, a wayfinding aid was provided, with colored dots representing hospital workers. Three aids were developed for navigation: dynamic map with a static orientation pointer, static map with dynamic orientation pointer, and static map with dynamic circle pointer.

In the future, the effectiveness of the wayfinding aids on spatial cognition will be evaluated. Also, more safety hazards and an advanced feedback system will be added. When completed, trainees should be better equipped to identify risks to patient safety in a real hospital environment.

**MC-08**

# Analyzing the Releases of Toxic Chemicals Over Time: Is it the Economy or the Environment?

English (North Carolina State University), William James (North Carolina State University), Bomin Kim (North Carolina State University), Advisor: William Hunt (North Carolina State University)

Over the past decade toxic releases in the United States have been steadily decreasing. During the same time period, we have also seen a major economic downturn, prompting many US industries to move production overseas. It is possible that this trend is impacting the amount of toxic releases within our border. We investigated the Toxic Release Inventory emissions provided by the Environmental Protection Agency (EPA) for our client Dr. Barry Nussbaum, EPA's Chief Statistician, in order to examine whether these changes are a result of environmental policy or more a result of economic troubles. We compared this data with economic data using exploratory statistical methods. We will develop a statistical model using major economic measures as predictors for toxic chemical releases. This will give us a good idea of how the economy is impacting toxic releases. We also plan to examine how chemical release data changes after a major environmental policy is implemented. After exploring all of the data with various statistical methods, we will be able to answer the question at hand: is it the environment or is it the economy?

Key Terms: Statistics
Environment
Economics

**MC-09**

# Palmetto Island: Developing Computer Science Awareness in Middle and High School Students

Charles Jones (Clemson University), Kaylee Nichols (Winthrop University), Brittany Green (Clemson University), Advisor: Dr. Larry Hodges (Clemson University)

In recent years, the number of computer science majors has decreased dramatically. Simultaneously, many students majoring in computer science leave the program within their first two years because they find introductory courses boring or difficult. In particular, students with no previous computer science experience are more likely to leave the program. Palmetto Island is a possible solution to this problem. The virtual environment based on the OpenSim software offers a fun and interactive way to introduce middle school and high school students to basic modeling and programming concepts. By doing so, Palmetto Island hopes to increase the number of computer science majors, while at the same time, giving students the skills they need to succeed in their introductory computer science classes.

The middle school and high school students participating in the program are called Citizens, and they work one-on-one with Mentors, who are Clemson University faculty and students. Citizens learn universal programming skills by completing challenges to "level up". Upon completion of the second level, Citizens should have mastered modeling and be familiar with variables, states, events, functions, if statements, and for loops. During the course of the summer, several students participated on Palmetto Island to complete the challenges and provide feedback. The next step for Palmetto Island will be to develop the remaining challenges for the last two levels and to increase the number of participants. Afterwards, pre and post testing will be analyzed to determine whether participation affects student attitudes about majoring in computer science.

Key Terms: Computer Science Education
CS Enrollment
Virtual Worlds

**MC-10**

## A Mathematical Model of Police Search Methods

Jeremiah Coleman (Appalachian State University), Advisor: Mary Searcy (Appalachian State University)

Law Enforcement agencies frequently use software with optimizing algorithms to organize their daily patrol routes. However, there have not been any published methods of roadblocks or patrol routes for finding suspects for whom the police are actively searching. An example is an armed robbery; if police have information on the getaway vehicle, they will establish roadblocks and have patrol officers look for the suspects. This problem requires a solution to these two parts; where to establish roadblocks and where officers should patrol. Our method for finding roadblock locations involves betweenness centrality of the road network and an iterated node removal process. A method for the patrol routes is being investigated, with the possibility of using the newly defined K-Path centrality as a solution. We use the Python package NetworkX for our calculations, due to the size of these problems.

Key Terms: Social Network Theory
Mathematical Modeling
Law Enforcement

**MC-11**

## Graph Algorithm – Efficient Shortest Path Estimation

Peiyang (Yonk) Shi (University of California, San Diego), Mentor: Arijit Khan (University of California, Santa Barbara), Advisor: Xifeng Yan (University of California, Santa Barbara)

Graph systems are getting more and more complex with the boom of social networks and advancements in data mining. Many problems arise as the graphs become massive. Many traditional algorithms for graphs are becoming too time consuming. Therefore, our goal is to design more efficient algorithms for large graphs.

In this project, we proposed a shortest path algorithm that uses MultiDimensional Scaling(MDS) technique to speed up the traversal time. MDS converts graphs into two dimensional maps, and with the assist of MDS, we use greedy routing to find the shortest path. Our greedy algorithm traverses to the closest neighboring node to destination, and repeats the process until the destination is reached. However, since MDS is only an approximation of coordinates, many obstacles arise, such greedy algorithm often comes up with far longer paths than the real shortest path. By creating a statistical model of 200 pairs of samples from the graph, we find that the ratio between real shortest path and direct distance path is no larger than 1.5, therefore by setting such parameter on our algorithm, it drastically increases the accuracy and efficiency. However, there are currently a 10% failure rate at which no paths are returned. Our algorithm is 171.3 times faster than Dijsktra's algorithm on a 1981 nodes graph, while the distances is, on average, 1.54 times longer than Dijsktra's path.

Key Terms: Graph Mining
Social Network
Efficient Algorithm

**MC-12**

## A Simple Visualization Approach to the Multiple Changepoint Problem

Praveen Suthaharan (The Early College at Guilford), Advisor: QiQi Lu (Virginia Commonwealth University)

Changepoints are important features of time series in many applications including climate data homogeneity, biomedical signal processing and DNA sequence segmentation. In general, the multiple changepoint detection can either be formulated as a hypothesis test problem or a model selection problem. However, most of these traditional methods are mathematically difficult and computationally intensive, and thus difficult to automate. Therefore it is important to address this problem to facilitate automated technologies. In this research, we propose a simple visualization technique to estimate the multiple changepoints in a time series.

We first compute a moving average version of the time series data to reduce the variance of the sequence. For the noise reduced data, we apply a higher degree polynomial regression globally to model the segment means. The endpoints of segments with less fits have the large residuals that represent the locations of changepoints. In the regression residuals those endpoints can be treated as outliers. Since the residuals of the polynomial regression asymptotically follow a Gaussian distribution, we can apply the outlier detection methods for Gaussian errors with 2-sigma or 3-sigma rules. Then the changepoints, as the outliers, will be easily identified in the residual plot. We demonstrate the performance of our method using 1000 simulated data. We will also apply this approach to the monthly mean temperature series at Tuscaloosa (Alabama) and a biomedical data. The proposed approach in this study is simple, but efficient and easily implemented. The findings will provide easy-to-compute staring configurations for other multiple changepoint detection methods.

Key Terms: Climate Data Homogeneity
Biomedical Signal Processing
DNA Sequence Segmentation

**PA-01**

## A Study of Nodal Errors in Fixed-Node Diffusion Monte Carlo Simulations of Many-Body Quantum Systems

Kevin Rasch (North Carolina State University), Advisor: Lubos Mitas (North Carolina State University)

In principle, Fixed-Node Diffusion Monte Carlo is an exact many-body method if the nodal surface of the trial wave-function is identical to the nodal surface of the true wave-function. We study the errors in the calculation of total energies and associated properties when the trial wave-function's nodes are imperfect, what is referred to as the fixed-node error, in a full range of systems. First, by comparing trial wave-functions from different theories, we show that in the presence of a flawed nodal structure increasing the charge density increases the fixed-node error, but has no effect when the nodal structure is nearly exact. Second by comparing results for a lithium systems of different sizes to experimental results, we show that the fixed-node errors can be of the order of 1-3% of the correlation energy of the system.

Key Terms: Electronic Structure
Many-Body Quantum Mechanics
Monte Carlo Methods

**PA-02**

## Transfer Function of the Photoelastic Modulator in Circular Dichroism Spectroscopy

Julie DiNitto (East Carolina University), Advisor: John M. Kenney (East Carolina University)

Interpreting spectra in Circular Dichroism (CD) spectroscopy can be influenced by the polarization state of the light. By adjusting the phase difference on the photoelastic modulator (PEM), the modulating polarization state can be analyzed and adjusted to optimize the signal and determine the state or states of polarization being detected. Determining the polarization state will indicate the existence of leakage into the CD signal. This presentation addresses this theoretically and experimentally.

The transfer function of the CD spectrometer can be represented in terms of a Bessel function expansion. When expanding, the presence of Linear Dichroism (LD) signal leaking into the CD signal is theoretically possible. By modeling the CD spectrometer transfer function, a theoretical representation of the simultaneous presence of LD and CD can be obtained by Stokes parameters and eventually applied experimentally with an analyzer.

An experimental approach to determining the time averaged phase difference of the PEM and the polarization state of the light in CD spectroscopy will be addressed.

Key Terms: Circular Dichroism
Photoelastic Modulator
Stokes Parameters

**PA-03**

## The Evolution of the Polar Coronal Hole During Solar Cycles 23 and 24

Nishu Karna (NASA GSFC/ George Mason University), Shea A. Hess Webber (NASA GSFC/ George Mason University), William .D. Pesnell (NASA GSFC) M. S. Kirk (NMSU), Jie Zhang (George Mason University), Advisor: Jie Zhang(George Mason University) and Research Advisor: William D. Pesnell (NASA GSFC)

We have used the analysis of EUV and magnetic field synoptic maps and the perimeter tracking algorithm to extend our time series of polar coronal hole areas through solar minimum between cycles 23 and 24 (through 2010). Both EUV algorithms use 171, 195, and 304 Å images from the Extreme ultraviolet Imaging Telescope (EIT) on SOHO. The synoptic method calculates the area of the polar coronal holes from the meridional boundary through each Carrington rotation while the perimeter tracking algorithm measures the polar coronal hole boundaries as they appear on the limbs over each polar rotation and calculates the enclosed area. Line-of-sight magnetic field synoptic maps from SOHO's Michelson Doppler Imager (MDI) instrument are used to estimate the polar coronal hole areas by measuring the polar hole boundary having a unipolar field strength. We remain convinced that the northern polar hole area is measurably smaller in the recent minimum than it was at the beginning of cycle 23, while the southern polar hole area is roughly the same. The annual periodicity in the polar coronal hole areas is due to projection effects that cannot be completely removed. This work is supported by the Solar Dynamics Observatory.

Key Terms: Polar Coronal Hole
Area
Solar Minimum

**PA-04**

**Towards Measuring the Metallicity Distribution of Kepler Target Stars**

Keith Hawkins (Ohio University), Advisors: John Johnson (California Institute of Technology), Tim Morton (California Institute of Technology)

One of the most interesting correlations that has come out of large statistical studies of exoplanets is a relationship between the occurrence rate of giant planets and the metallicity of their host stars. The primary goal of this project is to develop an automated pipeline to measure stellar parameters (e.g. effective temperature, surface gravity and metallicity) of a large number of stars. We use a spectral index-based method that employs a Bayesian approach to determine the stellar parameters of stars. Results will be presented. This method will be applied to a large number of stars in the Kepler field in order to determine the planet-metallicity correlation for small planets for the first time.

Key Terms: Astronomy
Exoplanets

**PA-05**

**Molecular Polarizabilities Partitioned into Atomic Polarizabilites**

Kaitlynne Rethman (Central Michigan University), Advisor: Juan Peralta (Central Michigan University)

Motivated to understand how molecules and clusters respond to external stimuli, we developed a new method for the partitioning of the electric static polarizability, $\alpha_{kl}$, of a molecule or finite system into contributions from atoms or fragments. It serves as a starting point to analyze how other properties are affected by electric fields and potentially use external fields as a mechanism to control these properties. Also, it provides a proof-of-concept for a similar partitioning of the dynamic (frequency-dependent) polarizability. The electric dipole is partitioned into atomic contributions using the Hirshfeld partitioning scheme. All calculations were carried out using a local version of the Gaussian program. To test our method of partitioning polarizabilites into local contributions, we chose to use a silicon cluster, $Si_3$, and the water molecule $H_2O$. We compared our results with available data from the literature.

**PA-06**

**Lithium in Low Mass Stars in the Scorpius Centaurus OB Association**

Marc Schaeuble (Clemson University), Advisor: Jeremy R. King (Clemson University)

The question of the source of the dispersion of lithium abundances in cool Pleiades stars has gone unanswered in stellar astrophysics. We utilize the Li I λ6104 subordinate line, and the λ6708 doublet to derive lithium abundances for 12 members of the Scorpius Centaurus OB Association to try to shed some light on the solution to this problem. The results indicate any intrinsic Li scatter in our 0.9-1.4 solar mass stars is limited to a factor  1.4, consistent with the lack of dispersion in ≥1.0 solar mass stars in the 100 million year old Pleiades. Both ab initio uncertainty estimates and the derived abundances themselves indicate that the λ6104 line yields abundances with equivalent or less scatter than is found from the λ6708 doublet as a result of lower uncertainties for the subordinate feature. Because non-local thermodynamic equilibrium corrections are less susceptible to changes in surface gravity and/or metallicity for the 6104 Å line, the subordinate Li feature is preferred for deriving lithium abundances in young Li-rich stellar association stars with a temperature ≥ 5200 K. At these temperatures, we find no difference between the Li abundances derived from the two Li I lines. However, at temperatures ≤ 5200 K, the λ6708-based abundances may give more reliable estimates of the mean Li abundance in cool young stars. While stellar models suggest that Li depletion of at least a factor of 2.5 should have occurred in our lowest mass star(s), our Li abundances show no decline indicative of such depletion.

Key Terms: Astronomy
Stellar Astrophysics

**PA-07**

## Microwave Telescope Dewar Design

Brittany Christy (Santa Barbara City College), Advisor: Philip Lubin (University of California Santa Barbara) and Ishai Rubin (University of California Santa Barbara)

The future of the study of the structure and evolution of our universe depends on understanding variations in the cosmic microwave background, or CMB; the cooled microwave remnant of the hot big bang that fills the entire universe. Unfortunately, the plane of our Milky Way galaxy emits extra microwave radiation that prevents accurate mapping of the CMB. My project is to help design and build a microwave telescope in order to better understand these interfering emissions so we can subtract them out. An antenna in the telescope collects microwave signals, which are then amplified. The main amplifier needs to stay very cold in order to reduce thermal noise, so we are building a device called a Dewar; an insulated, vacuum pumped, cryogenically cooled thermos made to thermally isolate the amplifier. Although previous Dewars have been relatively successful, it is still unclear how much heat leakage there is from outside sources, particularly infrared radiation. I am working on making the Dewar design more efficient by using heat transfer equations to calculate how much heat from radiation is leaking into the system, creating a visual simulation of radiative heat transfer using an engineering program called Solidworks, and doing a real-life heat transfer experiment with a small test Dewar in my lab in order to compare the data with my theoretical predictions. Although little data has been gathered so far due to technical difficulties, my future research will hopefully help make future microwave telescope Dewar design more efficient.

Key Terms: Cosmology
Microwave
Cryogenics

**PA-08**

## A Cross-Examination Of Saturnian Kilometric Radiation (SKR) Emission Observed By Cassini And Ulysses

Robert Albarran (University of Hawai'i at Hilo), Melissa Guzman (NASA Lunar and Planetary Science Academy), Roger Hess (NASA Goddard Space Flight Center), Advisor: Robert MacDowall (NASA Goddard Space Flight Center)

Saturnian Kilometric Radiation (SKR) is an auroral radiation of Saturn that has been observed by the Voyager 1 and 2, Cassini and Ulysses spacecraft. Previous studies show that the SKR periodicity varies with time; it was not locked to a fixed rotation period for Saturn. In this study, we compare radio observations from the Cassini and Ulysses spacecraft to determine a geometric model for the SKR emission. We localize peak SKR frequencies within Saturn's magnetosphere via models governed by the Cyclotron Maser Instability (CMI). Subsequently, by correlating spacecraft signals and triangulating detection times, we use the CMI model with Saturn's offset dipole model to survey SKR emission cone orientations through time. Such radio data reduction will allow for further constraint of the SKR rotational modulation. Ultimately, we examine the question - is the SKR source location fixed in Saturnian longitude or Local Time (LT)?

Key Terms: Radio Astronomy
Astrophysics
Solar System Exploration

**PA-09**

## Search for the Standard Model Higgs Boson Produced in Association with a Z and Decaying to Bottom Quarks

James Brandenburg (University of Florida), Advisors: Ivan Furic (University of Florida), Michele De Gruttola (University of Florida)

The Standard Model of particle physics has been extremely successful in predicting particle interactions observed over the last 20 years of collider experiments. The Higgs mechanism, which generates the masses of W and Z bosons, is one of the cornerstones of this theory but has not yet been experimentally observed. Limits from LEP and the Tevatron have excluded ranges of the Higgs mass, but it is now possible to probe previously inaccessible mass ranges with the CMS detector at the CERN LHC. We present the results from a recent search for the Higgs boson decaying to two bottom quarks. In order to reduce backgrounds from bottom quark production, we require the Higgs boson be produced in association with a Z boson. An analysis of this channel allows a direct search for the Higgs boson in the mass range of 115GeV to 135GeV, which is the range most favored by theory. We further focus on the Z boson decaying to two neutrinos. The analysis consists of a search for events with a final state of two neutrinos appearing as missing transverse energy and two bottom quarks appearing as jets. Requiring a high boost in the transverse plane further reduces experimental backgrounds. We present some of the data-driven techniques used to estimate background levels. We report the upper limit for the Higgs boson cross-section to be 12 to 20 times that of the standard model for this analysis optimized with 1/fb of data.

Key Terms: Particle Physics
Higgs Boson
Standard Model

**PA-10**

## GEANT4 Validation for MAJORANA

Christian Johnson (University of North Carolina), Advisor: John Wilkerson (University of North Carolina)

While much has been learned about neutrinos in recent years, a number of mysteries remain. The nature of the neutrino mass will be probed with the MAJORANA experiment. MAJORANA will search for a rare type of radioactive decay called neutrinoless double beta decay ($0\nu\beta\beta$), which can only occur if neutrinos are Majorana, and not Dirac, particles. The MAJORANA experiment will utilize ultra-sensitive germanium-based detectors to search for the characteristic spectrum of a $0\nu\beta\beta$ event. However, in order to characterize background radiation which could mask the signal, detailed simulations using GEANT4 are being performed. In order to ensure that GEANT4 accurately simulates particle physics events, validation simulations were run on several criteria. Data from GEANT4 simulations of radioactive decays and particle range experiments is presented here, and the results are found to be consistent with the literature.

Key Terms: Computational Physics
Neutrinos
Simulations

**PA-11**

## Lissajous Figures as a Model for Neutrino Oscillations

James Rowland (North Carolina State University), Advisor: Chueng Ji (North Carolina State University)

The phenomena of neutrino oscillations has been researched extensively since Bruno Pontecorvo proposed it in 1957. Our research proposes a novel model to visualize and interpret neutrino oscillations. Neutrino oscillation is the phenomena whereby neutrinos can change flavor. Motivated by two dimensional models for a simple harmonic oscillator, we discovered that Lissajous figures compose an analogous model to neutrino oscillations. These figures provide insight into neutrino oscillations with regards to the effect of interaction strength and relative masses of neutrinos.

Key Terms: neutrino
Oscillation
lissajous

**PI-01**

## Fascicle Lengths in the First Dorsal Interosseous Muscle

Brendan J. Casey (Philadelphia College of Osteopathic Medicine), Michael J. Ellis, Benjamin W. Infantolino and John H. Challis (Pennsylvania State University)

In musculoskeletal models a common assumption is that the properties of whole muscle can be considered to behave like a scaled individual muscle fiber or sarcomere. Gross dissection of muscles indicates that this conceptualization of muscle does not accurately reflect many aspects of muscle architecture. It is still commonly assumed that the fascicles of human muscles stretch the entire length of the muscle from proximal to distal tendon. There is limited evidence from anatomical studies that not all muscle fibers run from tendon to tendon, for example in cats, and in the long human muscles. Many of these muscle fibers terminated within the muscle belly, and some were arranged in series with other fibers.

Understanding the force-length properties of muscle is important, for example, for the parameterization of musculoskeletal models and can hold clinical significance, for example, in muscle tendon lengthening and transfer surgeries. Therefore the purpose of this study was to determine for a muscle the distribution of lengths of the fascicles and tendon comprising the whole muscle. The purpose of this study was to determine for a muscle the distribution of lengths of the fascicles comprising a muscle. The range of lengths was large but was normally distributed.

Some fibers are serially arranged meaning that the operating range of a whole muscle can be greater than that implied by the lengths of the individual muscle fibers. This also has implications for the force-velocity properties of muscle.

Key Terms: Muscle
Length Relationship
Muscle Architecture

**PI-02**

**Secreted West Nile Virus NS1 Modulates Toll-Like-Receptor Signaling**

Kristen Crook (North Carolina State University), Advisor: Frank Scholle (North Carolina State University)

The flavivirus, West Nile Virus (WNV), is a mosquito transmitted virus that can cause encephalitis as well as a debilitating illness known as West Nile fever. Toll-like receptors (TLRs) are involved in the earliest innate immune response to infection and our work focuses on delineating interactions between flaviviruses and TLRs. Recent studies have highlighted the importance of TLRs in the immune recognition of flaviviruses as TLR3 and TLR7 have been directly linked to flavivirus-induced responses. Previous research demonstrates that intracellularly expressed WNV nonstructural protein 1 (NS1) inhibits signaling through TLR3. WNV NS1 is required for viral replication, but is also secreted to high levels from infected cells and this secreted form was shown to associate with uninfected cells.

The study objectives were to identify a role for secreted NS1 (sNS1) in TLR signaling inhibition. We have shown association of sNS1 with uninfected cells and purification of sNS1 has allowed demonstration of reduced signaling through TLR3, TLR4, and TLR7 as analyzed by cytokine ELISA and reporter assays. The inhibitory function of sNS1 was not cell type specific as signaling was ablated in HeLa cells as well as murine bone marrow derived immune cells. Additionally, we have shown that purified sNS1 is able to modulate innate signaling *in vivo* after footpad inoculation into mice. Analysis of the draining lymph node by qRT-PCR indicates sNS1-dependent inhibition cytokine mRNA expression after stimulation with Poly(IC:LC). These data indicate that secreted NS1 likely has an important role in pathogenesis by interfering with important WNV-sensing immune components.

Key Terms: Virology
Immunology
Pathogenesis

**PI-03**

## Mutational Analysis Of The Multifunctional West Nile Virus NS1 Protein

Clayton Morrison (North Carolina State University), Advisor: Frank Scholle (North Carolina State University)

RNA viruses often maximize the impact of their small genomes by encoding multifunctional proteins. This is illustrated by the growing amount of literature describing the involvement of replication proteins in interference with the innate immune response. A mutational analysis of replication proteins, to identify characteristics involved in immune evasion, becomes problematic since many mutants will also abolish the replication function of the protein. West Nile Virus (WNV) is a human neurotropic flavivirus. Previous work by our group has demonstrated that WNV non-structural protein 1 (NS1) inhibits TLR3 signal transduction. NS1 is absolutely required for genome replication and truncation of the protein is lethal. We have conducted a FACS based screen to identify mutant NS1 proteins which retain replication competence, but have lost the ability to inhibit TLR3 signaling. A reporter cell line was created in TLR3-competent HeLa cells to express the fluorescent protein dsRed under the control of the NFκB promoter (HeLa-NFκB-dsRed). In addition this reporter cell line expresses a library of random NS1 mutant proteins (mNS1), introduced by retrovirus-mediated gene transfer. Further, a GFP-expressing WNV replicon containing an in-frame, lethal NS1 deletion (GFP ΔNS1 replicon) was constructed to only replicate in the presence of co-expressed functional NS1 (*trans*-complementation), and was packaged into virus replicon particles (VRPs). To perform the screen, the mNS1 expressing HeLa-NFκB-dsRed cell line was infected with GFP ΔNS1 VRPs and subsequently treated with the TLR3 ligand pIC, followed by FACS single-cell sorting. Several unique mutants were identified, individually reconstituted, and further characterized.

Key Terms: Innate Immunity
Viral Pathogenesis
West Nile Virus

**PI-04**

**Vascular PI3K-Akt Signaling contributes to Peripheral NMDAR-mediated Pressor Response in conscious rats**

Marie A. McGee ( Department of Pharmacology & Toxicology, Brody School of Medicine, East Carolina University), Advisor: Abdel Abdel-Rahman (Department of Pharmacology & Toxicology, Brody School of Medicine, East Carolina University)

Evidence has implicated the PI3K-Akt-NOS signaling pathway in neuronal responses mediated via NMDAR activation. However, the involvement of this pathway in the peripheral NMDAR-mediated pressor response is unknown. Recently, it has been demonstrated that PI3K-Akt-dependent phosphorylation of endothelial nitric oxide synthase (eNOS) at serine 1177 can lead to superoxide generation, linking eNOS-dependent reactive oxygen species (ROS) generation to vasoconstriction. In this study, we tested the hypothesis that vascular PI3K-Akt-NOS signaling contributes to NO and ROS generation and the subsequent pressor response mediated by peripheral NMDAR activation. Hemodynamic studies were conducted in conscious male Sprague Dawley rats that were pretreated with the selective inhibitor of: (i) eNOS, N5-(1-iminoethyl)-l-ornithine (L-NIO), (ii) neuronal NOS (nNOS), $N^{w}$-propyl-l-arginine (NPLA) or (iii) the upstream PI3K-Akt inhibitor, Wortmannin. L-NIO produced no change while NPLA pretreatment significantly attenuated the NMDA-mediated pressor response. These findings are the first to implicate nNOS-derived NO in the peripheral NMDAR signaling. Wortmannin pretreatment significantly ($p<0.05$) suppressed the dose (125, 250 and 1000 µg/kg) dependent NMDA mediated pressor response. Molecular and biochemical studies were conducted to substantiate these interesting pharmacological findings. Vascular nitrate and reactive oxygen species levels were significantly increased following peripheral NMDAR activation; interestingly, both levels were significantly abrogated following wortmannin pretreatment. Collectively, these novel findings suggest that the PI3k-Akt-nNOS signaling pathway serves as an underlying cellular mechanism for the peripheral NMDAR-mediated pressor response in conscious rats [NIH grant AA07839].

Key Terms: Pharmacology & Toxicology
Cardiovascular
PI3k-Akt signalling

**PI-05**

## Supplementing a Sows Diet to Promote Good Intestinal Health of Their Piglets

Lauren Kloc (North Carolina Agricultural and Technical State University), Dawn Conklin (North Carolina Agricultural and Technical State University), Steven Hurley(North Carolina Agricultural and Technical State University), Advisor: Radiah Minor (North Carolina Agricultural and Technical State University)

The immune response within the gastrointestinal tract is a fine balance between the release of pro-inflammatory and anti-inflammatory cytokines. Weaning associated intestinal inflammation has been demonstrated in many animals. In piglets, increased levels of inflammatory cytokines such as IL-6 have been observed in the intestine immediately following weaning. Diets rich in probiotic, prebiotic, or synbiotics (a combination of probiotics and prebiotics) are known to enhance intestinal health. Moreover, research shows that a sow's diet can play an important role in the health of their piglets. Therefore, a study was designed to investigate whether feeding probiotic, prebiotic, or synbiotic diets to sows during lactation would affect the intestinal health of their piglets. Specifically, the expression of the pro-inflammatory cytokine, IL-6, was measured in the small intestines of piglets sacrificed on the day of weaning (d0) and 28 days post-weaning (d28). In this study, the diet did not affect the expression of IL-6 on d0 in the small intestines. However on d28, IL-6 was detected in the small intestines of piglets whose dams received a diet with the probiotic yeast supplement suggesting that the addition of yeast culture to the diet of sows may promote intestinal inflammation in their piglets.

Key Terms: Immunology
Animal Science

**PI-06**

## Role of Mer in Apoptotic Cell Clearance in the Germinal Center

Tahsin Khan (Thomas Jefferson University), Eric Wong (Thomas Jefferson University), Advisor: Ziaur Rahman (Thomas Jefferson University)

Germinal centers (GCs) are specialized micro-environments that generate high affinity Ab-forming cells (AFCs) and memory B cells. Many B cells undergo apoptosis during clonal selection in GCs. The TAM (Tyro-3, Axl, and Mer) family receptor tyrosine kinases including Mer, facilitate macrophage clearance of apoptotic cells. We previously showed that tingible body macrophages (TBMφs) in GCs express Mer. We observed that apoptotic cells (ACs) accumulated in GCs of mice deficient in Mer ($Mer^{-/-}$), after immunization with T-dependent Ag. Accumulation of ACs in GCs of $Mer^{-/-}$ mice resulted in significantly increased AFCs, GCs, and Th1-skewed IgG2c Ab responses. We report here that increased GC response in $Mer^{-/-}$ mice compared to controls is due to increased proliferation of GC B cells. We also found that AC accumulation in $Mer^{-/-}$ GCs is not due to increased B cell apoptosis. We show that TBMφs express two other members (Tyro-3 and Axl) of TAM family receptors, which are similar in both $Mer^{-/-}$ and controls. TBMφs in GCs of both strains express similar levels of milk fat globule EGF factor (Mfge8) and T cell immunoglobulin 4 (Tim-4), which are believed to aid in AC clearance. These data indicate the critical role for Mer in the clearance of ACs in GCs. This is further strengthened by the efficient clearance of ACs from GCs in mice deficient in Axl ($Axl^{-/-}$) in the presence of Mer. Together, these data indicate a vital role of Mer in regulating B cell response and in the maintenance of B cell tolerance.

Key Terms: Immunology
Germinal center
B cell tolerance

**PI-07**

**Mesothelin: Good Protein Vaccine Target Or Dud For Pancreatic Cancer Treatment?**

Andrew Freistaedter (East Carolina University), Gwendolyn Jones (East Carolina University), Emmanuel Zervos (East Carolina University), Advisor: Rachel Roper (East Carolina University)

Pancreatic cancer is the fourth leading cause of cancer-related deaths in the United States. Pancreatic tumors over-express the protein mesothelin, and therefore, we used mesothelin as a tumor target antigen for vaccine development. Our current research focuses on using an improved Modified Vaccinia Ankara (MVA A35RΔ) poxvirus that we developed to present mesothelin to the immune system to treat pancreatic tumors in mice. Wild-type (normal) and A35RΔ MVA viruses were constructed to express mouse mesothelin to create an anti cancer vaccine. PCR, flow cytometry, and Western Blot confirmed virus construction, purity and protein expression. Our hypothesis was that the A35RΔ virus would be more efficient at stimulating the immune system and better protect against tumors caused by the Panc02 pancreatic adenocarcinoma cell line. MVA was found to both kill and replicate in Panc02 cells, showing it is an oncolytic virus. However, multiple schemes of infection/vaccination and boosts were used without any significant protection from tumor challenge in mice. Assays to determine immune response against mesothelin suggested that mice vaccinated with the mesothelin expressing vaccine virus did not generate a strong immune response to mesothelin as expected, however the mice had robust immunity to the poxvirus. Together these results suggest that native mesothelin may not be a good vaccine target antigen for cancer treatment, possibly because immune cells responding to this self-protein are deleted during development of the immune system as a protection against autoimmunity. Strategies for improving anti-mesothelin immunity are being explored.

Key Terms: Virology
Immunology
Oncology

**PI-08**

**Pyridoxine Administration in Chick Embryos Causes a Decrease in Number of Large Diameter Axons but has no Effect on the Expression of Activated Caspase-3 in DRG Neurons.**

Yuri Fedorovich (Southern Illinois University-Carbondale), Advisor: Andrew A. Sharp (Southern Illinois University School of Medicine-Carbondale)

A better understanding of sensory feedback in neural development would be achieved if specific sensory modalities could be altered. Pyridoxine (vitamin $B_6$) overdose causes large fiber deafferentation in adult mammals, but the mechanism of toxicity and the specificity of the resulting lesions are not fully understood. Our lab has shown that embryonic pyridoxine administration kills trkC positive DRG neurons but has no effect on Substance-P or CGRP positive neurons in chick embryos. Therefore, we hypothesize that the effects of pyridoxine are restricted to large diameter axons in motor nerves and that these neurons are eliminated through an apoptotic pathway. To test this, embryonated eggs were injected with pyridoxine or physiological saline on embryonic day (E) 7 and E8. Spinal columns were collected on E8.25 and E9 and the third lumbosacral DRG was reacted with an antibody to activated caspase-3 (AC3) to assay for apoptotic neurons. The effect on peripheral axons was determined by measuring the number and diameter of axons in Toluidine Blue stained sections of the lateral branch of the femoral nerve (skin) and the lateral branch of the tibialis nerve (muscle) collected on E13. We found no change in the number of apoptotic neurons, but this may be due to the short duration of AC3 expression. Additionally, we only found a significant change (decrease) in large axons (1-3µm) in motor nerves. These results support the conclusion that the effects of pyridoxine are restricted to large sensory axons of motor nerves, but the mechanism of cell death remains unclear.

Key Terms: Neuroscience
Anatomy
Physiology

**PI-09**

## Identification of the Gene Responsible for the Chicken L Alloantigen by Whole Genome Association Mapping and Assessment of Potential Implications on Poultry Immunological Response

Mary Pat Bulfin (North Carolina State University), Advisor: Chris Ashwell (North Carolina State University)

Parasitic disease, such as cecal coccidiosis caused by the parasite *Eimeria tenella*, remains a significant concern within the commercial poultry industry due to increasing resistance to anticoccidial supplemental treatment. Improving the chicken's inherit immunological response to coccidial infection is a potential method for combating resistance to and can be determined by considering alloantigen genes. Chicken erythrocyte alloantigen system L has two haplotypes, $L^1$ and $L^2$, and is associated with multiple factors involved in immunological response in the chicken. A resource population was produced by mating a heterozygous male chicken ($L^1L^2$) with four heterozygous females ($L^1L^2$), the F2 progeny were characterized for their L type. DNA was extracted and birds were sexed by PCR. DNA pools were prepared representing each L haplotype from each family for SNP typing. The 4 parents and pools from each of the 4 families were genotyped using a 42,000 single nucleotide polymorphisms (SNPs) assay on a custom Illumina Bead Array SNP panel. A single marker association analysis was performed using JMP genomics as a case/control population and P values were adjusted for multiple testing using false discovery rate (FDR). Significant association was observed with L alloantigen type and a distal region of chromosome 4. Investigation of this L alloantigen locus on chromosome 4 indicates that there are multiple candidate genes present whose protein products are localized on the cell surface. Further study is required to determine the causative variation responsible for the L alloantigen system.

Key Terms: Poultry
Genomics
Immunological Response

**PI-10**

## Characterization of B16-F1 and D5.1G4 Melanoma Tumors and Profiling Melanoma-Induced Suppression of Dendritic Cell Function

Yonathan Ararso (Hampden-Sydney College), Advisor: Kristian Hargadon (Hampden-Sydney College)

Tumor-derived factors contribute to the dysfunction of immune responses by suppressing the production of proinflamatory cytokines, chemokines, and costimulatory molecules. In this group of experiments, we attempted to characterize the immunosuppressive agents released by B16-F1 and D5.1G4 melanoma tumors and to identify the effects of these tumor-derived agents on the production of the cytokines IL-6 and MCP-1 and on the production of the costimulatory/coinhibitory molecules MHC I, MHC II, CD40, B7-H3, CD80, B7-H7, CD86, and B7-DC using DC2.4 murine-derived dendritic cell line as a host. Real-time RT-PCR results confirmed a very high expression of the immunosuppressant TGFβ1 at 91.4 folds higher in B16-F1 than in D5.1G4. TGFβ2, VEGF-A, VEGF-B, and VEGF-C, also displayed higher gene expression at 1.2, 4.5, 2.9, and 2.9 fold higher in B16-F1 while VEGF-D displayed a 2.4 fold higher expression in D5.1G4 tumor line. However, subsequent ELISA and flow cytometry test results indicated that despite its abundant presence, TGFβ did not significantly alter the production of the cytokines IL-6 and MCP-1 or the production of the costimulatory/coinhibitory molecules MHC I, MHC II, CD40, B7-H3, CD80, B7-H7, CD86, and B7-DC.

Key Terms: Tumor Immunology
Immune Cell Disfunction
Dendritic Cell Function

**PI-11**

## A potential mechanism to describe the role of DRAK 2 in T cell activation

Patricia Lopes (University of California, Irvine), Advisors: Craig Walsh (University of California, Irvine) and Brian Weist (University of California, Irvine)

DRAK 2 (death-associated protein-kinase-related 2) is a serine/threonine kinase which is part of the calcium/calmodulin-dependent superfamily. It is highly enriched in lymphocytes and is known to raise the threshold for T cell activation and maintain its subsequent survival. Importantly, DRAK 2 knockout mice are resistant to organ-specific autoimmune disease models, yet retain normal responses to viral infection, thus suggesting a possible role as a key target for therapeutic intervention of autoimmune diseases.

Controlled calcium signaling is imperative for the prevention of abnormal T cell activation. Previous studies show that DRAK 2 plays an important role in calcium signaling regulation, as cells lacking DRAK 2 exhibit enhanced calcium responses to T cell stimulation. Additionally, kinase activity of DRAK 2 is itself promoted by calcium entry following T cell activation and is dependent upon the subsequent generation of reactive oxygen species, a byproduct of mitochondrial respiration. Thus, we set to test the hypothesis that DRAK 2 may be involved in a negative feedback loop that functions to limit calcium influx in the mitochondria.

Through immunofluorescence labeling and fluorescence microscopy we are able to stain conjugated T cells and antigen presenting cells for mitochondria and DRAK 2. This allows us to better understand how DRAK 2 may be regulated during T cell activation and potentially answering specific questions such as: Where is DRAK 2 localized during T cell activation? What is required for DRAK 2 to go to the synapses? Ultimately, we hope to better comprehend how DRAK 2 controls calcium homeostasis and its correlation to autoimmune disease development.

Key Terms: DRAK 2
immunofluorescence labeling
Immunology

**PI-12**

## The Effect of Phosphorylation on DRAK2 Function

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It is no secret that though the immune system protects the human body from foreign pathogens it is seldom thought as the cause of disease. Autoimmune diseases stem from the fact that rogue lymphocytes have been generated and matured enough to cause damage in the body by reacting aggressively to self-antigen. To do this, these T cells (of which this paper is concerned with) have to have escaped negative selection where they would have gone through apoptosis due to binding strongly to self-peptide. Cell death in thymocytes was believed to be monitored mainly by DRAK2, a DAP-kinase. However, recent studies have shown that DRAK2 is not sufficient to induce cell death. DRAK2, being a serine/threonine kinase, phosphorylation is thought to be a key factor to its function in apoptosis in lymphocytes. By retroviraly knocking down DRAK2 and comparing these cells to DRAK2 kinase activation site mutants, the function of DRAK2 in these cells can be monitored via western blot. The DRAK2 knockdown cells were created via co-transfection with Ψ Eco and retrovirus pSM2.

Key Terms: Autoimmunity
Drak2
T cells

**PI-13**

## Preliminary findings for the activation of a MyD88-independent TLR4 pathway after infection with H1N1 virus

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Infection with H1N1 virus has resulted in an increased number of emergency hospital visits for pneumonia and other influenza-related diseases (Perez-Padilla et al., 2009; Chowell et al., 2009). The mechanism(s) by which this occurs are not known. Influenza infection is characterized by inflammation and an increase in inflammatory cytokines in the lung. We investigated the role of toll like receptor (TLR), a component of the body's innate immune defense, against H1N1 infection in the lung. Previously, H1N1 infection was shown to have more deleterious effects on mice deficient in TLR4 ($TLR4^{-/-}$) than in mice deficient in myeloid differentiation primary response gene (88) ($MyD88^{-/-}$) or C57BL/6 control wild-type mice. As such, $TLR4^{-/-}$ mice had greater weight loss, higher total bronchoalveolar lavage (BAL) cell counts, and decreased lung compliance at day 7 post-infection than $MyD88^{-/-}$ and C57BL6 mice. Viral titers were not significantly different between the groups. Collectively, our findings suggest that a MyD88-independent TLR4 pathway is critical to controlling the severity of the inflammatory response to H1N1 infection. Future research will repeat these experiments, as well as focus on determining which components of the TLR pathway are important in regulating the differential responses seen to H1N1 infection in the lung.

**PI-14**

## Development of Lentiviral Infected Cell Line to Test The Role of TMPRSS2 In Influenza Infection

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The cleavage of hemagglutinin (HA) protein with the use of host cell protease is required for influenza virus to gain entry into the cell. Privous studies have found that TMPRSS2 protease plays a significant role in the infectivity of influenza virus. During this study Lentivirus was used for the insertion of shRNA against TMPRSS, Red fluorescent expression, Puromycin selection gene, as well as Doxycycline induction to create a stable cell line which can be tested to determine the role of TMPRSS in influenza infection. The cell line was passage through fluorescent cell sorter as well as Puromycin selection to create clone cell lines. Gene silencing was validated with the use of PCR which demonstrated that there was a significant difference in the level of TMPRSS2 between Doxycycline induced and non-induced clones. Upon induction with Doxycyclin, TMPRSS2 silencing RNA is produced which blocks the production of TMPRSS2 RNA. The blocking leads to a decrease translation of TMPRSS2 and without the protease activity of TMPRSS to cleave influenza hemagglutinin (HA), the infection of host cell is reduces. The assay results demonstrated that the induction of the clone does decrease the infection of influenza virus.

Key Terms: Virology
Immunology
Infectious Disease

**PI-15**

## Antimicrobial Activity of PHYTO-MAST® on Four Mastitis Causing Bacteria

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PHYTO-MAST® intramammary infusion is currently being used on organic dairy farms to manage mastitis and maintain udder health. Over the last decade, there has been a 20% growth in the organic dairy industry. Cows from organic dairy herds are only treated with antibiotics for mastitis when mastitis threatens the health of the animal. Once organic dairy cows are treated with antibiotics, they are considered conventional dairy cows and their milk is no longer considered organic. There is no medication that is FDA approved for use in organic dairy herds. PHYTO-MAST® is being investigated as an antibiotic substitute. It is a botanical phytoceutical, meaning it is made entirely from a plant base.

There is no data regarding *in vitro* studies of PHYTO-MAST® and its effect on mastitis causing bacteria. Therefore, four different strains of bacteria that can cause bovine mastitis were tested for their susceptibility to PHYTO-MAST®. *Esherichia coli*, *Staphlycoccus aureus, Streptococcus bovis,* and *Streptococcus agalactiae* were incubated and tested according to the Clinical Laboratory Standards Institute (CLSI) techniques for antimicrobial susceptibility. A few modifications to the CLSI procedures were made to allow emulisification of the phytoceutical into nutrient broth and facilitate quantification of the results. At this time preliminary results indicate that PHYTO-MAST® may be effective against *E. coli* and *S. bovis*.

Key Terms: Microbiology
Antimicrobial
Animal Health

**PI-16**

## Effect of Chlamydial Infection on Interferon-γ Receptors and the JAK/STAT Signaling Pathway in Human Epithelial Cells

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Binding of interferon-gamma (IFN-γ) to its receptor on the surface of a cell produces a signal cascade via the JAK/STAT signaling pathway that leads to an upregulation of indoleamine-2,3-dioxygenase (IDO) expression. Increased IDO activity can starve obligate intracellular pathogens such as *Chlamydia* of the essential amino acid tryptophan. A previous study found increased levels of IFN-γ receptor α-chain (IFNGR-α) on the surface of cells infected with *Chlamydia psittaci*. However, the presence of additional IFNGR-α does not lead to an increase in IDO activity in IFN-γ stimulated cells. The objective of this study is to examine why an increase in surface IFNGR-α does not lead to an increase in IDO activity in *Chlamydia*-infected cells. Western blot analysis and quantitative real-time PCR (qRT-PCR) were used to analyze changes in protein and mRNA levels of members of the IFN/JAK/STAT pathway in response to infection with *C. psittaci*. Preliminary results suggest that infection with *Chlamydia* does not influence mRNA levels of members of the IFNGR/JAK/STAT pathway, but instead might affect glycosylation of IFNGR-α and degradation or trafficking of IFNGR-β. By altering or destroying IFNGR-α and IFNGR-β, *Chlamydia* may be able to impair the host cell's ability to upregulate interferon-induced IDO expression and therefore avoid destruction by the host.

Key Terms: Microbiology
Immunology
Host Pathogen Interaction

**PI-17**

## The Identification of Sepsis Biomarkers Using High Throughput Real Time PCR Analysis

Danielle Tyson (William G. Enloe High School), Advisor: Shila K. Nordone (North Carolina State University)

Sepsis, a deadly condition caused by bacterial infection of the blood, affects up to 10% of dogs in veterinary teaching hospital critical care units each year. The leading cause of sepsis-related deaths is our inability to rapidly diagnosis the condition. Previous research regarding the pathogenesis of sepsis suggests that proinflammatory and proapoptotic proteins may serve as biomarkers for sepsis.

Using Real Time PCR, we analyzed a number of critical proinflammatory and proapoptotic genes in healthy dogs and dogs diagnosed with sepsis. Blood samples were collected and total RNA was extracted. RNA quality was tested using the Agilent Bioanalyzer before cDNA was synthesized using a reverse transcription enzyme kit. Proinflammatory and proapoptotic transcripts from cDNA were measured by Real Time PCR using custom high throughput 96 well plates pre-loaded with primers specific for 86 individual genes of interest and five housekeeping genes. Data was analyzed using the $\Delta\Delta$Ct method to determine fold-difference in gene expression between healthy and septic animals.

Based on the program analysis parameters, 11 genes were found to be significantly different in expression between healthy and septic animals. These 11 proinflammatory and proapoptotic genes have potential utility as biomarkers in a molecular diagnostic assay for sepsis.

Key Terms: Molecular Biomedical Science
Veterinary Medicine

**PI-18**

**Neutralizatino of Gastric Fluid pH Does Not Affect Pulmonary Transplant Pathology Associated with Chronic Gastroesophageal Reflux Aspiration**

Amy Xie (North Carolina School of Science and Mathematics), Advisor: William Parker (Duke University)

Obliterative bronchiolitis (OB) is the primary factor limiting the long-term success of pulmonary allografts. Chronic aspiration of gastric fluid likely plays a central role in OB pathogenesis. Treatment of patients with acid blockers such as proton pump inhibitors has been shown to effectively reduce symptoms associated with gastroesophageal reflux disease (GERD), but the effects of stomach acid neutralization, potentially a more cost-effective solution, is unknown. Thus, the hypothesis that the two treatments equally reduce GERD symptoms was tested using standard models of rat lungs, treated weekly with aspiration of gastric fluid (GF, pH 2.5), neutralized gastric fluid (NGF, pH 7.4), or normal saline (NS, control). After 8 weeks of treatment, the lungs were harvested, and lung function measures, compliance and histology, were evaluated *ex vivo*. Airways in rats receiving aspiration with neutralized gastric fluid (NGF) displayed results similar to those of rats treated normal gastric fluid (GF), but both were statistically different from controls treated with normal saline (NS). It was observed that transplanted lungs receiving gastric fluid aspiration developed lesions consistent with OB. It appears that neutralization of gastric acid does not prevent injury to pulmonary allografts associated with chronic aspiration in GERD. Other factors in the gastric fluid, such as digestive enzymes or particulate matter, may be the key mediators of injury. These studies strongly suggest that effective management of lung transplant recipients, especially with respect to long term prevention of OB, should include more than simple neutralization of gastric fluid in those suffering from GERD-associated chronic aspiration.

Key Terms: Surgical Sciences
Pulmonary Transplant
Gastric Fluid Aspiration