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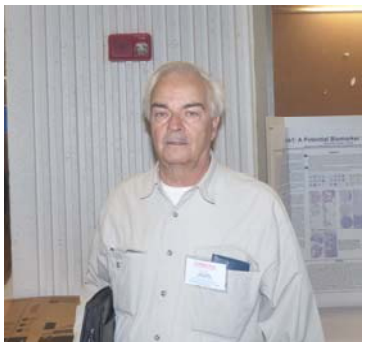






Instructions for Authors

IN VIVO is published three times yearly during the Fall, Winter, and Spring. Original research articles in the field of biology in addition to original articles of general interest to faculty and students may be submitted to the editor to be considered for publication. Manuscripts can be in the form of a) full length manuscripts, b) mini-reviews or c) short communications of particularly significant and timely information. Manuscripts will be evaluated by two reviewers.

Articles can be submitted electronically to *invivo@mec.cuny.edu* or mailed as a printed copy (preferably with a diskette that contains the file) to the Editorial Board at Medgar Evers College. All submissions should be formatted double spaced with 1 inch margins. The title of the article, the full names of each author, their academic affiliations and addresses, and the name of the person to whom correspondence should be sent must be given. As a rule, full length articles should include a brief abstract and be divided into the following sections: introduction, materials and methods, results, discussion, acknowledgments and references. Reviews and short communications can be arranged differently. References should be identified in the text by using numerical superscripts in consecutive order. In the reference section, references should be arranged in the order that they appeared in the text using the following format: last name, initials., year of publication. title of article, journal volume number: page numbers. (eg. - [1]Hassan, M. and V. Herbert, 2000. Colon Cancer. *In Vivo* **32:** 3 - 8). For books the order should be last name, initial, year of publication, title of book in italics, publisher and city, and page number referred to. (eg. - Prosser, C.L., 1973. *Comparative Animal Physiology*, Saunders Co., Philadelphia, p 59.). Abbreviations and technical jargon should be avoided. Tables and figures should be submitted on separate pages with the desired locations in the text indicated in the margins.

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Cryptococcus neoformans var. _grubii_ (serotype A) and var. _neoformans_ (serotype D) Survival Strategies Are Selected from Interactions with Other Environmental Microbes. **Asan F. Abdulkareem[1], Jade M. Greco[1], Cathleen Joseph[1] and Luis R. Martinez[1,2], [1]Long Island University-Post, Brookville, NY and [2]Albert Einstein College of Medicine, Bronx, NY.**

Cryptococcus neoformans is an opportunistic encapsulated fungus capable of causing meningoencephalitis in immunocompromised individuals. *C. neoformans* is frequently found in soil contaminated with pigeon droppings, where the fungus may be in contact with many soil predators, and this interaction might have influenced the evolution of factors associated with enhanced survival in challenging environments. *C. neoformans* var. *neoformans* (serotype D) and *C. neoformans* var. *grubii* (serotype A) differ in geographic prevalence and pathogenicity, with serotype D strains being more prevalent among isolates from temperate countries and causing localized cutaneous disease whereas serotype A strains are distributed worldwide and they cause systemic disseminated disease. In this study, we hypothesized that the survival strategies used by *C. neoformans* in the human host emerged and developed through environmental interactions, due to the constant selection by predation. Therefore, we compared the survival of 5 serotype A and D strains after interaction with soil organisms *Acanthamoeba castellanii* and *Acinetobacter baumannii*. In this regard, Serotype A strains displayed significantly higher survival rate, biofilm formation and capsular polysaccharide production than serotype D strains after interaction with *A. baumannii*. Similarly, serotype A strains were significantly less phagocytized and killed than serotype D strains by *A. castellanii*. Our findings suggest that the ability of serotype A and D strains to survive and cause disseminated or localized disease, respectively, within the human host might be acquired from variable interactions with other environmental species. This work was partially supported by NIH-NIAID 5K22A1087817-02 and LIU-Post Faculty Research Committee Awards.

Identification of Axial Protocadherin Interacting Proteins. **Alyson Abraham, Casie Spiteri and Michael Yoder, SUNY College at Old Westbury, Old Westbury, NY, USA.**

During gastrulation, a mass of cells is organized into distinct germ layers through invagination of the epithelial sheet, which establishes the structural and differentiation sites for the developing embryo. The cadherin family of cell-cell adhesion molecules is one of the most important adhesion groups that instructs proper tissue development during blastula formation, gastrulation and neural tube formation. In the frog, Xenopus laevis, C-cadherin is the only cadherin expressed in early development, so cadherin mediated cell sorting relies solely on the regulation of existing C-cadherin. Protocadherins, the largest subgroup of the cadherin family, have been identified as both positive and negative regulators of cell adhesion. Paraxial protocadherin (PAPC), expressed in the paraxial mesoderm, down-regulates C-cadherin activity, assisting in paraxial mesoderm separation. Axial protocadherin (AXPC), expressed specifically in the axial mesoderm, plays a crucial role is separation of the mesoderm, specifically in notochord morphogenesis. The loss of AXPC causes an altered phenotype defined by the loss of a clear notochord/somite boundary. It is known that loss of AXPC results in reduced mesodermal gene expression, however, it must be doing so through a secondary molecule. Since mesoderm is initiated as a common population, separation into axial and paraxial tissue is likely directed, in part, by the differential expression of AXPC in the axial mesoderm. Initial co-immunoprecipitation experiments tested negative for AXPC/N-cadherin interactions in the HEK293 cell line. We are currently looking to identify other potential interacting proteins, either intra or extra cellular, through mass spectrometry. These results will be verified through directed co-immunoprecipitation in cell culture and differentially staged embryo lysates. We thank all members of the Yoder lab. Special thanks to Dr. Mascareno SUNY, College at Old Westbury for reagents and equipment, and to CSTEP for reagents and funding. We would also like to thank Dr. Gerald Thomsen, Stony Brook University.

Anti-biofilm and Anti-fungal Efficacy of Nitric-Oxide Releasing Nanoparticles against *Candida albicans* Biofilms. Mohammed Ahmadi[1,2], Chitralekha Macherla[2], David Sanchez[3], Adam J. Friedman[3], Moses Tar[3], Joshua D. Nosanchuk[3] and Luis R. Martinez[2,3], [1]Adelphi University, Garden City, NY, [2]Long Island University-Post, Brookville, NY and [3]Albert Einstein College of Medicine, Bronx, NY.

An overwhelming majority of clinical manifestations associated with the fungus *Candida albicans* are associated with the formation of biofilms on implanted medical devices. These prosthetic devices are responsible for a significant percentage of clinical candidiasis and eradication of the infection often times requires the removal of the implant all together, a procedure not always possible due to the patient's condition. It is therefore imperative to develop novel approaches to impede the clinical repercussions associated with candidal biofilms. The aim of this study was to develop a strategy to prevent or treat biofilm colonization on implanted medical devices. In this regard, we developed a stable nanoparticle platform that rapidly deploys nitric oxide (NO) and hypothesized that NO-np can be microbicidal to fungal biofilms *in vitro*. Our results revealed that NO-np significantly decreases both the metabolic activity and the cell viability of fungal biofilms using XTT reduction and colony forming units assays, respectively. Evaluation by live light microscopy demonstrated that NO-np interferes on fungal growth and morphogenesis, therefore, preventing biofilm formation. Confocal microscopic examination demonstrated that NO-np penetrates mature fungal biofilms and destroys *C. albicans* cells encased on exopolymeric matrix. Moreover, comparison with commonly used antifungal drugs, fluconazole and voriconazole, in the clinical setting provided evidence that NO-np are more effective for treatment of *C. albicans* biofilms. Together, these data suggest that these NO-releasing nanoparticles have the potential to serve as a novel class of antimicrobials for the treatment of biofilm-infected prosthetic devices. This work was partially supported by NIH-NIAID 5K22A1087817-02 and LIU-Post Undergraduate Research Awards.

Role of Oral Surface Topographies on Polyclonal Antibody Interactions in Biofilm Formation. Anthony Arena[1], Thomas Owen[1] and Donna Leonardi[2], [1]Ramapo College of New Jersey, Mahwah, NJ, USA and [2]Bergen County Academies, Hackensack, NJ, USA.

Biofilm formation by the leading cariogenic oral flora strain, *Streptococcus mutans*, is initiated via the secretion of glycosyltransferase (GTF). GTF and other associated enzymes convert extracellular sucrose to glucans, facilitating bacterial adhesion to the tooth surface. Several microbiological studies have focused on serum therapy in a wide variety of scenarios, but little work has been done to investigate its potential role in prevention of oral biofilm formation that is associated with caries. This study initially began investigating the effect of polyclonal antibodies on biofilm formation, but has refocused to look at the roles that the surface topographies have on the antibody action. An IgG antibody, ab31181, is known to inhibit the function of GTF and was used in this study as a potential deterrent for biofilm synthesis. *S. mutans* was cultured on calcium hydroxyapatite (CHA) and porcelain fused to metal (PFM) discs. Antibody concentrations of 1:10000, 1:1000, 1:500, and 1:250 were added to these cultures growing on both CHA and PFM discs. A dose response relationship was found: higher concentrations of antibody reduced biofilm formation for both CHA and PFM samples. Data was found to be statistically significant for the CHA ($p<0.05$). Findings indicate that antibody serum therapy may be a viable option for the prevention of dental caries on calcium substrates. Future research goals include beginning molecular analysis of these interactions and improved EM imaging. Potential clinical tests in vivo using the antibody would be needed to investigate practical implications.

Fecundity of Estuarine Shrimp: A Comparison among Species. Afia Azaah, Allen Burdowski and Kathleen Nolan, St. Francis College, Brooklyn, NY 11201, USA.

Eggs carried on the abdomen were counted for over 100 shrimp, most of which were from the Gulf of Mexico (species *Palaemonetes vulgaris*). The free, downloadable program Image J was used in conjunction with a Motic camera. This data was compared to that obtained in *P. vulgaris* and other species in 2007-2008. Certain trends were noted in the data. There is an exponential

correlation of length with mass, and there is only a weak correlation of mass with fecundity. These ubiquitous organisms could be used as biomonitors of estuarine health, especially during times of environmental impacts such as oil spills, hurricanes and global warming. We will continue to collect data from various species in an attempt to examine the ecology of the estuaries.

In-vitro Antimicrobial Activity of Five Invasive Plants of New Jersey. Sana Baig, Elvinas Demereckas, Diego Morales and Daniela Shebitz, Kean University, New Jersey.

Since the evolution of new strains of disease-causing pathogens, a current concern for global health is the ever-increasing spread of antibiotic resistance. Simultaneously, ecosystems throughout the world are being altered by the abundance of invasive plants often through allelochemistry. While we anxiously wait on the development of new pharmaceuticals, cures may surround us in the form of secondary plant compounds of invasive species. This study explores the antifungal and antibacterial properties of invasive plants found in New Jersey. We examined whether extracts from these plants can be used to treat symptoms caused by infection by evaluating their antifungal and antibacterial properties in laboratory assays. Alcohol and aqueous extractions were made for the five plant species: ground Ivy (*Glechoma hederacea*) native to Europe and Southwestern Asia; mugwort (*Artemisia vulgaris*) native to China; multiflora rose (*Rosa multiflora*) native to eastern Asia; Japanese knotweed (*Fallopia japnica*) native to Japan; and garlic mustard (*Alliaria petiolata*) native to Europe, Asia, and northwestern Africa. These plants were screened against gram-negative bacterium *Escherichia coli*, gram-positive bacterium *Bacillus subtilis*, and fungus *Candida albicans* using replicate disc diffusion assays. All five plant species have been used for medicinal purposes in traditional medicine in their native range. Through this poster, we present our methods, preliminary results, and implications of our work for using both ecological and ethnobotanical indicators in screening potential medicinal plants. The strongest evidence of medicinal efficacy were found in Multiflora rose and Ground Ivy.

Red Algae Polysaccharide as a Potential Anti-*Pseudomonas* Agent. Margaret Bell and Tin-Chun Chu. Seton Hall University, South Orange, New Jersey.

Pseudomonas is a genus of gram-negative gammaproteobacteria with a large range of diversity. Because of its ability to grow at low temperature, *Pseudomonas* is a cause of food spoilage. This bacterium is also a very common nosocomial infection of hospital patients. In this experiment, we investigated the effects of a sulfated polysaccharide on *Pseudomonas*. The polysaccharide was obtained from the cell wall of red microalgae. The species *P. fluorescens* were used as a model for looking at these effects. The bacteria were cultured to stationary phase and a microtiter plate assay was performed to observe the effect of the red algae polysaccharide at 0.1%, 0.5%, and 1% concentrations. The inhibition of biofilm formation was also observed using crystal violet assay. From the microtiter plate assay, *Pseudomonas fluorescens* treated with 1% concentration of the sulfated polysaccharide inhibited cell growth. *P. fluorescens* treated with 0.5% showed a slight inhibition of cell growth and the *P. fluorescens* treated with 0.1% did not show any inhibitory effects. The results led to the conclusion that the polysaccharide extracted from marine red algae has antimicrobial effect and could be used to inhibit the growth of *Pseudomonas*.

Newly-Found Eastern Oysters (*Crassostrea virginica*) in Jamaica Bay, NY, Test Positive for MSX (*Haplosporidium nelsoni)*. Reniece Buchanan, Craig Hinkley and, Gary Sarinsky. Kingsborough Community College, Brooklyn, NY. USA.

The Eastern Oyster (*Crassostrea virginica*) is an ecologically and economically important organism. This species was abundantly found in Jamaica Bay, NY until the early 1920's when it is believed that pollution, over harvesting and pathogenic protozoan diseases caused their demise. Since then, no known oyster beds have been observed in Jamaica Bay, until these past two years when small clusters of oysters were detected. One of the suspected pathogenic diseases thought to have infected the oysters is MSX (*Haplosporidium nelsoni*). The mode of transmission of MSX to oysters is not known. However, it results in a gradual disruption of the digestive tubule epithelia. Our lab recently found that some oysters grown from spats in Jamaica

Bay in Taylor Floats under controlled conditions tested positive for MSX. This study attempts to determine whether any of the new oysters found in Jamaica Bay have MSX. We hypothesize that since the environmental conditions are similar to other bodies of water along the Eastern Coast where MSX is presently found to exist, that MSX will be observed in some of the newly-found oysters as well. Gill and mantle DNA was extracted from the new oysters using a DNeasy Blood and Tissue Kit. The DNA from 10 oysters and a positive MSX DNA sample were subjected to PCR with a MSX specific primer set. Two of the10 oysters were positive for MSX. We demonstrated that we could amplify MSX under the conditions used with the positive control. We further verified that DNA was extracted in all the samples by amplifying the oyster mitochondrial CO1 gene using Folmer primer, and the correct size (702 bp) was confirmed by gel electrophoresis. The 10 samples were submitted to Elim Biopharmaceuticals for sequencing and the results were subjected to a NCBI Blast Search which further confirmed that the two positive samples were MSX and the CO1 DNA were from *Crassostrea virginica*. This experiment showed that some of the oysters tested were infected with MSX and thus supported the hypothesis.This work was supported by grant 2R25GM0600309 of the Bridge Program of NIGMS and grant 0537121091 of the CSTEP Program of NYSED.

Research on the Antibacterial Activity of Garlic and Honey. Patricio E. Bueno, Mary T. Ortiz and Loretta Brancaccio-Taras, Kingsborough Community College, Brooklyn, New York, USA.

Garlic and honey are available. Studies are testing their antibacterial properties. This study focuses on the ability of garlic and honey, alone and in combination, to kill potential respiratory pathogens. Aqueous garlic extract (GE), garlic supplement pills (GP), honey (H), aqueous garlic extract combined with honey (GE+H) and garlic pills combined with honey (GP+H) were tested for antibacterial activity against 4 bacteria, 2 Gram-positives (S*taphylococcus aureus, Enterococcus faecalis),* and 2 Gram-negatives (*Klebsiella pneumoniae, Pseudomonas aeruginosa)*. The hypothesis was garlic, honey and their combination will be as effective as commonly prescribed antibiotics to treat potential respiratory pathogens. Antibiotics tested were bacitracin, erythromycin, gentamycin, penicillin and tetracycline. The procedure was an agar diffusion assay using tryptic soy agar plates inoculated with the bacteria. Disks containing GE, H, GE+H, GP, GP+H and the antibiotics were placed on the surface of the inoculated plates and incubated 24h@37^{o}C. Zones of inhibition were measured, and sizes were compared using the Mann-Whitney U test. Based on the analysis, H, GE, GP, GE+H, GP+H were not as effective as the antibiotics ($p \leq 0.05$, 2-tailed test) tested against *P. aeruginosa*, *K. pneumoniae*, and *E. faecalis.* Honey combinations (GE+H, GP+H) were less effective than GE or GP alone. For *S. aureus,* GE (28.00$\pm$0.7mm) ($x\pm$SEM) was more effective than bacitracin (14.25$\pm$0.7mm), erythromycin (22.81$\pm$0.39mm), tetracycline (24.06 $\pm$0.30mm), and gentamycin (21.40 $\pm$0.41mm). The only antibiotic that was more effective ($p \leq 0.001$, 2-tailed test) than GE was penicillin (32.40$\pm$0.60mm). Based on the results the hypothesis is only accepted for GE against *S. aureus*. Further studies may confirm garlic extract could possibly be used to inhibit growth of potential respiratory pathogens. Supported by grants 2R25GM0600309 Bridge Program (NIGMS), 0537121091 NYSED CSTEP.

Pollination Biology of *Petunia hybrida*: Differential Pollen Receptivity of Buds at Different Ages. Nicole Burton and Farshad Tamari, Kingsborough Community College, Brooklyn, New York, USA.

Our research focuses on the pollination biology of *Petunia hybrida*. We set out to determine pollen receptivity, measured through seeds set, throughout bud development. We measured seeds set for buds at four, three, two and one day prior to anthesis and for open flowers. We hypothesized that stigma of young buds four days before anthesis are least receptive to pollen grains compared to older buds. We also hypothesized that pollen receptivity increases as buds mature until the opening of the flowers at which stage they are optimally receptive. To test our hypothesis, we compared pollination data from pollination of stigma of flowers at anthesis (+ control) and non-pollinated flowers (- control) with that of flower buds one to four days before anthesis. For all pollination, other than the negative control, mature pollen from an open flower was used. Seed set was used as a measure of pollen receptivity. Seed set for buds at four, three, two and one day before anthesis were

found to be 0 (±0), 0 (±0), 13.67(±23.7), and 187 (±16.0), respectively. That of the positive and negative controls were 176(±17.2) and 0(±0). A one way ANOVA on these preliminary results from replicate pollinations on one plant indicate that pollination using flower buds at one day before anthesis yields the same number of seeds as the positive control. Seed set from pollination of buds younger than one day before anthesis was not statistically different from the negative control. Knowledge of the pollination and reproductive biology of *Petunia hybrida* is valuable as it is a commercially important plant. This work was supported by grants 2R25GM0600309 of the Bridge Program of NIGMS and grant 0537101091 of the CSTEP Program of the NYS Department of Education.

Ack1: A Potential Biomarker for Lung Cancer. Emily Chen and Azad L. Gucwa, Department of Biomedical Sciences, Long Island University at Post .

In recent years, there has been a great movement towards personalized medicine and the identification of clinically significant biomarkers. Identification of biomarkers that are both sensitive and specific for various types of cancers has proven to be challenging. Nonetheless, to date, numerous biomarkers have been identified that are routinely used in the clinical decision-making process. Most patients diagnosed with lung cancer are not diagnosed at an early stage, often with a poor prognosis. The stage in which a patient is diagnosed greatly affects the 5-year survival rate. According to the National Cancer Institute, diagnosis while the tumor is still localized results in a 5-year-survival rate of 52.6% as compared to 16.3%. Recognizing the lack of useful biomarkers in lung cancer and the subsequent poor survival rate, we have identified Ack1 as a potential biomarker for lung cancer metastasis. Ack1, a member of the Rho family of GTPases, has been highly implicated in the progression of a wide variety of cancers, including that of the lung. Amplified activity and overexpression of the Ack1 results in increased invasiveness, a hallmark of cancer progression as well as metastasis. With the goal of developing Ack1 into a useful biomarker for lung cancer, we have applied the molecular method of fluorescence *in* situ hybridization (FISH) to determine the levels of Ack1 amplification in a lung tumor tissue array. While our results are still in the preliminary stages, the use of FISH for this purpose has shown some promise. Work is being continued to optimize our protocol, to further test whether the detection of Ack1 via FISH is suitable for use in the clinical laboratory.

Multifunctional, Stimuli-responsive Protein Polymer-gold Nanoparticle Hybrids for Small Molecule Delivery. *Raymond Chen[1], Min Dai[1], Ekta Sharma[1], Navjot Singh[1] and Jin K. Montclare[1,2], [1]Polytechnic Institute of NYU, Brooklyn, NY and [2]SUNY Downstate Medical Center, Brooklyn, NY.

Stimuli-responsive, multifunctional proteins capable of self-assembling and forming defined, nanometer-scale structures have been closely studied for their potential in therapeutics, particularly in drug delivery vehicles and tissue regeneration systems. In a previous study, a library of protein diblock copolymers – E_nC and CE_n -derived from naturally occurring self-assembling domains (SADs) elastin (E) and the coiled-coil domain of the cartilage oligomeric matrix protein (C) were generated, where n represents the number of elastin repeats. The entire engineered library exhibited self-assembly, inverse transition temperature, and small molecule binding. In order to further induce the self-assembly and subsequent small molecule release, we have templated gold nanoparticles (GNPs), which exhibit surface plasmon resonance enabling the conversion of light energy into thermal energy. This self-assembly is dictated by the length of the E domain. Out of the engineered protein diblock library, E_1C and CE_1 have been chosen to template the GNPs due to their high inverse transition temperatures (38.0°C and 59.0°C, respectively), high small molecule binding capacity, and thermo-stability. The block orientation affects GNP templation, thermo-responsiveness and overall small molecule binding and release of the GNP-protein polymer composite. In particular, GNP templation leads to a slightly less ordered structure for both protein types as well as an increase in inverse transition temperature. Both Protein-GNP polymer complexes demonstrate enhanced thermostability, binding capacity to the anti-inflammatory, antitumor agent curcumin, and exhibit extended release times of curcumin compared to the non-templated protein polymer. Furthermore, the un-complexed and hybrid complex proteins bound to curcumin exhibit uptake into the breast cancer cell line MCF_7, making them suitable for potential use in drug delivery. This work was supported by NSF DMR and MRSEC.

Septin Could Regulate Distribution of Phosphatidylinositol-4,5-bisphosphate in the Plasma Membrane of Cells. Jia Cheong and Urszula Golebiewska, Queensborough Community College, Bayside, NY.

Phosphatidylinositol-4,5-bisphosphate (PIP2) comprises about 1% of the phospholipids of a typical plasma membrane of mammalian cells. It performs wide range of roles during cells signaling. Several investigators proposed and subsequent experiments confirmed existence of separate pools of PIP2. One of the events requiring enhanced concentration of PIP_2 is cytokinesis, the last step during the cell division. It involves the separation of cellular material into two daughter cells and requires three steps: formation of a cleavage furrow, ingression through contraction of an actomyosin ring and abscission via membrane fusion. PIP2 plays roles in regulating the cytoskeleton and vesicle trafficking. Enrichment of PIP2 might regulate the attachment of the contractile ring. How the enrichment of PIP2 in the furrow is generated is not understood. Possibly a region enriched in saturated lipids (i.e. raft) prevents movement of PIP2 from the furrow. If this is the case then how such a region is formed? We investigated whether septin, a cytoskeletal protein is responsible for regulating the distribution of PIP_2 during cytokinesis using fluorescent microscopy and spectroscopy techniques. We determined that the septin 2 protein upon binding to lipid vesicles penetrates the hydrophobic region of the bilayer allowing it to perturb the bilayer. We observed that the co-localization of PIP_2 and septin is modest in quiescent mammalian cells. It does not significantly increase in dividing cells. We also investigated the distribution of PIP2 in giant unilammelar lipid vesicles composed of raft forming lipids. This work was supported by C3IRG R9 grant to UG.

Induction of Adipogenesis in Mesenchymal Cells Isolated from Limb Buds of Early Chicken Embryos. Lauren Clancy, Adam Drucker, Kristene Hirsch, LeighAnn Mulholland and Anthony Tolvo, Molloy College, Rockville Centre, NY, USA.

Chicken embryo mesenchymal cells have been used to study developmental aspects of multipotent and pluripotent stem cell populations. One of our goals was to establish and characterize a chick embryo derived mesenchymal cell line to use in future studies. We report the ability of chick mesenchymal cells to undergo adipogenic induction *in vitro.* Limb buds from early embryos (stages 25 – 28) were dissected under aseptic conditions and the tissue explants were teased apart to free the mesenchymal cells. Cells were cultured for several passages, assessed for viability and used directly for adipogenic induction. For induction, cells were initially plated in 60 mm dishes (experimental and control) at 2 x 10^4 cells/ml in α-MEM with 10% FBS, high glucose and 1% antibiotic solution. For differentiation, 0.5 µl/ml IBMX, 1µl/ml insulin and 2 µl/ml and dexamethasone were added to the experimental culture medium and all cells were cultured for 2 – 3 additional days. After removing the medium, cells were stained for neutral lipid deposits by using oil-red-o stain. The cells were photographed using bright field phase 1 microscopy. Results revealed that treatment of the mesenchymal cells with the induction medium caused a dramatic increase in triglyceride and neutral lipid droplets within the cytoplasm over controls. The results show that chick embryonic limb bud mesenchymal cells can undergo rapid differentiation into adipogenic cells at this stage of development and validate the avian embryonic model for such differentiation studies. Future studies examining the potential of these cells for osteogenic and chondrogenic differentiation will complete their characterization as mesenchymal stem cells.

Manganese Accumulates in Leaves of Radishes Grown in Manganese Supplemented Soils. Shellyann Clarke-Lambert, Melissa Stapleton, Karl Ruddock and Dereck Skeete, Medgar Evers College, Brooklyn, NY.

Manganese is a naturally occurring element, essential in trace amounts for living organisms, but is toxic in high concentrations. Certain occupations including mining, welding and steel manufacturing can expose workers to chronically high levels of airborne manganese, leading to a clinical condition known as Manganism, a Parkinsons-like condition. Recent studies report excess dietary manganese can impair immune and reproductive functions in birds. Previously we showed manganese is present in some commercially available fertilizers. We hypothesize plants grown in soils high in manganese or supplemented with fertilizers containing manganese will accumulate manganese in their leaves and fruits. To test this we grew radishes in soils supplemented with fertilizers containing

manganese, as well as in soil without added manganese. Samples (0.5 g) of each of the fertilizers as well as radish leaves were digested with HNO_3 in a microwave digester. Digested samples were analyzed for manganese levels using electrothermal vaporization with deuterium lamp background correction in a Perkin Elmer AA800 Atomic Absorption spectrophotometer with a THGA graphite furnace. We found leaves from plants grown in soils supplemented with manganese accumulated manganese up to about 104 µg/gm tissue. Control leaves contained 25.28 µg/gm of manganese, which was significantly less than all the experimental groups. On the other hand, the soil that contained fertilizer had a significantly higher concentration of manganese than the plant tissue. The highest concentration of manganese recorded in the soil with manganese supplement fertilizer was 1709 µg/gm, while the lowest concentration was 1280 µg/gm. The study shows plants will accumulate manganese from the soil and that use of fertilizers with high concentrations of manganese will increase the accumulations, possible creating a situation where animals and people ingesting the fruits and vegetables might be subjected to elevated manganese levels. This work was supported by grants 0516041071 of NYSDOE and 0622197 of the DUE Program of NSF.

The Effect of Silver Nanoparticles and Silver Bulk Particles on Mustard Plants. Laeticia Compas, Mohammad Rana and Tetiana Delaney. St. Joseph's College, Patchogue, NY, USA.

The mustard plant *Brassica juncea* can be found in multiple areas such as Asia and the Middle East. The usage of nanoparticles in the modern world might support or demote the growth of cultivated vegetation. This study shows the effects of the silver nanoparticles (AgNPs) and silver bulk particles (AgBPs) on the mustard plant, particularly the *Brassica juncea*. Different concentrations of 0 ppm, 20 ppm, 100 ppm, and 200 ppm of AgNPs and a concentration of 100 ppm and 1000 ppm of AgNO3 were utilized. During the AgNO3 bulk particles treatment, the root length, stem length and growth of leaves were negatively affected the greater the concentration was. The AgNP treatment of higher concentrations (100 ppm and 200 ppm) generally stimulated the growth of the *B. juncea* seeds in root length and stem length but caused deformation of the leaves during the 7-day growth period. DNA analysis of the plants will be performed.

Correlating Conserved *Cis*-Regulatory G-quadruplex Motifs Distribution With Gene Function. Matt Crum, Camille Menendez, Scott Frees and Paramjeet S. Bagga, Ramapo College of New Jersey, NJ.

Three-dimensional structures called G-quadruplexes can form in single-stranded segments of nucleic acids which have high guanine content. There is sufficient evidence to support G-quadruplex role in biological processes as *cis*-regulatory elements of post-transcriptional gene expression. Consequently, G-quadruplex motifs have been implicated in human disease and are being targeted for therapy. G-quadruplex motifs found in the translated as well as untranslated regions of the mRNAs have been shown to play important roles in the expression of several genes. However, there is a lack of large scale systematic studies for analyzing G-quadruplex distribution patterns in functionally diverse genes. Characterization of genes based on G-quadruplex distributions within them and their relationship with gene function can help better understand the biological significance of these structures and how they affect post-transcriptional gene expression. We have developed two web applications, QGRS-H Predictor and QGRS-DB, which identify and make accessible data relating to G-quadruplex distribution across multiple exomes. Using these tools, we have analyzed the entire human exome for evolutionarily conserved G-quadruplexes. Our results show that genes associated with brain development, negative regulation of cell proliferation, and transcription factors have a higher frequency of G-quadruplex occurrence within their mRNAs. In oncogenes, we noticed a particularly high occurrence of G-quadruplexes in the 5'-untranslated region, between 160-280 nucleotides upstream of the translation initiation site. It has been well documented that G-quadruplexes in the 5'-untranslated regions can regulate gene expression by inhibiting or enhancing translation. Therefore, prevalence of evolutionarily conserved G-quadruplex motifs in the 5'-UTR suggests their regulatory roles which are much needed for tightly controlled expression of oncogenes. Our studies suggest that the distribution of G-quadruplex regulatory motifs differs among various functional categories of human genes and correlates with the requirements of their post-transcriptional gene expression.

Newly Discovered Eastern Oysters (*Crassostrea virginica*) in Jamaica Bay, NY Were Not Found to be Positive for Dermo (*Perkinsus marinus*). Philip Cussimano, Craig Hinkley and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY. USA.

Attempts are underway to re-establish the Eastern Oyster (*Crassostrea virginica*) in Jamaica Bay, New York. It is thought that one of the reasons for their decline in the 1920's was as a result of the pathogenic parasitic protozoan Dermo (*Perkinsus marinus*). There have been no known natural oyster beds observed in the Bay until this year when divers found small clusters of oysters in several locations. Our lab recently tested one and two year old oysters that had been grown from spats in Jamaica Bay in Taylor Floats under controlled conditions. A number of them tested positive for Dermo. The purpose of this study was to determine if any of the newly found oysters were infected with Dermo. We hypothesize that Dermo will be observed in the new oysters. Gill and mantle DNA was extracted from the new oysters using a DNeasy Blood and Tissue Kit. The DNA from 10 oysters and a positive Dermo DNA sample were subjected to PCR with a Dermo specific primer set. None of the oysters were positive for Dermo but we demonstrated that we could amplify Dermo under the conditions used with the positive control. Since no Dermo was amplified from the oysters tested we further verified that DNA was extracted by amplifying the oyster mitochondrial CO1 gene using Folmer primer, and the correct size(702 bp) was confirmed by gel electrophoresis. The 10 samples were submitted to Elim Biopharmaceuticals for sequencing and the results were subjected to a NCBI Blast Search which further confirmed that the CO1 DNA was from *Crassostrea virginica.* Contrary to our hypothesis, this experiment showed that the oysters tested were not infected with Dermo. This work was supported by grant 0537121091 of the CSTEP Program of NYSDOE.

Microbial Characterization of Composted Material. Prasha Das, Elizabeth Kulko, Belal Ibrahim, Edward Veloz, Thomas Flannery, Jacqueline Mateo, Jeyson Gil, Ana Polanco, Veena Methner, Brenda Margolies, Teresa Aponte, and Luis Jimenez. Bergen Community College, Paramus, NJ, USA.

The culturable microbial communities in compost produced by the Rocket® Composter system were characterized using phenotypic and molecular analyses to understand the numbers and diversity of microorganisms responsible for transforming organic waste into compost. Mesophilic and thermophilic bacterial numbers ranged from 10^6 to 10^{10} cells/gram of soil. Anaerobic bacterial counts ranged from 10^6 to 10^8 cells/gram. Predominant culturable aerobic and anaerobic species were identified by 16S rRNA analyses as members of the phyla Firmicutes and Actinobacteria. Within the Firmicutes, the family Bacillaceae was found to be predominantly present in samples with bacterial species identified as *Bacillus thermoamylovorans* detected in aerobic and anaerobic growth media. *Escherichia coli* was isolated from lactose enrichments and identified by DNA sequencing of ribosomal RNA gene and PCR amplification of the *uidA* gene. During the sample period, seven percent of samples exhibited the presence of *E. coli* but isolation was sporadic with numbers below acceptable levels for compost maturation. The Rocket composter produced a robust and metabolically active microbial community that converted cafeteria waste into composted soils.

Moms and Music: An Assay for Female *Drosophila* Decision Making. Alexa Decker, Nathan Kemper, Olivia Focazio, Lisa Applegate, Jessyka Venchkoski and Julian Paul Keenan, Montclair State University, Montclair, NJ.

Egg laying location in female drosophila is an under-used, but potentially powerful assay. Female drosophila have been known to discern oviposition site selectively. This study utilized and replicated previous findings in order to determine if a tone would deter or encourage egg laying. After being exposed to either tone or no tone during breeding, females were tested in a Petri dish with tone or no tone and a small area of substrate (containing sucrose, caffeine or only agar). It was found that more eggs were laid on sucrose and in the presence of a tone.

Black Tea Theaflavins as a Novel Way to Inhibit Herpes Simplex Virus. Aline de Oliveira, Derek Prince and Tin-Chun Chu. Seton Hall University, South Orange, New Jersey.

Tea is the second most consumed drink in the world. Black tea is derived from the leaves of *Camellia sinensis* plant, and it is rich in theaflavin polyphenols, in particular theaflavin (TF1), theaflavin-3-monogallate (TF2A), theaflavin-3′-monogallate (TF2B), and theaflavin-3,3′-digallate (TF3). Vero cells were used to evaluate the effect of black tea theaflavins as anti-herpes simplex 1 agent. Results of the cell viability and proliferation assay showed that TF1, TF2, and TF3 are not toxic to Vero cells at a concentration up to 100 μM. Plaque forming assay showed that TF1, TF2, and TF3 inhibit the production of viral plaques at a concentration of 50 μM and above. TF3 showed the highest anti-herpes simplex 1 effect on Vero cells. Thus, black tea theaflavins may serve as a natural remedy against herpes simplex viral infections.

Testing the Anti-Cancer Effect of Curcumin, a Turmeric Extract. Deanna Doctor, Lauren Geyman and Thomas Owen, Ramapo College of New Jersey, Mahwah, NJ, USA.

School of Theoretical and Applied Science, Ramapo College of New Jersey.

As students hoping to pursue naturopathic medicine in the future, we have chosen to study natural paradigms of healing for our research. Curcumin is an extract from turmeric, a root from the ginger family, and is widely used as a natural healer, specifically in Ayurveda, India's 5,000 year old natural medical system. Curcumin, the principle curcuminoid of three in the turmeric root, gives turmeric its orange color and is said to have anti-cancer properties. In the studies reported here, our first goal was to determine the highest dose of curcumin that is not toxic to rat osteosarcoma (Ros) cells. We conducted several growth assays using concentrations of curcumin ranging from 75 μg/ml to 0.075 μg/ml. Cells growing in 96 well dishes were exposed to curcumin at plating and 3 days later were treated with a dye which when acted upon by mitochondria, forms a colored compound which is measured by spectrophotometer (Cell Titer 96, Promega, Inc). After conducting these tests, we determined that 0.1 μg/ml of curcumin appears to be the best dose and we will use this dose in our continuing research. Ongoing experiments are monitoring the effects of curcumin on alkaline phosphatase, an enzyme whose activity in Ros cells correlates with osteoblastic differentiation. This is being done in order to determine if curcumin can affect cell growth and differentiation separately. In the coming year, we plan to extend our research from rat osteosarcoma cells to human breast and ovarian cancer cells to determine if curcumin affects tumor-derived and normal cells differently and to begin to assess its mechanism of action.

The Effect of Melatonin on Genomic Instability in Cells Defective in Homologous Recombinational DNA Repair. Kimberly Doyle and Maureen Sanz. Molloy College, Rockville Centre, NY, USA.

The primary defect in the genetic disorder Bloom's syndrome (BSyn), is caused by mutation in *BLM*, the gene that encodes BLM, a RecQ DNA helicase. BSyn cells are defective in homologous recombinational repair and are hyperrecombinable and hypermutable. The cellular phenotype is characterized by chromosomal aberrations, a strikingly elevated frequency of sister chromatid exchange, and oxidative stress. The unrepaired DNA damage, increased rate of somatic mutation and recombination between homologous chromosomes may explain the increased predisposition to neoplasia observed in persons with BSyn. Melatonin (MLT) is a molecule naturally produced by the human body. Its reported oncostatic activity, antioxidant properties, and lack of toxicity distinguish MLT as a potential cancer therapy to reduce the side effects of and protect healthy cells from radiation- and chemotherapeutic drug- induced cytotoxicity. This study investigates the potential use of MLT to reduce the constitutional genomic instability in cells from persons affected with BSyn. Exponentially growing cultures of lymphoblastoid cell lines derived from an unaffected individual and from an individual with BSyn were treated for 48 hours with varying concentrations of MLT. Cultures were harvested by standard cytogenetic technique and slides prepared. Controls and treated cultures were analyzed for cytostaticity by quantitative determination of mitotic index and genomic instability by quantitative evaluation of micronuclei formation. One thousand giemsa stained cells from each culture were analyzed microscopically(100x) and scored for the number of cells in metaphase and for micronuclei formation. A cytotoxic effect was not observed in

either normal or BSyn control or MLT-treated cell cultures. A slight reduction in the frequency of micronuclei formation as compared to control cultures was observed in normal and BSyn cultures treated with increasing concentrations of MLT. These preliminary results may demonstrate an *in vitro* ameliorative effect of melatonin on the constitutional genomic instability of cells from persons with BSyn.

Role of Histamine in the Sensory Motor Integration of Gill Lateral Cilia in the Bivalve Mollusc, *Crassostrea virginica*. Jened Duncan[1], Patrick Akande[2], Edward J. Catapane[1] and Margaret A. Carroll[1], [1]Kingsborough Community College and [1]Medgar Evers College, Brooklyn, NY.

Lateral cilia of gill of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervations. The motor aspects of this control have been well studied over the years. The sensory side has not been. There is limited information about sensory inputs. We found *C. virginica* can sense and adjust gill cilia beating appropriately to the presence of food and other chemical cues including histamine. Histamine doesn't alter beating when applied to gill, but when applied to mantle rim causes a slight, but statistically significant decrease in beating rates. Detaching the mantle rim or transecting the branchial nerve prevented histamine's actions. We hypothesize histamine is a sensory neurotransmitter in mantle rim involved in the sensory-motor integration of gill lateral cilia activity. Other tested neurotransmitters/ neuroactive substances including serotonin, dopamine, acetylcholine, GABA, and FMRFamide had no effects on gill lateral cilia beating rates when applied to mantle rim. We conducted a study of the actions of histamine, and 3 classes of histamine receptor antagonists when applied to mantle rim on their ability to influence gill lateral cell cilia beating. Cilia beating was measured by stroboscopic microscopy in whole animal preparations. Applying histamine (10^{-6} - 10^{-3} M) to mantle rim decreased beating. The H1 antagonists, diphenhydramine and H2 antagonist famotidine, produced dose-dependent blockages of histamine. Conessine, a H3 antagonist was not effective in blocking histamine. The study further demonstrates a sensory-motor integration of beating of lateral cilia that involves the sensory mantle rim and the visceral ganglia and suggests histamine is a putative sensory neurotransmitter in mantle receptor cells that synapses with afferents going to the VG where signals are integrated resulting in a motor response to the gill lateral cells. This work was supported by grants 2R25GM06003 of the Bridge Program of NIGMS, 0516041071 of NYSDOE and 0622197 of the DUE Program of NSF.

The Lapatinib-Induced Gene Expression Program in HER2-Positive Breast Cancer Cells. Mercedes Duran-Paez and Marc Y. Fink, LIU Post, Brookville, NY.

HER2 positive breast cancer is caused by the over expression of the HER2 receptor. This over expression is seen in 20-30% of all breast cancers and is cause by the amplification of the HER2 gene on chromosome 17. HER2 positive breast cancer is treated with lapatinib, a small molecule tyrosine kinase inhibitor that targets HER2 and HER1 receptors. Prolonged exposure to lapatinib is known to cause resistance. To study the mechanism of resistance, a HER2 positive cell line model was used. When the BT474 cells are treated, the AKT pathway is inhibited. The inhibition of AKT prevents the phosphorylation of the transcription factor FOXO3a which allows it to translocate to the nucleus. Data presented here further characterize the kinetics of this translocation. FOXO3a is hypothesized to be an important factor in resistance since it is known to transcribe genes that are pro-apoptotic and genes that are pro-survival. To assess the role of FOXO3a, siRNA was used to silence its expression. The absence of FOXO3a decreased the induction of the known lapatinib-induced genes *irs2, depp.* Further screening of lapatinib-induced genes will provide a comprehensive regulatory map of the signaling-gene circuitry underlying the decision of a cancer cell to survive or die in response to drug treatment.

The Depressed Mud Crab (*Eurypanopeus depressus*) Does Not Appear to Be a Vector for the Pathogenic Protozoan Dermo (*Perkinsus marinus*) in Jamaica Bay, NY, Chantal Edouard, Craig Hinkley and Gary Sarinsky. Kingsborough Community College, Brooklyn, NY USA.

The Eastern Oyster (*Crassostrea virginica*) has not been observed in Jamaica Bay, NY since the early 1920's. Our lab has been growing oysters from spats in Taylor Floats under controlled conditions for the past 9 years. Tests to determine whether the pathogenic protozoan

known as Dermo (*Perkinsus marinus*) would be present in these oysters have shown some to be positive. Dermo is a single celled protozoan which is known to be transmitted from oyster to oyster. If Dermo is spread from oyster to oyster and there are no known oysters in the bay, how did they become infected with Dermo? Some literature suggests that Dermo can be transmitted by vectors. The Depressed Mud Crab (*Euryponopeus depressus*) seeks refuge from direct sunlight as well as from predators by hiding in the clusters and valves of the Eastern Oyster. Because of the close proximity to the oysters, it is hypothesized that the Depressed Mud Crab serves as a vector for Dermo. DNA was extracted from the tissues of the Depressed Mud Crab by using a DNeasy Blood and Tissue Kit. The DNA and a positive Dermo DNA sample were subjected to the Polymerase Chain Reaction (PCR) using Dermo specific primers. The PCR products were subjected to agarose gel electrophoresis to determine the presence or absence of Dermo. None of the crabs tested were positive for Dermo but the control was positive and at the correct size (365bp). We further verified that DNA was extracted from all samples by amplifying the Depressed Mud Crab mitochondrial COI gene using Folmer primers. All the samples were positive and the correct size (702bp) was confirmed by agarose gel electrophoresis. The COI gene was found to be present in all samples and was sent to Elim Biopharmaceuticals to be sequenced. The sequences were subjected to a NCBI Blast search which further verified that the COI gene was from *E. depressus*. The experimental results showed that the Depressed Mud Crabs tested were not vectors for Dermo and our hypothesis is rejected.

Identification and Isolation of Phytoplankton and Their Viruses from Barnegat Bay in New Jersey. Nicole Elia and Tin-Chun Chu. Seton Hall University, South Orange, New Jersey.

In 2011, the Barnegat Bay Partnership issued a report stating that the environmental conditions of Barnegat Bay are declining due to high levels of nitrogen in the water. Increased nitrogen levels have led to eutrophication and the formation of harmful algal blooms (HABs) caused by various species of phytoplankton such as cyanobacteria, dinoflagellates, and diatoms. The resulting HABs cause a decrease in dissolved oxygen levels in the water as well as the release of toxins affecting organisms that inhabit the bay. In this study, water samples were obtained from 16 different sites ranging from the northern to southern locations of Barnegat Bay. Each sample was filtered and analyzed using Chelex DNA extraction followed by PCR based assay. General and specific DNA primers were use to detect the presence of marine phytoplankton. In conjunction with the phytoplankton study, a second study was implemented involving phage isolation and identification from the same Barnegat Bay water samples. Water samples were concentrated and used in plaque assays to confirm the presence and lytic effects of phage that can be used as a natural controlling method to prevent cyanobacteria populations from forming HABs. Initial plaque assays were able to detect cyanophages at following six sites: Westeconk West, Westeconk East, Silvery Bay West, Silver Bay East, Double Creek West, Forked River West.

The Effect of H4 Mutation on H3 Acetylation. Timi Elvuchio and Daniel S. Ginsburg. LIU Post, Brookville, NY, USA.

Chromatin is the DNA-protein complex that makes up the chromosomes in eukaryotic cells. The basic unit of chromatin is the nucleosome, consisting of DNA wrapped around histone proteins. Chromatin impedes transcription by blocking access of the RNA polymerase to DNA. Thus, transcription can only take place if chromatin is altered. One way in which chromatin is altered is through post-translational modification of histones. Acetylation of lysines in histone tails neutralizes their positive charge and weakens DNA/histone interactions. Histone acetylation is key to the disassembly of chromatin. The two major lysine acetyltransferase complexes in yeast are NuA4 and SAGA. They have been shown to work together to stimulate transcription initiation and elongation. We have previously shown that SAGA-mediated H3 acetylation decreases in NuA4 mutants, suggesting that H4 acetylation (H4Ac) stimulates H3 acetylation (H3Ac). To test the hypothesis that H4Ac stimulates H3Ac, we examined H3Ac in H4 mutants that cannot be acetylated. We observed a 3 fold decrease in tetra-acetylated H3 in bulk histones in an unacetylatable H4 mutant (K5,8,12,16R) as compared to WT H4 and an acetylated H4 mimic (K5,8,12,16Q) by western blot. Because histone acetylation stimulates chromatin disassembly, we analyzed histone eviction at the inducible *ARG1* and *GAL1* genes by chromatin immunoprecipitation (ChIP). We did not observe

much histone eviction at *ARG1* but unexpectedly at *GAL1* histone eviction at the ORF was stimulated by the K5,8,12,18R mutant. We are in the process of tagging SAGA subunit *ADA2* to check SAGA occupancy in the K5,8,12,16R mutant. Our data suggest that H3Ac is stimulated by H4Ac and that the effects on histone eviction are more complex than was previously thought. This research was funded by a grant from the LIU Post Research Committee.

Role of Sit-1 in Osteoblast Function. Emily Emmet[1], Garrett McConville[1], Steven Popoff[2] and Thomas Owen[1], [1]Ramapo College of New Jersey, Mahwah, NJ and [2]Temple University School of Medicine, Philadelphia, PA.

The objective of these experiments was to use rat osteosarcoma cells to begin to elucidate the role of the Sit-1 protein in osteoblast differentiation. Sit-1 is a member of a family of transmembrane adapter proteins (TRAPs) and has been reported to function in T-cell receptor activation in the immune system. The TRAPs are phosphorylated by members of the c-src family of kinases. Interestingly, when the c-src gene is knocked out of mice, bone formation increases, suggesting that Sit-1 may also play a role in osteoblast function, although Sit-1 has not yet been associated with any functions in bone. To test this hypothesis, rat osteosarcoma (Ros 17/2.8) cells were transfected with either an expression plasmid carrying the rat SIT-1 cDNA or the empty plasmid (the control group). Cells that that took up the plasmid were selected by resistance to the antibiotic G418 and pools of them were used in our experiments. SIT-1 transfected cells and control cells were plated in 12 well dishes and then harvested every 3 days for 15 days. At each day, some cells were fixed in paraformaldehyde and histochemically stained for alkaline phosphatase enzyme activity while other cells were lysed and frozen. These lysates then assayed for alkaline phosphatase activity using a quantitative enzyme assay. We found that while alkaline phosphatase activity increased with osteoblastic differentiation as expected, at each time assayed, the overexpression of Sit-1 led to a further increase in enzyme activity. These data strongly suggest that an increase in Sit-1 expression enhances the osteoblast phenotype through increasing the extent of their differentiation. This work was supported by the Ramapo College Foundation and the Research Honors Program in the School of Theoretical and Applied Science.

Effects of Lipopolysaccharide-induced Inflammation on Hypoxic Gene Expression Pathways in the Rat Testis. Genevieve Fasano and Michael A. Palladino Monmouth University, West Long Branch, NJ.

Research in male reproductive biology is an active area because it helps to gain a greater understanding of infertility, cancers of the male reproductive tract, erectile dysfunction, and fetal development. Inflammation of the male reproductive tract is of particular interest because bacterial and viral infections are known causes of infertility. We hypothesize that antimicrobial protection of the male reproductive organs is achieved through both classic inflammatory pathways and hypoxic pathways involving the protein hypoxia-inducible factor-1 (HIF-1). The overall goal of our research is to determine the effects of lipopolysaccharide (LPS)-induced inflammation on gene expression pathways of the rat testis. The objective of this project was to identify hypoxia pathway genes that are up-regulated or down-regulated following LPS administration and to determine the role of these genes in the overall cellular response of the testis to inflammation. Induction of inflammation in rats was accomplished via intraperitoneal administration of LPS from *P. aeruginosa* at a dosage of 5 mg/kg body weight for 3 or 6 hours (n = 6-7 animals/time point). RNA was isolated from testes and cDNA was synthesized using reverse transcriptase. A quantitative polymerase chain reaction (qPCR) array was used to evaluate expression of a panel of 91 genes involved in hypoxia pathways. Array results demonstrated that 9 genes (*Adm, Angptl4, Egr1, Fos, Ier3, Nfkb1, Pgf, Serpine1, Slc2a1)* showed statistically significant up-regulation after 3 hours of LPS-induced inflammation and expression of 3 genes (*Angptl4, Egr1, Serpine1)* remained elevated after 6 hours. No genes were down-regulated by LPS. Future experiments will investigate gene expression in the inflammatory pathway following LPS-induced inflammation. The role of these genes and their relation to genes up-regulated in the hypoxic pathway will then be studied to develop potential models for understanding molecular mechanisms of antimicrobial responses in the testis. Funding: ICFNJ– Merck Undergraduate Science Endeavors Scholarship.

Curcumin as an Inhibitor of Herpes Simplex Virus 1 Infection in Cultured Vero Cells. Daniel Flores and Sandra D. Adams, Montclair State University, Montclair, NJ.

Herpes simplex virus 1 (HSV-1) a member of the *Herpesviridae* family, is a common human pathogen known to cause oral lesions. Worldwide the incidence of HSV-1 is estimated between 65% and 95% with most infected persons unaware of infection. Those infected with HSV-1 are associated with life-long latent infection. Current treatments that work to reduce transmission of HSV are not cost effective and hard to obtain in under-developed countries, where HSV is the most prevalent. Plant derived products have gained popularity as promising antiviral agents. One promising antiviral plant derived product is curcumin (diferuloylmethane), a polyphenol extracted from the plant *Curcuma longa,* a member of the ginger family *Zingiberaceae*. Curcumin is widely abundant, cost effective and has been employed in Ayurveda, the Indian system of medicine, for approximately 6000 years. Curcumin has been demonstrated to contain antioxidant, anti-inflammatory, antitumor and antiviral properties. The purpose of this project was to determine if curcumin exhibits antiviral properties against HSV-1 in cultured Vero cells. The maximum non-cytotoxic concentration of curcumin (62.5 mM) on Vero cells was determined by microscopic examination of treated cells and quantification by trypan blue assay. The direct effect of infectivity was determined by treating cells and virus with the maximum non-cytoxic concentration, the results of this reveled a significant decrease of cytopathic effect of Vero cells by curcumin. Adsorption, attachment, and penetration assays determined that treatment with curcumin reduced the ability of HSV to enter Vero cells. A PCR-based assay was used to determine the effect on viral DNA replication. Use of curcumin has the potential for development of a safe, effective, and inexpensive topically applied therapeutic agent to reduce transmission and replication of HSV-1. This work was supported by the 2013 Benjamin Cummins/MACUB Research Grant and the Montclair State Science Honors Innovation Program.

***Paguris longicarpus* (Long-Armed Hermit Crab) Does Not Appear to Serve as Vector for Dermo (*Perkinsus marinus*) in Jamaica Bay. NY. Jessica Fraser, Craig Hinkley and Gary Sarinsky. Kingsborough Community College, Brooklyn, N.Y. USA.**

Perkinsus marinus (Dermo) is one of the factors that are suspected of causing the loss of *Crassostrea virginica* (eastern oyster) in Jamaica Bay, NY. Dermo is an intracellular parasite infecting the blood cells of the oyster. Natural infections are most often caused by parasites released from the disintegration of dead oysters. The disease is thought to be transmitted from oyster to oyster. Some one and two year old oysters that have been grown from spats in Jamaica bay in Taylor floats under controlled conditions have been shown to be positive for Dermo. Our research problem is: If there are no known oysters in the bay how did they contract Dermo? Recent literature suggests that the transmission may occur by vectors such as scavengers feeding on infected dead oysters or by parasitic snails. This study attempts to determine if *Pagurus longicarpus (Long-Armed* Hermit Crab) is a potential vector. We hypothesize that hermit crabs are scavengers and will be found to be a vector for Dermo. DNA was extracted from six hermit crabs using the DNeasy Blood and Tissue Kit. The tissue samples were subjected to PCR with a Dermo specific primer set. We demonstrated that we could amplify Dermo under the conditions used with a positive control for Dermo. Since no Dermo was amplified from the hermit crabs tested we verified that DNA was extracted by amplifying the hermit crab mitochondrial CO1 gene using the Folmer primer and the correct size (702 bp) was confirmed by gel electrophoresis. Amplified DNA was sequenced by ELIM Bio pharmaceuticals and they were subjected to a NCBI Blast search which further verified that the CO1 DNA was from *Pagurus longicarpus.* The hermit crabs tested were not positive for Dermo and therefore do not support our hypothesis. This work was supported by grant 2R25GM0600309 of the Bridge Program of NIGMS and grant 0537121091 of the CSTEP Program of NYSED.

Associative Learning for Tone in *Drosophila melanogaster.* Brad Gold, Alexa Decker, Nathan Kemper and Julian Paul Keenan. Montclair State University, Montclair, NJ.

Music is an innate human activity expressed in every culture on Earth. However, explaining the ultimate and proximate reasons for how man evolved the capacity to comprehend music has long confounded researchers. Previous studies have demonstrated that humans instinctively prefer consonant tones over dissonant tones. Other species of the animal kingdom show sensitivities to certain pitches, tones, and sound intensities– including birds, crickets and various mammals. In this study, we conditioned 3rd instar Drosophila melanogaster larvae to prefer consonant tones over dissonant tones via Pavlovian conditioning. One group (n=20) was placed in a petri dish of neutral agar for three minutes. A small, circle of fructose-infused agar (UCS+) was inset on one side of the dish. Above this inset was a headphone that played a consonant sine tone harmony (CS+). On the other side of the dish was placed a second headphone that played white noise of the same intensity. The group was then placed into another petri dish for another three minutes – this one with a sodium chloride-infused inset (UCS –). Above this inset was headphone that played a dissonant sine tone harmony (CS –). A second group (n=20) was conditioned reciprocally (USC+/CS – and USC – / CS+). For the critical test trials, five larvae from each group were tested with one following dipolar headphone setups: 1) Consonant harmony vs. dissonant harmony, 2) dissonant vs. white noise, 3) consonant vs. white noise, and 4) white noise vs. white noise. Initial results indicate that larvae tend to spend more time on the side with the tone condition with the positive stimulus. This suggests associative learning and "conscious" differentiation of separate tones among the larvae. This study hopes to result in a better understanding of how tonal preferences and the comprehension of music first evolved in humans.

Ack1 Disruption of the Trans-Golgi Network (TGN) is Independent of Kinase Activity. Li Guan[1], Victoria Prieto-Echagüe[2], Deborah A. Brown[3], W. Todd Miller[3] and Azad L. Gucwa[1], [1]Long Island University, Brookville, NY. [2]Institut Pasteur de Montevideo, Montevideo, Uruguay and [3]School of Medicine, Stony Brook University, Stony Brook, NY.

Ack1 (activated Cdc42 kinase 1), is a non-receptor tyrosine kinase and a direct effector molecule of Cdc42, a member of the Rho GTPase family. It is activated in response to several different ligands as well as cell adhesion and plays a role in clathrin-mediated internalization of EGFR and cell signaling. Unpublished results from our lab suggests that Ack1's effects on endocytosis are not limited to the clathrin pathway. Overexpression of Ack1 in various cell lines efficiently blocked internalization of the caveolar pathway, as well as a clathrin- and caveolin-independent pathway. In the present study, we found that Ack1 overexpression induced the tubularization and disruption of gamma Adaptin, a marker of the trans-Golgi network (TGN). To test the importance of kinase activity, we expressed a kinase-dead construct (K158R) as well as the N-terminus and kinase domain (NKD), and the kinase domain alone (KD). Cells expressing the K158R construct displayed the same phenotype, suggesting kinase activity is not required for the disorganization of the TGN. In contrast, NKD and KD did not have any effect on the TGN; however, it is unclear whether this due to the difference in localization of these two constructs as compared to wild-type Ack1. Expression of the clathrin-binding mutant (D572A) also resulted in the disruption of the TGN, indicating that binding to clathrin is not required. We also overexpressed wild-type Ack1 and studied its effect on mannose 6-phosphate receptor (MPR). This receptor binds newly synthesized lysosomal hydrolases in the trans-Golgi network (TGN) and delivers them to pre-lysosomal compartments. A GFP-tagged form of cation-independent MPR (CI-MPR) was sequestered at the plasma membrane when co-expressed with Ack1, suggesting Ack1 also has an effect on retrograde transport. Taken together, our results indicate overexpression of Ack1 plays a significant role in endocytosis as well as intracellular trafficking.

A Role for BIM in Lapatinib-Induced Apotosis in HER-Positive Breast Cancer. Elizabeth A. Haughney and Marc Y. Fink. LIU Post, Brookville, NY, USA.

Overexpression of HER2 occurs in 20-30% of breast cancer and is associated with poor prognosis. HER2 heterodimerizes with HER3 to drive cancer cell proliferation and survival. Lapatinib, a dual inhibitor of HER2, is used to treat HER2-positive breast cancer patients. When the HER2 receptor is inhibited, the cellular signaling pathways (ERK and AKT) are suppressed and the cell undergoes apoptosis. The exact mechanism of growth factor receptor-deprivation driven apoptosis is not well understood and was the subject of the current study. Within the cell there are BCL-2 family proteins, some are pro-survival and others are pro-apoptotic. BIM is a pro-apoptotic protein in the BH3 only group that activates BAX/BAK, thereby, initiating the apoptotic pathway. Previous studies have shown that BIM protein levels are dramatically elevated in response to lapatinib in HER2-positive breast cancer cell lines. The data presented here, utilizing cleaved-PARP as an apoptotic marker in BT474 cells, show a fairly rapid onset of apoptosis. Apoptosis was detected at 1 hour and peaked at 4 hours post addition of lapatinib. Preliminary data show that BIM levels are weakly increased within this time frame. These results support the hypothesis that BIM is involved in lapatinib-induced apoptosis in breast cancer cells.

Dual Actions of Octopamine on Heart Rate of *Crassostrea virginica*. *Addy Jean Louis, Margaret A. Carroll and Edward J. Catapane, Medgar Evers College, Brooklyn, NY.

Octopamine, biogenic amine first identified in octopus, is well studied in arthropods and gastropods serving as a neurotransmitter and hormone. Octopamine's presence and functions have rarely been reported in bivalves. Previously we found octopamine in cerebral and visceral ganglia (VG), gill, palps and hemolymph of the oyster *Crassostrea virginica* and that octopamine was cardio-acceleratory when applied to whole animal preparations,but cardio-inhibitory when applied to isolated hearts. Oyster heart is innervated by a cardiac nerve from the VG and can also respond to hormones. To study these divergent results we examined effects of octopamine on heart rate by applications to VG with and without transecting the cardiac nerve, on isolated hearts and on ventricular muscle strips. Heart rate was monitored with a Physiograph. Data were collected and analyzed with a DATAQ DI-700 Data Acquisition System. Average basal heart rate of whole animal preparations was 15 beats/min. Superfusing octopamine (10^{-6}-10^{-3}M) onto whole animal or VG preparations caused a dose-dependent increased up to 70%. Applying octopamine to isolated hearts or heart strips decreased rates to 0. The octopamine antagonist, metoclopramide (10^{-6}-10^{-4}M), produced a dose-dependent blockage of octopamine's actions on both whole animals and heart strips. Transecting the cardiac nerve prevented the cardio-acceleratory effects of octopamine. The study shows octopamine affects heart rate in 2 different fashions depending on the site of application, inhibitory when applied to isolated heart, acceleratory when applied to the whole animal or VG. At the VG, octopamine may be stimulating cardio-acceleratory neurons innervating the heart via the cardiac nerve. In should be noted superfusing a drug to a ganglion could cause stimulation of receptors on different neurons, which is not a normal physiological situiation. This work was supported by grants 2R25GM06003

Expression of Monoamine Oxidase-A (MAO-A) in Cancerous and Non-Cancerous Cell Lines. Odile Jean-Pierre, Roselie Pierre-Bois and Tammy A. Castro, Bloomfield College. Bloomfield, NJ.

Monoamine oxidase-A (MAO-A) is an enzyme that catalyzes the breakdown of serotonin (5-hydroxytryptamine). The enzyme is coded for by the X-linked MAO-A gene which presents a well characterized functional polymorphism. A published analysis of genechip datasets points to a consistent decrease of MAO-A expression in cancers among a variety of tissues. The purpose of this study is to measure MAO-A activity in tumorigenic and non-tumorigenic cell lines in order to determine if the predicted decrease can be measured and correlated to tumorigenicity. Preliminary data obtained using a luminescent method, suggests that MAO-A expression is negatively correlated to malignancy of breast cancer. Future work will examine the levels of MAO-A message and activity in a wider cell population and determine the polymorphic state of the gene in each cell type.

Evaluating Mitochondrial Dysfunction in Autism: Mitophagy as a Putative Causative Mechanism. Charlotte Jimenez[1], Rujin Tian[2] and Guomei Tang[3]. [1]Hunter College, NY, [2]Bronx Community College, NY and [3]Columbia University, New York.

Autism spectrum disorders (ASD) are complex neurodevelopmental disorders characterized by impaired social interactions, deficits in communication and repetitive behaviors. It occurs in approximately 1 out of every 110 children in the U.S by the age of 8 years. While synaptic pathology, denoted by increased dendritic spine density and loss of normal GABAergic neurotransmission, has been identified by postmortem assessments of the brains of autistic children as a hallmark feature of ASD brain, the precise signaling pathway and intracellular mediators for synaptic abnormalities in ASD are largely undefined, limiting treatment and prevention strategies. Mitochondria are essential for neuronal survival and synaptic transmission. Proper degradation of long-lived and/or damaged mitochondria through mitophagy is a key cellular pathway for mitochondrial quality control. Recently, patient derived lymphoblast cell lines were utilized as an ASD cell model, in which mitochondrial dysfunction and oxidative stress have been reported. Here, we show that mTOR dependent autophagy is disturbed in postmortem autistic brains exhibiting dendritic spine pathology, which points to the possibility that autophagy dependent mitochondria degradation (mitophagy) is inhibited in autism patients. This may lead to accumulation of damaged mitochondria, and consequently mitochondria dysfunction as demonstrated by ASD lymphocytes.

Preliminary Characterization of a Streptomyces Strain Collection. Kanchanpreet Kaur, Kimberly Deleon, Chung Tse, Mangala Tawde and Monica Trujillo, Queensborough Community College, CUNY.

Streptomyces are Gram-positive filamentous bacteria highly abundant in soils, sediments and seawater and they belong to the Actinomycetes order. The mechanisms to elicit the production of secondary metabolites are very diverse and not completely understood. We have characterized a collection of Streptomyces isolated from New York State soil environments by studying interspecies interactions. We studied interactions between ten isolates among themselves and with the model organism *Streptomyces coelicolor*. The resistance profile of each strain was used to discard putative repeats existing in the collection. We detected changes in the developmental cycle of some of the strains induced by secondary metabolites produced by other strains in the collection. We also identified strains that produced compounds with antibiotic activity only when they were growing next to other strains from the collection. This approach of isolating pure cultures and then studying their interactions with other pure cultures in the laboratory is very useful strategy to build a collection with no repeats and also can be powerful tool to reveal the production of new natural products previously undetected.

Use of DNA Barcoding to Examine the Origin of Eastern Oysters Used in a New York Restoration Project. Michelle Kelmansky, Gary Sarinsky and Craig Hinkley. Kingsborough Community College, Brooklyn, NY. USA.

Crassostrea virginica, the eastern oyster, is native to North America. There were many oyster beds in NY bays, including Jamaica Bay (JB); however, there are no longer any known natural oyster beds. This large decline in oysters has raised interest in restoration and management of oyster populations. One example is the Oyster Restoration Research Project in NY in which oysters grown by students from NY Harbor School (NYHS) were seeded into NY Harbor. Our overall goal is to examine the genetic background of these oysters since this will help determine how they spread within the NY harbors. In 2001, our lab showed that oysters were able to survive and reproduce in JB. Since the oysters from our study and the NYHS were obtained from local oyster farms, we wanted to know whether they were from the same farm. Our hypothesis is that the oysters from NYHS are from the same farm as the 2001 study. To test our hypothesis, we first amplified a 700 bp region of the cytochrome c oxidase I (COI) gene using PCR. The size of the PCR products were confirmed by agarose gel electrophoresis and the PCR products were sequenced by Elim Biopharmaceuticals. A BLAST search showed the PCR products were from COI gene of *Crassostrea virginica.* The COI genes from 69% of oysters in the 2001 study contain a polymorphism that distinguishes them from eastern oysters of other regions. An alignment using the sequences of the NYHS

oysters and sequences from our 2001 study showed the NYHS oysters did not have this polymorphism. These results suggest the NYHS oysters are not from the same oyster farm as those used for our 2001 study and we therefore reject our hypothesis. This work was supported by grant 0537121091 of the CSTEP Program of NYS Department of Education.

Enhanced Removal of Carbamazepine in Biochar Amended Soil. Azel King[1], Stephen A. Boyd[2], Hui Li[2] and Mark Bezdek[2], [1]Medgar Evers College, Brooklyn, NY and [2]Michigan State University, East Lansing, MI.

This research analyzed effects of biochar as a soil amendment. Evidence shows a significant increase in levels of pharmaceuticals in soil, resulting from the application of livestock waste, which has value as fertilizer but often contain pharmaceuticals. We studied the sorption of the anti -depressant carbamazepine by biochar because it frequently occurs in natural waters. To quantify sequestration of carbamazepine by biochar, a batch equilibration method was used, involving adding a series of aqueous carbamazepine solutions to known masses of biochar. Samples were centrifuged to separate liquid and solid phase. The liquid phase was analyzed for its carbamazepine concentration by HPLC coupled to tandem mass spectrometers. The differences between the initial and final concentrations of carbamazepine in solution allows for the calculation of the mass sequestered by a unit mass of biochar. This quantifies carbamazepine's affinity for biochar and provides perspective on the efficacy of biochar as a soil amendment to reduce transport of carbamazepine to ground waters and surface waters. This study showed biochar is a more effective sorbent for carbamazepine than soil. Experiments were made using soil and water as controls and 1% and 10% biochar amended soil were used to observe how carbamazepine is sorbed. In 1% biochar amended soil, it decreased to 4.5% and in 10% biochar amended soil to 0.2%, whereas controls reduced to 16%. The use of biochar as an *in situ* soil or sediment amendment reduces the bioavailable fraction of toxic organic chemicals, and hence the threats they pose to human and ecosystem health. This represents a new direction in the management of contaminated soils and sediments. It has been estimated that the cost to treat contaminated sediments on a per hectare basis is reduced from $2.5 million for conventional dredging and disposal to $75,000 for in -situ biochar amendments.

Anti-biofilm and Anti-microbial Efficacy of Cetrimide and Chlorhexidine against *Acinetobacter baumannii*. Suvarna Krishnamoorthy[1] and Luis R. Martinez[1,2], [1]Long Island University-Post, Brookville, NY and [2]Albert Einstein College of Medicine, Bronx, NY.

Acinetobacter baumannii is a rapidly emerging and problematic pathogen that causes nosocomial infections worldwide. The majority of clinical *A. baumannii* isolates display high-level resistance to commonly utilized antimicrobial drugs, which severely compromises our capacity to care for patients with disease. As a result of its resistance to most antibiotics available, *A. baumannii* infections are costly to treat. *A. baumannii* can survive in dry conditions and during outbreaks has been recovered from various sites in the patients' environment, including bed curtains, furniture and hospital equipment. Therefore, radically new approaches are urgently needed for its eradication. The purpose of this study was to assess the efficacy of cetrimide (CT) and chlorhexidine (CHX), either alone or in combination, in eradicating *A. baumannii* biofilms formed on stainless steel washers (SSW) were used as a tool to mimic abiotic environment found in the hospital setting. Seven clinical strains isolated from wound cultures at the Montefiore Medical Centre, Bronx, NY were used in this study. Using colony forming units (CFU) and crystal violet (CV) assays, we demonstrated that increasing doses of each disinfectant alone or combination of low CT and CHX concentrations were able to efficaciously damage *A. baumannii* biofilms formed by 8 different isolates. Additionally, a strong correlation (R^2= 0.99) was found between the two methods- CFU and CV assays employed. Our findings suggest that either CT or CHX or combination of both disinfectants might be utilize to eradicate *A. baumannii* from the hospital setting in order to reduce infections caused by this troublesome microbe. This work was partially supported by NIH-NIAID 5K22A1087817-02 and LIU -Post Faculty Research Committee Awards.

Composite Gel Electrophoresis Resolves Large Human Lung Glycoproteins (Mucins) that Control Lung Inflammation. Melanie Krongold[1], Steve M. Fernandes[2], Anabel Gonzalez Gil[2], HuiFeng Yu[2], Yadong Wei[2] and Ronald L. Schnaar[2], [1]Wagner College, Staten Island, NY and [2]Johns Hopkins University, Baltimore MD.

The immune system is highly regulated, in part by cell-cell interactions that either activate or inhibit immune responses. When these interactions are disrupted, the resulting misdirected immune responses can lead to immune diseases such as allergic asthma and chronic obstructive pulmonary

disease (COPD). Siglec-8 and Siglec-9 are cell surface molecules on eosinophils and neutrophils, respectively, that normally inhibit immune responses. They recognize and bind to specific sialylated glycans on target tissues (like the lung), then induce immune cell apoptosis. Large (>500 kDa) sialylated proteins called mucins on the surface of human lung tissues were identified as likely Siglec counter receptors. The goal of my research was to resolve, transfer, and identify these large mucins, or Siglec-8 and Siglec-9 counter receptors, from human lung tissue using detergent and/or guanidine extracts of human lung parenchyma, bronchus and trachea. I have developed SDS-urea agarose polyacrylamide composite gel electrophoresis as a tool to identify very high molecular weight proteins that bind Siglec-8-Fc and Siglec-9-Fc recombinant proteins. Their identification will help us understand the control of lung inflammation in allergic asthma and COPD, and perhaps develop new ways to halt misdirected immune responses.

Distribution and Frequency of Microbial Genes in Compost and Compost Bacteria Isolated from the Rocket Composter. Elizabeth Kulko, Belal Ibrahim, Edward Veloz, Thomas Flannery, Brenda Margulis, Prasha Das, Jacqueline Mateo, Teresa Aponte and Luis Jimenez, Bergen Community College, Paramus, New Jersey, USA.

Compost produced by the Rocket Composter (RC) were analyzed by direct DNA extraction, PCR, DGGE, and DNA sequencing analysis. Culturable bacterial isolates were analyzed for the presence of cellulose degradation genes. Direct detection of microbial genes in compost DNA showed Eubacterial and Actinobacterial 16S rRNA genes present in all samples tested. Mold was not culturable by the media and only 8% of compost DNA exhibited mold genetic sequences. Beta-glucosidase genes were found in 96% of compost samples. Bacterial isolates showed 74% reaction with the primer pair. Cellulase gene *cel48* was detected in 46% of compost samples while the numbers for culturable isolates were 26%. Lower numbers were found with primers amplifying cellulase gene *cel5*. Only 19% of compost samples showed a positive reaction while 21% of culturable isolates showed positive PCR amplification. Ammonia monooxygenase genes, *amoA*, were found in 88% of compost samples tested. DGGE analyses of compost DNA demonstrated a non-culturable bacterial community dominated by species belonging to the phyla Firmicutes and Actinobacteria. Only one of the species detected by DGGE was found to be culturable with the media used.

Sudy of the Effect of CuO Nanoparticles on the Morphology and DNA Damage in Radish Plants. Sonali Kumari, Mohammad Rana and Tetyana Delaney. St. Joseph's College, Patchogue, New York, USA.

Nanotechnology is a fast growing field which is used in various areas ranging from environment to industries. Although nanotechnology has brought benefits to the world, nanoparticle's harmful effects on plants have led researchers to study nanoparticles in more detail. ZnO, TiO2 and CuO nanoparticles are the most commonly studied. CuO have shown to cause the most DNA damage in plants. A study on CuO nanoparticles induce DNA damage and also cause structural abnormalities in plants has been conducted to further support the studies on nanoparticle's harmful effects. The affect of different concentrations of CuO nanoparticles 1ppm, 10ppm, 100ppm, and 1000ppm on structural and DNA damage on radish seeds were studied. The result showed that increasing concentration of CuO nanoparticles led to a decrease in the root length of the radish plants. Furthermore, the radish seeds were also exposed to 100ppm and 1000ppm of CuO bulk particles. The result showed that increasing concentration of CuO bulk particles also led to a decrease in the root length of the radish plants. The CuO nanoparticles caused the most damage to the root length of the radish plants when compared to CuO bulk particles.

Analysis of the Genetic Structure of Eastern Mud Snail Populations from Fort Wadsworth and Plumb Beach in New York. Goldy Landau, Gary Sarinsky and Craig Hinkley. Kingsborough Community College, Brooklyn, NY. USA

The eastern mudsnail, *Ilyanassa obsoleta*, is native to estuaries along the North America coast. However, it is an invasive species on the west coast where it has taken over habitats of native shellfish including *Cerithidea californica*. In order to control the distribution of mudsnails, we need to understand the genetic structure of their populations. This will help determine whether we need to manage local populations separately or

can treat them as one large population. Since *Ilyanassa obsoleta* populations are abundant in many NY bays, including Fort Wadsworth (FW) and Plumb Beach (PB), we examined the genetic structure of mudsnails from these locations to determine if they are from the same or different populations. Our hypothesis was that mudsnails from FW and PB are from the same population. To test our hypothesis, we PCR-amplified a 700 bp region of the cytochrome-c-oxidase I gene using DNA isolated from mudsnails collected at FW and PB. We verified the length of the PCR-amplified DNA by agarose gel electrophoresis and the DNA was sequenced by Elim Biopharmaceuticals. A BLAST search was performed to ensure our DNA is from *Ilyanassa obsoleta*. Estimates of average evolutionary divergence over sequence pairs within groups (d) for mudsnails from FW was d=0.01046 (S.E.=0.00179) and from PB was d=0.01023 (S.E.=0.00112). Using a two-tailed t-test with alpha=0.05, we were unable to reject the null hypothesis that average diversity between the two groups was the same, p-value=0.9407. Phylogenetic tree analysis using the neighbor-joining method showed that DNA sequences from FW and PB were not grouped into separate clades. In conclusion, these data suggest that the mudsnails from FW and PB do not represent two populations; therefore, we accept our hypothesis that they are from the same population. This project was supported by grant 0537121091 of the CSTEP Program of NYS Department of Education.

Effects of Green Tea Polyphenols on Endospore Germination in *Bacillus cereus*, *B. megaterium*, and *B. subtilis*. Nozrin Laskar, Hassan Tahir, Oliqua McKenzie and Lee H. Lee, Montclair State University, Upper Montclair, New Jersey.

Endospores pose high concern when found in various environments due to their highly resistant characteristics. To investigate a method in controlling endospore germination, particularly outgrowth, purified endospores from *Bacillus cereus*, *B. megaterium* and *B. subtilis* were treated with four types of green tea polyphenols: GTP (mixed green tea polyphenols), LTP (lipophilic green tea polyphenols), EGCg (epigallocatechin gallate), and EGCg-Stearate. Ten-day grown spore crops were purified using American Society for Testing and Materials (ASTM) method, and were boiled at 100°C for 20 minutes to kill any remaining vegetative cells. Heated samples were treated with 1%, 5%, 10% of GTP, LTP, EGCg or EGCg -Stearate for 2 hours, diluted and plated onto nutrient agar plates, and subsequently incubated at 37°C for 24 hours. Non-starved cells and starved cells without treatment were designated as controls; separate controls were used for hydrophilic and lipophilic treatments. Transmission electron microscopy (TEM) photographs with EGCg treatment illustrate stressed damage to spore's structural integrity, while treatment with EGCg-Stearate display complete spore surface disruption. Inhibition of hydrophilic (GTP and EGCg) treatments ranged from 88.41% - 100%, and lipophilic (LTP and EGCg-Stearate) treatments ranged from 85.86% - 100%. Results obtained suggest that green tea polyphenol compounds significantly inhibit endospore germination. This experiment proposes that natural antimicrobial compounds may aid in preventing food and beverage spoilage caused by spore-forming bacteria, prevention of contamination of devices in the medical industry, and overall aid in controlling harsh endospore conditions.

Methamphetamine Enhances *Streptococcus mutans* Adhesion and Biofilm Formation to Abiotic Surfaces. Hiu Ham Lee[1] and Luis R. Martinez[1,2], [1]Long Island University-Post, Brookville, NY and [2]Albert Einstein College of Medicine, Bronx, NY.

Methamphetamine (METH) is a powerful central nervous system stimulant drug and a major public health problem in United States (US). A common sign of METH abuse is extreme tooth decay, a condition known in the media as "METH mouth" and highly prevalent in prisoners, impacting the US correctional facilities' budgets. Users with "METH mouth" have blackened, stained, or rotting teeth, even among young or short-term users. The exact causes of "METH mouth" are not fully understood. The leading hypothesis is that METH constricts blood vessels thereby limiting blood supply resulting in "dry mouth" (xerostomia). A reduction in saliva impairs the mouth's capacity to neutralize harsh acids produced by oral bacteria after metabolizing carbohydrates, resulting in erosion of the teeth and gums and increasing the susceptibility of teeth to damage. This process is exacerbated by behaviors common in users on a

METH high: a strong desire for sugary foods and drinks, compulsive tooth grinding (bruxism), and neglect of brushing and flossing. Hence, our project investigates the relationship between METH use, microbial surface colonization, and increased dental disease using *Streptococcus mutans* as a model organism. *S. mutans* is a Gram-positive coccus-shaped bacterium commonly found in the oral cavity and a significant contributor to tooth decay. Using colorimetric XTT reduction and colony forming unit assays, we observed that bacterial cells grown in the presence of METH adhered and formed more robust biofilms than controls. To complement the cell viability methods, *S. mutans* biofilm mass was measured by crystal violet staining obtaining similar results. Our findings suggest that METH might increase the risk of microbial dental disease in users, information that may help the development of more effective public health strategies to deal with this scourge on our society. This work was partially supported by NIH-NIAID 5K22A1087817-02 and LIU-Post Faculty Research Committee Awards.

Screening the *Saccharomyces cerevisiae* Genomic Library for Genes Involved in Copper Induced Cell Death. Weiwu Li and Nidhi Gadura, Queensborough Community College, Bayside, NY.

The broad goal of our study is to understand the mechanism(s) by which copper alloy surfaces kill microorganisms. It has been known that copper kills microorganisms but the mechanism of cell death is still not clear. Previous results from our lab indicate that copper surface mediated cell death of bacteria and yeast correlates with increased levels of lipid peroxidation. *Saccharomyces cerevisiae FLEXgene* ORF collection in the BY011 expression vector was acquired from the Harvard Institute of Proteomics (HIP). There are a total of 5533 clones in the collection. We hypothesize that screening this overexpression library for survivors on lethal doses of copper will reveal genes involved in the copper induced cell death. Plasmids are extracted from the library collection, DNA is pooled together and WT yeast strain BY4741 is transformed. Our results indicate that in a 96 well format, cell death occurs in wild type *Saccharomyces cerevisiae* strain BY4741 at 30mM $CuSO_4$ concentration between 40-50 min. Screen results reveal that overexpression of some ORFs protect the yeast strain from copper induced cell death. The genes discovered in this screen will expose the cellular pathways involved in copper induced cell death. This project was funded by PSC – CUNY and Copper Development Association grant to Dr. Gadura. Funding for Weiwu Li is provided by QCC NSF – STEP grant.

Overexpression of Ack1 Interrupts Endocytosis and is Dependent on its Interaction with Cdc42. Ting-Nien Lin[1], Chao Ye[1], Victoria Prieto-Echagüe[2], Deborah A. Brown[3], W. Todd Miller[3] and Azad L. Gucwa[1], [1]Long Island University, Brookville, NY, [2]Institut Pasteur de Montevideo, Montevideo, Uruguay and [3]School of Medicine, Stony Brook University, Stony Brook, NY.

Ack1 (activated Cdc42-associated kinase1) is a direct effector of activated Cdc42 and is amplified and overexpressed in a number of tumors. Its strong implications in cancer and associations with the Rho family member make it of great interest. However, until recently, little was known about this non-receptor tyrosine kinase and its regulation. Ack1 is known to play an integral role in clathrin-dependent internalization and the downregulation of activated EGFR. Our lab is interested in studying the effects of Ack1 overexpression on the trafficking of ErbB2, a member of the ErbB family of growth factor receptors. Treatment of cells in culture with the ansamycin antibiotic, geldanamycin (GA), results in the internalization and degradation of ErbB2 in a clathrin-independent manner. We found that overexpression of Ack1 disrupts the downregulation of ErbB2 in GA-treated cells. Interestingly, we also discovered that overexpression of Ack1 has an extensive influence on intracellular trafficking. Endocytosis of cholera toxin, which occurs via caveolae, was also blocked by the overexpression of Ack1. To test the importance of kinase activity, we expressed a kinase-dead construct (K158R). Cholera toxin accumulated at the plasma membrane in cells expressing K158R, suggesting kinase activity is not required. In addition, we found there to be only a partial block in cholera toxin uptake with the expression of the autophosphorylation mutant construct, Y284F. In contrast, the Cdc42-binding mutant (ΔCrib) did not block cholera toxin uptake, indicating Ack1's interaction with Cdc42 is important for this to occur. Taken together, this data strongly suggests overexpression of Ack1 has a global effect on endocytosis and vesicular transport.

p-Aminosalicylic Acid Prevents the Loss of Immunofluorescence Emissions of Post-Synaptic Dopamine D2 Receptors due to Manganese Treatment. Kurt Loney-Walsh[1], Yelena Chekayev[2] Margaret A. Carroll[2] and Edward J. Catapane[2], [1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY.

Manganese a neurotoxin causing Manganism, a Parkinsons-like disease, disrupts dopamine neurotransmission. The toxic mechanism is not fully resolved. Reports postulate it more related to dysfunction of dopamine D2 receptors than degeneration of dopamine neurons. Lack of effective treatments is an obstacle in management of Manganism. *Crassostrea virginica* gill lateral cell cilia of are controlled by serotonergic-dopaminergic innervations. Our lab showed dopamine receptors in these cells are D2 type and manganese blocks cilio-inhibitory effects of dopamine. We also showed toxic effects of manganese are blocked by p-aminosalicylic acid. Questions exist whether manganese decreases the number of D2 receptors. We used immunohistofluorescence to test if manganese decreases the number of D2 receptors in gill and if p-aminosalicylic acid prevents the decrease. Using 1° antibodies against D2 receptors and FITC -linked 2° antibodies, we quantified D2 receptors. Animals were treated up to 6 days with 500 μM of manganese. Gills were excised, fixed, exposed to 1° and 2° antibodies and paraffin embedded. Sections were viewed with FITC excitation and emission filters. Control gill showed bright FITC fluorescence. Fluorescence intensities were quantified using ImageJ software from NSF. Intensities in sections from animals treated up to 6 days with manganese showed progressive decreases in fluorescence up to 36%. Animals co-treated with manganese and p-aminosalicylic acid did not show reduced fluorescence. The study shows negative correlation between fluorescence intensities of D2 receptors in manganese treated animals vs controls and shows p-aminosalicylic acid negates the effect manganese. The question whether the loss in fluorescence intensity is due to a decrease in D2 receptor number or if manganese is altering the protein conformation and ligand binding site of D2 receptors needs to be further explored. This work was supported by grants 2R25GM06003 of the Bridge Program of NIGMS, 0516041071 of NYSDOE and 0622197 of the DUE Program of NSF.

Survey of Soil Bacteria, from Brooklyn NY, with Potential Commercial Applications. Lissette Lopez-Guzman, Roger Mitchell and Carolle Bolnet, Ph. D. Medgar Evers College, Brooklyn, New York, USA.

Our previous work examined the types of volatile organic compounds (VOCs) metabolites produced by four soil bacteria (D1 to D4) isolated in our lab using Headspace Solid-Phase Microextraction coupled to Gas Chromatography—Mass Spectrometry. There were sufficient differences in the profiles to distinguish D1 from the other tree bacteria. In the present study, we conducted literature surveys for each of the one hundred and twenty four VOCs emitted by our samples to assess the potential of these strains for medical, pharmaceutical and industrial applications. Our preliminary results about the relevance of the VOCs revealed that D1 emitted more compounds involved in fragrance and flavor while D2 and D3 emitted more compounds involved in antibiosis. D4 was the only one emitting compounds currently involved in non-pharmaceutical industrial applications. In conclusion, our literature surveys confirmed the potential importance of our isolates in producing compounds for commercial use. This work was supported by PSC-CUNY Award # 66457-0044.

Engineered Protein-based Delivery Agents for the Treatment of Osteoarthritis. Michael Lupo,[1] Liming Yin[1], Carlo Yuvienco[1], Thorsten Kirsch[3] and Jin Kim Montclare[1,2], [1]Polytechnic Institute of New York University, Brooklyn, NY, [2]SUNY-Downstate Medical Center, Brooklyn, NY and [3]NYU Hospital for Joint Disease, New York, NY.

Osteoarthritis (OA) is a disease that brings about joint degradation and affects the normal function involved in the joints. OA is hypothesized to be induced by excessive levels of all-*trans* retinoic acid (a*t*RA). In order to combat this pathological up-regulation of a*t*RA, another small molecule is needed to compete for receptors involved in a*t*RA-induced OA. The molecule being studied to compete is a pan retinoic acid receptor (RAR) inverse agonist known as BMS 493. Our group is researching the development of a biomolecular delivery vehicle to facilitate the transport of BMS 493 to affected chondrocytes. The vessel being studied is the coiled-coil domain of cartilage oligomeric matrix protein (COMP), which is a non-collagenous extracellular matrix glycoprotein that exists in cartilage, tendons, and ligaments. The coiled-coil domain (COMPcc) is known to self-assemble into a homopentamer with a hydrophobic pore at its center, within which

small molecules are also known to bind within hydrophobic pore. For example, it has been shown to bind curcumin, vitamin D, all-trans retinol, and retinoic acid. Two specific variations of COMPcc protein are studied, the first being based off of the wild-type sequence; the second is a mutant of COMPcc where the residue Q54 is mutated to an alanine (Q54A). Previous studies have shown that Q54A has a higher affinity to bind small molecules such as all-trans retinol, which is structurally similar to *at*RA. The variants were generated in this study and used in binding studies to measure its affinity towards BMS 493 within its pore. We intend to compare the binding capacity of both these proteins with *at*RA as well as the inverse agonist, BMS 493.

Inhibition of C-SRC Activity in Osteosarcoma Cells Leads to Decreased Expression of the Osteoblast Phenotype. Joshua Luster, Sofija Vlasevska, Joseph Tarr and Thomas Owen. Ramapo College of New Jersey, Mahwah, NJ.

In the human body, bone is constantly produced and recycled. Osteoblasts are responsible for the creation of bone and osteoclasts are responsible for recycling bone by dissolving it with acid and enzymes, releasing calcium into the blood stream. To maintain proper bone density, the activity of these two types of cells must be balanced. The c-src kinase is an enzyme known to play an important role in the functioning of both of these cell types. When the c-src gene is deleted in mice, there is a decrease in osteoclast activity and an increase in the rate of differentiation of osteoblasts. This effect on bone formation can be shown in vitro using cultures of normal osteoblasts which undergo a series of developmental steps ultimately resulting in the formation of multilayered nodules of cells with a structure similar to normal bone. When the c-src kinase is inhibited in these normal cells using the inhibitor compound PP2, their differentiation increases. To further study this mechanism, we inhibited c-src kinase in Ros 17/2.8 osteosarcoma cells with PP2 and used PP3 (an inactive form of the inhibitor) or vehicle (DMSO) as controls. We found that when c-src was inhibited in these tumor-derived cells, alkaline phosphatase, a marker of osteoblastic differentiation was decreased, not increased as it is in the normal cells. This suggests that the downstream targets of phosphorylation are different between the normal and tumor cells or that the c-src enzyme itself is mutated in the tumor cells, leading to deregulation of its function.

Inferring Gene Regulatory Networks Based on Mutual Information. Ahmed Mahmoud, Wenwei Xiong and Chunguang Du, Montclair State University, New Jersey, USA.

Gene Regulatory Networks (GRN), which diagram interactions between large numbers of genes and regulators, have recently been a highly studied topic. The nonlinear and complex nature of biological networks require robust and effective algorithms to infer relationships between genes. Here we present a recent study coupling a traditional method (Mutual Information) with a new method (Conditional Mutual Information). Together, this novel method aims to calculate the dependency of genes on each other in a network. Based on this method, we present a pseudo code script to infer Maize gene expression array data.

Comparison of Water from Five Reservoirs in Bergen County, New Jersey. Samantha Maksoud and Charles Sontag, Bergen Community College, Paramus, NJ.

The waters from five reservoirs, while from the same general area, vastly differ in their quality. This study measured the temperature of each water supply at a specific point in the day, their oxygen content, their water clarity, pH, carbonate hardness, general water hardness, nitrite, nitrate and ammonia levels. The study was conducted between 5am and 7am every morning for 50 days. Hillsdale was first, followed by Dumont, Oradell, River Edge and Teaneck. At each site, water was hauled up in a bucket to take for testing. An oxygen meter was used to check the oxygen content and the temperature. A Secchi disk was used to judge the water's clarity. Solutions kits for testing the waters for an aquarium were acquired for testing the pH, KH, GH, nitrite, nitrate and ammonia levels. Each time it rained, the oxygen levels rose, the ammonia rose, and the clarity rose. Then the water had been stagnant for a couple of days, and it was humid, the nitrate and nitrite rose. This work was supported by the S.T.E.M. department at Bergen Community College in Paramus New Jersey.

The Presence of Histamine in Ganglia and Tissues of the Bivalve Mollusc, *Crassostrea virginica.* Daniel Mantone[1], Kisha LeFleur[2], Jarreau Harrison[2], Edward J. Catapane[2] and Margaret A. Carroll[2], [1]SUNY at Stony Brook University, Stony Brook, NY and [2]Medgar Evers College, Brooklyn, NY.

Histamine is a biogenic amine serving as a neurotransmitter in the nervous system and sensory receptors in a variety of invertebrates. Histamine has rarely been reported in bivalves. Our physiology work showed it involved in sensory reception in the sensory-motor integration of gill lateral cell cilia in the bivalve Mollusc, *Crassostrea virginica.* We hypothesize histamine is present in ganglia and innervated tissues of *C. virginica*. We used HPLC with pre-column derivatization and fluorescence detection to identify and measure histamine in cerebral and visceral ganglia, and peripheral tissues of *C. virginica.* HPLC was performed isocratically with a Phenomenex Gemini 5µ C18 column, Beckman HPLC system and a Jasco FP 2020 Spectrofluorometer. The mobile phase was 40/60 acetonitrile /phosphate buffer (50 mM, pH 6.8, 2 ml/min flow rate). Tissues were dissected, blotted, weighed and homogenization on ice with a Brinkman Polytron in 0.4 M HCl, then centrifuged at 4℃ for 15 minutes at 600g followed by centrifugation at 12,000g for 15 minutes. The supernatant was filtered through 0.24 micron filters, adjusted to pH 9.5 with NaOH and derivatized for 15 minutes by adding 0.6 ml of sample, borate buffer (0.2 ml, pH 9.5) potassium cyanide (0.2 ml, 20 mM) and NDA (2,3-naphthalene-dicarboxaldehyde, 0.3 mM in methanol). Samples were injected into the HPLC and fluorescence measured at 450 nM excitation and 484 nM emission. Results show histamine present in ng amounts in cerebral ganglia, visceral ganglia, gill, palps, heart, hemolymph, posterior adductor muscle, mantle and mantle rim. This study confirms the identity of histamine in the nervous system and innervated organs, including sensory tissue, and coupled with our other work shows histamine is an important endogenous biogenic amine in the bivalve *C. virginica*. This work was supported by grants 0516041071 of NYSDOE and 0622197 of the DUE Program of NSF.

Measuring Algal Growth of *Chlorella vulgaris* Under Different Levels of Nutrients Using Spectrophotometry. Marie Manzan, Jacqueline Mateo, Carlos Olivares, Jan Siess, Sheryl Wong, Katarzyna Czechowicz, Joseph Sivo and Bruce Benjamin, Bergen Community College, Paramus, New Jersey, USA.

The transportation industry is responsible for a significant amount of greenhouse gas emissions in the atmosphere. Many commercial airlines are beginning to use biofuels to offset the use of traditional fossil fuels. Microalgae are a sustainable energy resource and a feasible source of biodiesel. Researchers have been exploring methods to maximize growth and lipid production in algae. Algae are the most promising candidates for future fuels because of their unique ability to produce a high lipid concentration, much higher than that obtained from food crops. The algae are harvested and lipids are extracted from the algal cells. The lipids, high energy hydrocarbons, are refined to produce biodiesel. The microalgae *Chlorella vulgaris* were selected in this research for its ability to produce high lipid content. An increase in general algal growth can be accomplished by exposing the organisms to optimal conditions, which include various parameters such as nutrient source, light intensity, oxygen level, carbon dioxide level, pH, and photobioreactor design. All these factors are known to have an effect on the lipid production by *C. vulgaris*. In this study, the best nutrient source for *C. vulgaris* was investigated. After testing several potential nutrient sources, it was discovered that *C. vulgaris* responds extremely well to Miracle-Gro (MG) as a primary nutrient source. This study compared growth of *C. vulgaris* in a serial dilution of MG (0.065M, 0.0065M, 0.00065M, and 0.000065M). Growth and quantity were monitored daily by measuring the absorbance of light by the algae with a spectrophotometer set at 690 nm. A growth curve was established for each concentration. The results indicated that at the end of the study (day 10) the highest concentration of algae was found in the 0.065M solution of MG. The highest concentration of nutrient was linked to most optimal algal growth. With this increase in biomass, the expectation is that lipid content also increased. This work was supported by the STEM grant.

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The Impact of Beach Renourishment on the Atlantic Horseshoe Crab (*Limulus polyphemus*) Spawning Activity on Plumb Beach, Brooklyn NY. Vanessa Maria and Christina P. Colon, Kingsborough Community College, Brooklyn, NY.

This study investigates initial outcomes of beach replenishment on horseshoe crabs, to better understand its impact on egg survivorship. It was hypothesized that despite a beach replenishment project on the Western portion of Plumb Beach, Brooklyn NY in fall 2012, the Atlantic horseshoe crab's (*Limulus polyphemus*) egg density will show no significant increase compared to the numbers in 2012 prior to the beach renourishment. It was further hypothesized that in 2013 horseshoe crabs will continue to prefer to use the existing natural beach (Eastern area) for spawning activities and will show a preference for this area over the restored area. The beach renourishment project that took effect in the Fall of 2012 shortly before Hurricane Sandy, may negatively impact horseshoe crab spawning. Horseshoe crabs, a species that dates back to 500 million years may have specific spawning habitat requirements that a large scale beach renourishment project may disrupt. The observed 50% decrease in eggs on the Western area in 2013 compared to 2012, and the lower numbers on the Western end compared to the Eastern end in 2013 support both hypotheses. These data suggest that perhaps beach renourishment is not the right approach when trying to protect or increase habitat suitability. However, this may also suggest that horseshoe crabs need time to adapt to the renourished environment, or perhaps that the sand itself needs to settle and become integrated into the existing biota. Gratitude is extended to Dr. Mark Botton and Dr. Yumiko Iwasaki, Kang Lee, Richard Ramsundar of Fordham University, New York City Audubon, NY Seagrant, NYC Parks, NY State DEC, National Park Services and the Army Corps of Engineers. This work was supported by grant 2R25GM0600309 of the Bridge Program of NIGMS and grant 0537121091 of the CSTEP Program of NYSED.

Evidence That Eastern Oysters Have Spread Into Jamaica Bay, New York. Isaac Mazile, Gary Sarinsky and Craig Hinkley, Kingsborough Community College, Brooklyn, NY. USA.

The eastern oyster, *Crassostrea virginica*, is indigenous to North America. Once abundant in many bays, their numbers have declined due to pollution and destruction of their habitats. In Jamaica Bay (JB) in New York, there are no known natural oyster beds. In 2001, a group of oysters was introduced into JB and shown to both survive and reproduce. Recently, five new oysters were found in various regions of JB and we wanted to know whether they were offspring of those introduced in 2001 or from another source. My hypothesis was that the new oysters were offspring of the 2001 oysters. This hypothesis was tested by first extracting DNA from the tissues of the new oysters. A 700 bp region of the cytochrome c oxidase I (COI) gene was then amplified using the polymerase chain reaction (PCR) and agarose gel electrophoresis was used to verify the correct size of the PCR products. The amplified DNA was sequenced and a BLAST search confirmed the sequences were from the *Crassostrea virginica* COI gene. The COI genes from 69% of oysters in the 2001 study contain a polymorphism that distinguishes them from oysters of other regions. Alignment of sequences from the new oysters and the 2001 study oysters showed that one of the new oyster sequences contained this distinguishing polymorphism. This suggests the oyster is offspring of the 2001 oysters. Although the other new oysters do not contain this polymorphism, it is still possible they are offspring of the 2001 oysters since 31% of the 2001 oysters did not contain the polymorphism either. In conclusion, my hypothesis that the new oysters were offspring of the 2001 oysters was partially supported. This work was supported by grant 2R25GM0600309 of the Bridge Program of NIGMS and grant 0537121091 of the CSTEP Program of NYSED.

The Effect of Na^+/H^+ Exchanger 6 on Tau Protein Aggregation. Pakinam Mekki[1,2], Hari Prasad[1], Kalyan Kondapallai[1] and Rajini Rao[1], [1]Johns Hopkins University School of Medicine, Baltimore, MD and [2]Wagner College, Staten Island, NY.

Na^+/H^+ exchangers are highly conserved ion transporters found in all branches of the evolutionary tree. Members of the NHE family are classified based on their subcellular localization, either residing on the plasma membrane or on the membrane of intracellular organelles. Specifically, isoform NHE6 regulates the luminal pH of early/ sorting and recycling endosomes. Patients with loss of function mutations in NHE6 have a form of Angelman syndrome, characterized by epilepsy, mental retardation, and deposition of Tau protein in the brain. In this study, the effect of NHE6 overexpression, knockdown, and loss of function mutations on Tau-expressing HEK 293 cells was investigated using immunofluorescence, confocal imaging, and Western blotting. Our preliminary results indicate that NHE6 levels have a direct effect on the Tau protein levels in the cell.

Exome Wide Identification of Evolutionarily Conserved Cis-Regulatory G-quadruplexes Near PolyA Signals. Camille Menendez, Matt Crum, Scott Frees and Paramjeet S. Bagga, Ramapo College of New Jersey, Mahwah, NJ.

We have used our previously developed web application (QGRS-H Predictor) and database (QGRS-H DB) to identify evolutionarily conserved G-quadruplex motifs within 500 nucleotides upstream and downstream of polyA signals in the entire human exome. A G-quadruplex is a three-dimensional structure formed by guanine rich nucleic acids which has been identified as a cis-regulatory element of post-transcriptional gene expression with significant roles in important biological processes, human disease and as a therapeutic target. One particular interest is in the role of G-quadruplexes in 3'-end mRNA processing, particularly the alternative polyadenylation. Several previous studies have identified genes in which G-quadruplexes downstream of the polyA signal play active roles in the polyadenylation complex. It has been observed that the efficiency of the polyadenylation complex can be improved by the binding of hnRNP H to the G-rich sequence (GRS) downstream of the polyA signal. Polyadenylation can also be inhibited by the binding of hnRNP F in this same region. Association of G-rich sequences capable of forming G-quadruplexes within polyA signals has also been shown to be involved in alternative polyadenylation, mRNA shortening, and tissue-specific localization. Our computational approach of identifying conserved G-quadruplexes near polyA signals in the human exome was successful in determining their distribution patterns in this region. We have identified many human genes which have G-quadruplexes mapped to upstream as well as downstream of their poly A signals This project has provided important information about the regulation of human gene expression associated with 3'-end formation.

The Potential Impact of Super Storm Sandy: Egg Density of the Atlantic Horseshoe Crabs *(Limulus polyphemus)* on Plumb Beach (Brooklyn NY). Cassandra Mezalon and Christina P. Colon, Kingsborough Community College, Brooklyn, NY.

Atlantic Horseshoe Crabs (*Limulus polyphemus*) one of Earth's oldest living species, date back five hundred million years. Every year, from April to June, the horseshoe crabs come ashore at the night high tide during the new and full moon to lay and fertilize many thousands of eggs in the sand. Throughout the investigation, a team of researchers went to Plumb Beach (Brooklyn NY) a pivotal Limulus breeding beach and collected egg samples from 3 parts of the Eastern section of Plumb Beach to see whether Hurricane Sandy had a negative impact on egg density. It was hypothesized that the storm would have no long term impact on breeding success but could reduce egg densities in the short term. Egg data collected in 2013 were indeed much lower than numbers collected in the 2012 breeding season. Numerous studies of other storms such as hurricane Dennis, Floyd, and Irene, reveal long term negative impacts that led to declines in spawning and survival of marine invertebrates as well as breeding birds. Although the reason is unknown for the decline of the horseshoe crab eggs in 2013, Hurricane Sandy may have been a contribution factor along with other climate or environmental changes on the beach. To better understand factors that lead to the declining of the egg density, and to test for long term impacts, further studies and continued monitoring need to be conducted. I would like to thank, Dr. Mark Botton and Dr. Yumiko Iwasaki, Kang Lee, Richard Ramsundar of Fordham University, New York City Audubon, NY Sea Grant, NYC Parks, NY State DEC, National Park Services and the Army Corps of Engineers. This work was supported by grant 2R25GM0600309 of the Bridge Program of NIGMS and grant 0537121091 of the CSTEP Program of NYSED.

Methamphetamine Alters Adaptive Immune Responses after Exposure to T-Cell Dependent or Independent Antigens. Anum N. Mitha[1], Valerie Vaval[2] and Luis R. Martinez[2,3], [1]The Wheatley School, Old Westbury, NY, [2]Long Island University-Post, Brookville, NY and [3]Albert Einstein College of Medicine, Bronx, NY.

Methamphetamine (METH) is a potent and highly addictive central nervous system (CNS) stimulant. This drug of abuse is a major public health problem in many communities of the United States. It is estimated that >12.3 million Americans (4.9% of US persons aged 12 or older have used METH at least once, 1.4 million persons aged 12 or older (0.6% of the US population) had used METH during the past year, and 600,000 (0.2% of the US population) had used it during the past month. Also, the transmission of HIV, hepatitis B

and C, and other transmissible diseases are possible serious infectious consequences of METH use. These infectious diseases can be spread via contaminated needles, syringes, and other equipment used by multiple people who inject METH. Additionally, METH adversely impacts immunological responses, which might contribute to the higher rate and more rapid progression of certain infections in drug abusers. However, no studies have specifically addressed the impact of METH on adaptive immune responses after exposure to T cell dependent, ovalbumin (OVA) and independent, lipopolysaccharide (LPS) antigens. Therefore, we hypothesized that METH would alter adaptive immune responses after antigenic challenge. Using a murine model of METH administration, we demonstrated that METH modifies, with variable degrees, lymphocyte recruitment in the lungs and spleen of challenged mice. Histological analysis confirmed that animals treated with METH and challenged with OVA or LPS exhibited delayed inflammatory response compared to untreated and sensitized controls. Furthermore, we showed that METH reduced circulating antibody levels in the serum of antigenically challenged animals. Our findings demonstrate the pleotropic effects of METH on the adaptive immune response. These alterations have profound implications on tissue homeostasis and the capacity of the host to respond to diverse insults, including invading pathogens. This work was supported by NIH-NIAID 5K22A1087817-02.

The Danger Zone: Plumb Beach's Condition, and Its Effect on Juvenile Atlantic Horseshoe Crab (*Limulus polyphemus*) Population. **Anthony Mora and Christina P. Colon, Kingsborough Community College, Brooklyn, NY,**

Plumb Beach in Brooklyn, New York is an important spawning ground for Atlantic horseshoe crabs. Over the past three years researchers counted and measured adults and juveniles in order to monitor their numbers. Few crabs were found on the Western end of Plumb Beach due to its eroded and inhospitable state, while adults and juveniles were more abundant on the sandier and healthier Eastern end. It was hypothesized that due to Superstorm Sandy, fewer juvenile horseshoe crabs would be found on the Eastern side compared to 2012. It was also hypothesized that due to the storm and a beach renourishment project, there would also be no juvenile horseshoe crabs on the Western end. We observed that older juvenile horseshoe crabs tend to be more abundant early in the summer; as the season progressed smaller crabs were more common, indicating a disappearance of the older crabs, perhaps due to predation. There was an overall decline in the total count of juveniles found on the Eastern end from 2011 to 2013, but an increase in the number of hatchlings on the Western end. This increase could be due to the beach renourishment project carried out in October, 2012 on the Western end of the beach, which had previously been severely degraded. However, other factors could be at play such as natural inter-annual variation, therefore further research is warranted. Gratitude is extended to Dr. Mark Botton and Dr. Yumiko Iwasaki, Kang Lee, Richard Ramsundar of Fordham University, New York City Audubon, NY Sea Grant, NYC Parks, NY State DEC, National Park Services and the Army Corps of Engineers. This work was supported by grant 2R25GM0600309 of the Bridge Program of NIGMS and grant 0537121091 of the CSTEP Program of NYSED.

Mutualist and Antagonist Interactions in Heterogeneous and Homogeneous Plant Communities in a Lakeshore Restoration. **Britany L. Morgan[1], Elena Tartaglia[2] and Steven N. Handel[1], [1]Rutgers, The State University of New Jersey, New Brunswick, NJ and [2]Bergen Community College, Paramus, NJ.**

The design of restoration projects is often complex, as it must take into account all facets of the ecology of the system to be restored. The question of optimal plant community composition for restorations has been an issue of some disagreement. Heterogeneous plant communities, which offer a higher overall diversity, attract a higher diversity of beneficial mutualists such as seed dispersers, but provide a low signal strength for both mutualists and harmful antagonists, such as herbivores. Homogeneous plant communities, while low in diversity, provide a bigger signal strength for attracting beneficial mutualists but also attract more harmful antagonists. In this experiment, we aimed to answer the questions (1) are beneficial seed dispersal interactions greater in heterogeneous or homogenous communities? and (2) are harmful herbivore interactions greater in heterogeneous or homogeneous communities? We planted 150 individuals of five species of native hydrophilic shrubs and trees in 30 plots of

five individuals each. The communities were located around a lakeshore at Duke Farms in Hillsborough, NJ. Twenty-five plots were homogenous communities, and five plots were heterogeneous communities with one individual of each species. We compared seed dispersal and herbivory levels between the two community types for each species. Herbivory levels did not significantly differ for any species between community types, but seed dispersal for one of the species that bore fruit did show significantly greater levels of dispersal in homogeneous communities than in heterogeneous communities. This experiment provides insight on ecological functions in restored communities to allow restoration ecologists to create environments that are self-sustaining and require minimal maintenance. This work was supported by grants from the Aresty Foundation, the Duke Farms Foundation and Rutgers, The State University of New Jersey. The authors thank Pinelands Nursery for supplying the plants.

Conservation of G-Quadruplex Regulatory Motifs in Multiple Genes Involved in Neurological Disorders. Emma Murray, Lawrence D'Antonio and Paramjeet S. Bagga, Ramapo College of New Jersey, Mahwah, NJ.

The goal of this project has been to perform a comprehensive study of evolutionarily conserved regulatory G-quadruplex motifs found in several genes implicated in human neurological disorders. For this project we chose seven genes: NF1 and NF2 involved in neurofibromatosis; CHD8 and MECP2 involved in autism; and SNCA, MAPT, and Park7 involved in Parkinson's disease and dementia. We discovered higher than expected level of sequence conservation in the 5'- and 3'-UTR of all genes, suggesting the presence of *cis*-regulatory motifs in the untranslated regions. G-quadruplexes, known to regulate gene expression, are highly stable three-dimensional structures formed in guanine rich DNA and RNA sequences. G-quadruplexes consist of square coplanar arrays. RNA G-quaduplexes have received significant attention lately because of their importance in biological processes such as regulation of protein synthesis and mRNA turnover. Consequently, G-quadruplexes are being targeted for therapeutic purposes. Using computational tools developed in our lab, we adopted a bioinformatics approach to map evolutionarily conserved G-quadruplexes in the mRNAs of all seven genes. Conservation studies included up to five mammalian orthologs of the respective human genes. We found a large number of evolutionarily conserved G-quadruplexes in the untranslated regions. The 3'-UTR exhibited a higher number of G-quadruplexes than the 5'-UTR, suggesting their complex regulatory roles. G-quadruplexes in the 3'-UTR also had a higher predicted stability. In CHD8, MECP2, NF1, and NF2 mRNAs, conserved G-quadruplexes were located within close vicinity of polyadenylation sites. In CHD8 and MECP2, G-quadruplexes were found at a higher frequency near alternative splice sites then near constitutive splice sites. Our analysis suggests that evolutionarily conserved G-quadruplexes could regulate mRNA stability, polyadenylation, and alternative splicing of the genes involved in neurological disorders.

Characterization of Methionine Synthase in Peas. Rafia Muslim, Regina Hodges, Ceran Messam, Angie Yoshizu, Karla Alvarado, Denisse Martinez, Katherine Aumann, Juan Soto and James Murphy, Bloomfield College. Bloomfield, NJ.

We characterized the gene for Methionine Synthase from peas. We designed oligonucleotides based on orthologs of Methionine Synthase from the pea family. We used these oligonucleotides to perform the Polymerase Chain Reaction on pea cDNA. The PCR products were purified and sequenced. The sequences were analyzed and organized into a contiguous sequence corresponding to the complete cDNA. This will allow us to infer Methionine Synthase's Methionine Synthase amino acid sequence and then investigate chemical modification of its amino acids, such as acetylation, through mass spectrometry.

Zinc Stress Response in *Acinetobacter baylyi* ADP1. Robert Newby Jr. and Tin-Chun Chu. Seton Hall University, South Orange, NJ.

Exposure to heavy metals in freshwater from effluent or unregulated dumping causes not only an ecological issue, but can fundamentally change the microbial population present. To adapt to the stress, bacteria such as *Acinetobacter baylyi* ADP1 have many different heavy metal stress response mechanisms. *Acinetobacter baylyi* ADP1 was exposed to $ZnCl_2$ at 0, 50, 100, 200, 300, and 350 mg/L concentrations in LB, and the growth and viability was observed and recorded. *Acinetobacter baylyi* ADP1 appeared to be slightly inhibited by $ZnCl_2$ at concentrations greater than 200 mg/L, compared to 0, 50, and 100 mg/L. 300 mg/L $ZnCl_2$ caused a much more significant delay in growth with a prolonged lag phase compared to

the control. Concentrations in excess of 300 mg/L proved to be lethal to *Acinetobacter baylyi* ADP1. Phase Contrast microscopic observations of *Acinetobacter baylyi* ADP1 highlighted elongation of cells compared to control at concentrations greater than 100 mg/L, but the mechanism is yet to be determined. Heavy metal resistant and/or tolerant genes have been identified with bioinformatic analysis. Pilot sequencing and transformation indicated that *Acinetobacter baylyi* ADP1 may serve as a powerful model organism for physiological stress studies.

The Ability of *Capsicum annum* to Inhibit the Growth of *Bacillus subtilis, Escherichia coli, Enterococcus faecalis, Salmonella typhimurium, Enterobacter aerogenes,* and *Staphylococcus aureus*. Darshan Nimmons and Elizabeth Mulligan, Kingsborough Community College, Brooklyn, NY, USA.

Capsicum annuum is a species of plant including a variety of peppers ranging from mild Bell peppers to the extremely hot Bhot Jolokia. The compound responsible for the pungency of these peppers is Capsaicin which varies depending on the variety of pepper. The Scoville scale, measured in Scoville Heat Units (SHU), is an indirect measure of the average amount of Capsaicin found in peppers; higher capsaicin levels equal hotter peppers. In mammals, capsaicin acts as an irritant creating a burning sensation when in contact with mucus membranes. Capsaicin is produced by *Capsicum annuum* as a deterrent against mammals and fungi. The capsaicin compound is also known to have inhibitory effects on bacteria. We tested the ability of peppers from different levels of the Scoville scale (Bell, Poblano, Jalapeño, Serrano, Thai, Habañero, and Bhot Jolokia) to inhibit the growth of the following bacteria: *Bacillus subtilis, Escherichia coli, Enterococcus faecalis, Salmonella typhimurium, Enterobacter aerogenes, and Staphylococcus aureus.* We hypothesized that peppers containing more capsaicin, and a higher SHU, will have a greater amount of bacterial inhibition compared to peppers with a lower SHU. To test our hypothesis, we analyzed pepper extracts in isopropanol and utilized a disc diffusion method to determine the amount of bacterial inhibition. For this procedure we grew bacterial lawns on Müller – Hinton agar with paper discs containing extracts of each pepper, and an isopropanol control. After incubation we measured the zones of inhibition and were able to see inhibition of bacteria with our pepper extract. However, the amount of inhibition was not greater than the results of our control experiments. Therefore, we must conclude that our hypothesis is not supported by our results. This work was supported by grant 2R25GM0600309 of the Bridge program of NIGMS and grant 0537121091 of the CSTEP program of NYSED.

Intracranial Self Stimulation and Neurogenesis in a Rat Model of Alzheimer's disease. Lucia Nunez[1], Jessica Montes[1], Rudolf Nisanov[2], Jamel Travis[2], Taramati Shew[2] and Francisco Villegas, [1]Queensborough Community College and [2]York College of CUNY, NY.

Alzheimer's disease (AD) is a neurodegenerative brain abnormality that plagues the elderly. Characterized by the precipitous deterioration of cognitive and behavioral abilities, AD slowly progresses to chronic dementia, anterograde amnesia, and eventually death. As a potential "regenerative" therapy for a variety of cognitive impairments presented in an Aβ (25-35) rat model of AD, our research will attempt to determine whether the electrical intracranial self-stimulation (ICSS) will promote neurogenesis in the adult hippocampus. ICSS is believed to facilitate the excitation of "reward" circuitry and activity-dependent regulation of the entorhinal cortex in the hippocampus system. Thirty male Sprague-Dawley rats will form three randomized groups of control, sham control and experimental subjects. After surgical recovery, specific cognitive deficits in visual, temporospatial and non-spatial working short-memory will be tested using the Morris Water Maze (MWM) and Social Discrimination test. Immediately after the ICSS/ MWM procedure, Bromo-deoxyuridine will be administered via intraperitoneal (i.p.) injection in all animals to identify neuronal proliferation during the S stage of mitosis. Lucia and Jessica are participants in the NIH Bridges to the Baccalaureate Program at Queensborough Community College (R25 GM65096-11).

Use of a Stainless Steel Washer Platform to Study *Acinetobacter baumannii* Adhesion and Biofilm Formation on Abiotic Surfaces. Samantha J. Orsinger-Jacobsen[1], Shenan S. Patel[1], Ernestine M. Vellozzi[1], Phillip Gialanella[2], Leonardo Nimrichter[3], Kildare Miranda[4], and Luis R. Martinez[1,5,6], [1]Long Island University-Post, Brookville, NY, [2]Microbiology Laboratory, Montefiore Medical Center, Bronx, NY, [3]Instituto de Microbiologia Professor Paulo de Góes and [4]Instituto de Biofísica Carlos Chagas Filho, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil and [5]Albert Einstein College of Medicine, Bronx, NY.

Acinetobacter baumannii (*Ab*) is a frequent cause of hospital-acquired pneumonia and has recently increased in incidence as the causative agent of severe disease in troops wounded in Afghanistan and Iraq. Clinical approaches are

limited since *Ab* strains isolated from patients are extremely resistant to current antimicrobials. *Ab* can survive desiccation and during outbreaks has been recovered from various sites in the patients' environment. To better understand its prevalence in hospital-settings, we used a stainless steel washer (SSW) platform to investigate *Ab* biofilm formation in abiotic surfaces. Scanning electron microscopy demonstrated that *Ab* forms strong biofilms on stainless steel surfaces. This platform was combined with a colorimetric 2, 3-bis (2-methoxy-4-nitro-5-sulfophenyl)-5-[(phenylamino) carbonyl]-2H-tetrazolium-hydroxide (XTT) reduction assay to observe the metabolic activity of bacterial cells and facilitate the manipulation and comparison of multiple *Ab* clinical strains. A strong correlation between XTT and CFU assays was demonstrated. To complement the cell viability assays, *Ab* biofilm mass was measured by crystal violet staining. Furthermore, the effect of commonly-used disinfectants and environmental stressors on *Ab* biofilms and planktonic cells was compared and characterized. Biofilms on SSWs were significantly more resistant than their planktonic counterparts providing additional evidence that may allow us to understand the high prevalence of this microbe in hospital-settings. Our results validate that SSWs are a simple, versatile, and innovative method to study *Ab* biofilms *in vitro*. This work was partially supported by NIH-NIAID 5K22A1087817-02, Benjamin Cummings/MACUB Research, and LIU-Post Undergraduate Research Awards.

Enhanced Infectivity/Detection of Rotavirus in Monkey Kidney Epithelial Cell Cultures by CystiCran[R] 40. Fatma S. Ozen[1,2], Robert E Gordon[3], Laina Karthikeyan[4] and Steven M Lipson[1], [1]St. Francis Colllege Brooklyn, NY, [2]Celsuk University. School of Veterinary Medicine Konya, Turkey, [3]Mount Sinai Medical Cente, New York, NY and [4]NYC Technical College, CUNY, Brooklyn, NY.

Optimal sensitivity and specificity serve as cornerstones in the proper operation of the diagnostic/biomedical laboratory. In the discipline of medical microbiology for example, efforts are relentless in the establishment of new assays to improve one's detection of low viral microbial levels in the clinical specimen. Although the polymerase chain reaction and related amplification technologies are employed in the larger hospital virology laboratories, routine screening using cell cultures for the isolation of viruses in clinical specimens are still performed. Descriptive and mechanistic approaches to determine the effect of naturally occurring secondary plant metabolites on virus infectivity remains an area of interest in our laboratory. Although earlier studies with plant metabolites and juices [e.g. epigallocatechin gallate (EGCG), proanthocyanidins (PACs), cranberry juice] caused a loss of virus infectivity/antigen, a newly tested (proprietary) semi-synthetic plant metabolite, CystiCran[R] 40 (C-40) significantly increased virus infectivity titers after several days in host cell cultures. The rotavirus was used as a model enteric virus system. Measurement of transepithelial electrical resistance (TEER) in monkey kidney epithelial (MA-104) cell cultures revealed a premature loss of tight junction integrity by virus/C-40 but not EGCG treatment. Transmission electron microscopy (TEM) revealed amorphous virus particles 3 days post inoculation (P.I.), compared with that of EGCG-treated virus or the positive control. C-40 was not cytotoxic to MA-104 cells in monolayer culture. The ramifications of our findings are significant, as the use of C-40 in routine viral screening (or environmental pollution testing, plant virology, etc.) has the potential of affecting increased rates during specimen/sample testing in the isolation of currently circulating as well as new and re-emerging viruses which may be missed through the use of specialized nucleic acid amplification technologies.

Evaluate The Effect Of Selenium Dioxide On The Toxicity Of Zinc Chloride In Bacteria, Algae, Mammalian Cells And World Trade Center Dust. Jagruti I. Patel, AnnMarie DiLorenzo and Lee H. Lee. Montclair State University, Montclair, NJ, USA.

The effect of selenium dioxide (SeO_2) on toxicity of zinc chloride ($ZnCl_2$) was studied in different levels of organisms from prokaryote to human. *Synechococcus sp*. IU 625 (SIU 625) is a prokaryotic, unicellular freshwater photoautotrophic Cyanobacterium, *Chlamydomonas reinhardtii* is a unicellular photosynthetic eukaryotic green algae. Both are good environmental pollution indicators especially for heavy metal contamination. Human Pulmonary Fibroblast Cells (MRC- 5) and Chinese Hamster Ovary Cells (CHO) in vitro were also used to represent more complex system. In addition, the World Trade Center (WTC) dust containing high

concentration of Zn (57.4 mg/L) was also used to study this effect. The culture of SIU 625 and *Chlamydomonas reinhardtii* were grown in the presence of SeO_2 (1mg/L) with various concentrations of $ZnCl_2$ (0, 10, 25, and 50mg/L) for 25 days. The growth was monitored by turbidity study and direct cell count. A CellTiter 96® Non-Radioactive Cell Proliferation Assay was performed after cell exposed to SeO_2 in combination with various concentration of $ZnCl_2$ or WTC dust. The morphology of the cells was observed under microscope and the DNA was stained with DAPI. SeO_2 reduced the toxicity in SIU 625 with 25 and 50 mg/L of $ZnCl_2$, in *Chlamydomonas reinhardtii* with10 mg/L of $ZnCl_2$, and in mammalian cells with 25 and 50 mg/L of $ZnCl_2$. SeO_2 (0.125mg/L) increased proliferation in $ZnCl_2$/SeO_2 treated cells in both cell lines and WTC dust (1.25, 12.5, and 125mg/L) exposed CHO cells, but not in MRC-5. This study suggests that SeO_2 reduces the toxicity of zinc at different concentration in different organisms and aids to retain cell shape and DNA integrity.

The Inhibitory Effects of EGCG and EGCG-Stearate in Cultured Human Epithelial A549 cells. Shivani N. Patel, Lee Lee and Sandra Adams, Montclair State University, Montclair, NJ.

Epigallocatechin gallate (EGCG), a green tea polyphenol possesses antioxidant, antibacterial, anticancer and antiviral properties. EGCG-stearate (EGCG-s) is of interest for this study because of its stability and lipophilic properties. Herpes Simplex Virus-1 (HSV-1) from family *Herpesviridae* is a leading cause for human viral diseases in the United States. In this study, 25μM, 50μM and 75μM of EGCG and EGCG-s were used to study the effects of EGCG and EGCG-s on infection of HSV-1 in cultured human epithelial (A549 cells) using cytotoxicity, cell viability and cell proliferation assays. Infectivity assays were performed to study the effects of EGCG and EGCG-s HSV-1 infection. The results were quantified by determining the TCID50. A PCR based assay was performed to study the effects on viral DNA replication. The results of the cytotoxicity, cell viability and cell proliferation assays determined the maximum non-cytotoxic concentrations used to treat the virus. Infectivity assays demonstrated the inhibition of HSV-1 by EGCG and EGCG-s by showing no cytopathic effect. PCR based assay suggest inhibition of HSV-1 by EGCG-s. The long-term goal of this research is to develop a topical using EGCG-s as a possible novel treatment to limit the spread of HSV-1 infections. This research is supported by the Montclair State University Science Honors Innovation Program (SHIP).

Elucidating the Protective Effect of Phenylmercaptoacetamide (PMA) to As (V) Toxicity in *Caenorhabdites elegans.* Madeeha Rahat, Fernando Nieto and Duncan A. Quarless, SUNY College at Old Westbury, Old Westbury, NY.

Bioremediation methods of arsenate decontamination of soils include the use of specialized plants, hyperaccumulators, that extract arsenate out of the soil by using low molecular weight thiols. Phenylmercaptoacetamide (PMA) was synthesized in our laboratory as a functional model to determine the structural features related to the coordination and redox chemistry of arsenate detoxification. The goals of this study were to determine the nature of the interaction between As (V) and PMA and the chemical mechanism of its chemoprotection to the worm, *C. elegans*. Synchronized worms were pre-treated with PMA for thirty minutes, and then washed before arsenate exposure. The tested hypothesis is that in the pretreated worms PMA would diffuse into the worm where it would enhance the reduction of As(V) to As(III) and its subsequent sequestration in an intracellular compartment. Control worms were pre-treated with distilled water. After pre-treatment, the nematodes were exposed to arsenate concentrations of 1000 mg/L, 100 mg/L, 50 mg/L, and 10mg/L and incubated for 24 hours. PMA pretreated worms showed a significantly lower mortality (40 to 60% lower) than those exposed to As(V) alone. The mortality of PMA pretreated worms alone was not significantly different from the controls. The reactivity of arsenate and PMA was also studied *in vitro* by ^{1}H and ^{13}C NMR and electrochemical analyses. These experiments suggest that the reduction of arsenate by PMA *in vitro* is a non-spontaneous process. These results indicate that PMA outside of the worm is limited at best to a chaperoning interaction with arsenate. These experiments provide some mechanistic insights also for the actions of PMA *in vivo*.

Evaluation of Primers for Microbial Source Tracking in the Passaic River, New Jersey. Myla Ramirez, Dena Restaino, Jayesh Desai, Marco Finocchiaro, Meiyin Wu and Lee H. Lee. Montclair State University, Montclair, NJ.

Specific microorganisms, such as Escherichia coli, total coliform, and enterococci, are used as fecal indicators to signify the presence of potential pathogenic organisms. These pathogenic indicators are often used to assess point and non-point source pollution in water systems. Microbial Source Tracking (MST) is a method that incorporates biochemical and molecular biological techniques to identify animal sources from which the coliform and *E. coli* originate. This is accomplished by using specific genetic markers from diverse animals, and then employing distinct primers that correspond to a specific gene. In this study, coliforms from the Passaic River were analyzed and the animal hosts that were evaluated were humans, horse, dog, deer, and geese. The molecular markers utilized were the 16S rRNA in Bacteroides, lacZ gene in *E. coli*, and the cytB and ND2 gene from deer and geese. Preliminary trials show positive results for *E. coli* and dog hosts. Further extensive research can be done to identify non-point source pollution along the Passaic River.

Comparison of Water Quality through Coliform Bacteria Levels in Northern New Jersey Rivers. Myla Ramirez, Jewel Lipps, Paul Tomasula, Meiyin Wu and Lee H. Lee. Montclair State University, Montclair, NJ.

Biological organisms can pose a threat to water quality and can be responsible for waterborne diseases. Because it is very expensive and time consuming to test for each pathogenic organism, coliform bacteria, which originate in environmental and animal sources, serve as good pathogenic indicator organisms. This study focused on the water quality in two New Jersey Rivers: Flat Brook River and Passaic River, which contrast in urban and agricultural land use. Water samples were taken over three months and tested for coliforms using EPA approved methods, total coliform and fecal coliform tests. It was concluded that urbanized areas, specifically highly urban and agriculturally developed areas, had an increased level of coliforms. Further research, such as Microbial Source Tracking (MST), will be conducted to identify the origin of fecal contamination. This study was supported by the Research Experience for Undergraduates program of the National Science Foundation.

Eaf3 Stimulates NuA4 Interaction With Methylated H3K36. Anish Satianathan, Priyadarshini Ravichandran and Daniel S. Ginsburg. LIU Post, Brookville, NY.

NuA4 is the only essential lysine acetyltransferase (KAT) complex in *S. cerevisiae*, where it catalyzes acetylation of histones H4 and H2A. NuA4 has been shown to stimulate both transcription initiation and elongation. We have proposed a two-step mechanism for NuA4 occupancy of coding sequences in which NuA4 recruitment is stimulated by interaction with the RNA Polymerase II CTD, while interaction with nucleosomes is stimulated by H3K4 and H3K36 methylation. The mechanism by which NuA4 binds to nucleosomes is not well understood. NuA4 subunit Eaf3 is also present in the RPD3C (S) histone deacetylase complex (HDAC), where it stimulates binding of the complex to di- and trimethylated H3K36. We investigated the role of Eaf3 in NuA4 binding to nucleosomes. Deletion of Eaf3 leads to a significant decrease in H4 acetylation in bulk histones. *In vivo* Eaf3 stimulated NuA4 interaction with nucleosomes. Likewise, *in vitro* experiments revealed that Eaf3 specifically stimulated NuA4 binding to methylated H3K36. Our results indicate that Eaf3 plays an important role in NuA4 binding to nucleosomes. These results also suggest that the role of H3K36 methylation in transcription elongation may be more than just preventing the production of cryptic transcripts. This work was supported by the LIU Post Research Committee. We would like to thank Alan Hinnebusch for advice and reagents, Bing Li for the H3K36 tail peptides, as well as Tae-Soo Kim and Stephen Buratowski for technical assistance.

Characterization of Biological activities of MTE4a. Rawnok Rayeka[1], Kimberly DeLeon, Paola Estrada[2], Akira Kawamura[2] and Monica Trujillo[1], [1]Queensborough Community College and [2]Hunter College.

The Streptomyces family of bacteria has a multicellular life cycle in which extensive cell-cell signaling can regulate not only the formation of spore forming aerial hyphae but also the production of secondary metabolites. Soil Actinomycetes produce a wide variety of secondary metabolites; which may provide growth advantages in their microenvironments. Our research focuses on the biological characterization of a Streptomyces strain, MTE4a, which is known to produce 17-hydroxycyclooctatin (Kawamura et al, 2011). Our recent findings have shown that this diterpene

has anti-inflammatory activity (Nguyen A, personal communication) and we have data that suggest it is involved in cell signaling. MTE4a also produces a compound with antibiotic activity that has been partially purified. We describe here the various assays performed using MTE4a grown both in solid and liquid media to elucidate its potential to produce active secondary metabolites.

Does Stress Make You Fat? T. Rhodes, M. Pazienza, C. Nunez and J.F. Evans, Molloy College, Rockville Centre, New York, USA.

ACTH is a major hormone of the stress axis or hypothalamic-pituitary-adrenal (HPA) axis. It is derived from pro-opiomelanocortin (POMC) the precursor to the melanocortin family of peptides. POMC produces the biologically active melanocortin peptides via a series of enzymatic steps in a tissue-specific manner, yielding the melanocyte-stimulating hormones (MSHs), corticotrophin (ACTH) and β-endorphin. The melanocortin system plays an imperative role in energy expenditure, insulin release and insulin sensitivity. Bone marrow derived mesenchymal stem cells circulate in the blood stream and as progenitor cells have the potential to differentiate into many cell types such as osteoblasts, chondrocytes and adipocytes. Here we examine the effects of ACTH on the mouse D1 bone-marrow derived MSC. ACTH significantly increased lipid accumulation during the adipogenic differentiation of D1 cells in a concentration- dependent manner. ACTH also shifts the temporal pattern of D1 adipogenic differentiation to the left i.e. differentiation occurs earlier with ACTH treatment. No significant differences in protein expression of peroxisome proliferator-activated receptor gamma (PPAR-γ2), a regulating transcription factor of adipogenesis were found. Therefore the effects of ACTH are suggested to be mediated by an alternative pathway. Overall the results indicate a connection between increased adipose deposition and the elevated circulating ACTH associated with stress.

Preliminary Characterization of the *XRR1* Gene in the Yeast *S. cerevisiae.* Vanessa Rivera[1] and Marci J. Swede, Long Island University, Post, Brookville, NY.

We have characterized a novel gene, *XRR1* (eXhibits Rapamycin Resistance), whose null mutant exhibits temperature sensitive resistance to the anti-fungal drug rapamycin. The *XRR1* gene product was shown via a systematic yeast two-hybrid analysis (Uetz *et al*, 2000) to physically interact with FKBP12 (FPR1p). The FKBP12 protein is responsible for binding rapamycin and causing cell-cycle arrest via the *TOR* signaling pathway. The *XRR1* gene exhibits sequence homology to the A1pp (Macro) domain specific for binding ADP-ribose. This domain is found in the C -terminus of the mammalian macroH2A histone variant. Initial characterization of *XRR1* null mutants indicates that they have no overall growth defect across a temperature range of 25°C to 37° C. Further characterization of the *XRR1* gene suggests a role in the rapamycin resistance pathway. We have observed that the *XRR1* null mutation results in an increase in growth in the presence of 100 ng/ml rapamycin at 37°C compared to growth at 30°C when exposed to the drug. The degree of resistant growth observed in the null mutant is greater than that observed by wildtype isogenic yeast under the same growth conditions. This drug resistance is not observed when growth at 30°C. We propose a model in which the *XRR1* gene product is involved in stabilizing the FKBP12-rapamycin complex, which is responsible for cell cycle arrest in response to rapamycin treatment. The Swede lab gratefully acknowledges Dr. Hinnebusch at the NICHD for the gift of mutant strains. This research is supported by a grant from the Dextra Baldwin McGonagle Foundation in support of undergraduate research to MJ Swede and by a faculty research development grant from LIU, Post to MJ Swede.

The Effects of Resveratrol Compounds on the Motility and Proliferation of F10 Melanoma Cells. Christian Rivoira[1], Valery Morris[2] and Susan Rotenberg[2], [1]Queensborough Community College, Bayside, NY and [2]Queens College, Flushing, NY.

Resveratrol is a phytochemical found in grapes and wine and has been reported to possess anti-carcinogenic effects. The effects of several cis and trans isomers of resveratrol were tested on highly metastatic mouse B16 F10 cells to see the effect on cell motility. Cells were seeded onto 96-well plates, treated with each compound and then run through a proliferation assay. F10 cells were also plated on 6-well plates and allowed to grow until 100% confluent for a wound healing assay. These samples were then scratched and treated with the compounds.

Pictures of Time 0 and Time 5 were taken in order to quantify the closing of the wounds. Through western blots the effects of these compounds on β-tubulin were seen, as this has been reported to be the target of many of these compounds. It was found that compounds such as A2, CTM, and R52 were very effective in reducing the motility and proliferation of F10 melanoma cells. It was also found that A2 did not affect the β-tubulin of these cells, and that A2 seemed the least effective on Fibroblast cells, a good sign if this compound were ever to be used as a topical agent. Christian is a participant in the NIH Bridges to the Baccalaureate Program at Queensborough Community College (R25 GM65096-11).

The Toxic Effects of Manganese on Dopamine D2 Receptor Activation Is Not Due to Inactivation of the Phospholipase C Receptor Signal Transduction Component. Keisha Rogers, Isaac Beaubrun, Edward J. Catapane, and Margaret A. Carroll, Medgar Evers College, Brooklyn, NY.

Manganese is a neurotoxin causing Manganism, a Parkinsons-like disease. Manganese neurotoxicity involves disruption of dopaminergic neurotransmission. The toxic mechanism is not fully resolved. It is postulated to be more related to dopamine neuron dysfunction than degeneration. Lack of effective treatment for Manganism is an obstacle in its clinical management. *Crassostrea virginica* gill lateral cilia are innervated by serotonergic-dopaminergic neurons. Dopamine causes cilio-inhibition, serotonin cilio-excitation. Our lab showed post-synaptic dopamine receptors in gill lateral cells are D2 type, which are G protein-coupled ($G\alpha_{i/o}$) metabotrophic receptors. We also showed manganese blocks the cilio-inhibitory effects of dopamine by blocking dopamine post-synaptic receptor activity. The adenylyl cyclase component of the D2 receptor signal transduction pathway was not effected by manganese. Phospholipase C (PLC), another component of the dopamine D2 receptor signal transduction pathway, is inactivated by dopamine. We hypothesized this PLC component is not effected by manganese. To test this we measured cilia beating rates using stroboscopic microscopy. Applying serotonin (10^{-6}-10^{-3}M) to gill increased beating up to about 25 beats/min. Applying dopamine (10^{-6}-10^{-3}M) causes cilio-stasis, decreasing beating to 0. Applying manganese (100 μM) prevented this cilio-inhibitory response. Adding m3M3FBS (10^{-6}-10^{-3}M), a PLC activator, increased beating. Adding U73122 (10^{-6}-10^{-4}M), a PLC inhibitor, decreased beating. Repeating these experiments in the presence of 100 μM of managanese had no effect on either drug. The study helps elucidate the neurotoxic mechanism of action of manganese showing manganese disrupts dopamine's actions at the D2 post-synaptic receptor, but does not interfere at the level of adenylyl cyclase or PLC in the signal transduction pathway. This information is helpful to understand causes and potential therapeutic treatments of Manganism. This work was supported by grants 2R25GM0600309 of the Bridge Program of NIGMS, 0516041071 of NYSDOE and 0622197 of the DUE Program of NSF.

Optimization of Biofeul Production in *Chlamydomonas reinhardtii by* introduction of a synthetic *FATB2* gene. Joseph Saccente, J. Robert Coleman and Kerry A. Lutz, Farmingdale State College, Farmingdale, NY.

Fossil fuels are made from decomposed plants and animals that have been buried in the ground for millions of years. Since they are a limited resource, alternative fuel sources need to be developed. Biofuels are most commonly derived from plant biomass (bioethanol) or from plant oils (biodiesel). Plants and algae accumulate mostly C16-C18 fatty acid chains but short chain fatty acids (C8:0 and C10:0) are most desirable for biodiesel production due to their increased volatility, which can combust more readily. Use of crop plants for biofuel production has several drawbacks, such as a shortage in arable land needed for their planting and the increase in crop prices due to the higher demand. *Chlamydomonas reinhardtii* is a single celled alga that has a short generation time, grows in fresh water and does not take up arable land for growth. The *FatB2* gene from *Cuphea hookeriana* produces a protein that increases the presence of eight and ten carbon fatty acyl molecules. We describe here introduction of a codon-optimized *FatB2* gene into the chloroplasts of *Chlamydomonas.* The *FatB2* gene was cloned into a plastid transformation vector that targets insertion between the *psbA* and *rrn5* genes. The DNA was bombarded into the cells and transformants were identified by selection for spectinomycin resistance, conferred by the *aadA* gene, encoded in the transformation vector. Plastid transformants will be confirmed by PCR and Southern blotting. Expression of FatB2 will be confirmed by reverse-transcription PCR. Gas chromatography will be used to determine the fatty acid chain lengths

present in the transformants. Expression of the *FatB2* gene in *Chlamydomonas* is expected to increase the levels of short chain fatty acids, but is probably only one of multiple steps that will be needed to make large amounts of triacylglycerols needed for large-scale production of biofuels.

Methamphetamine Enhances *Cryptococcus neoformans* Melanization and Pathogenesis in a Murine Model of Infection. Sergio Salamanca[1], Swetha Manepalli[1] and Luis R. Martinez[2], [1]Long Island University-Post, Brookville, NY and [2]Albert Einstein College of Medicine, Bronx, NY.

Methamphetamine (METH) is a major public health and safety problem in the United States. Chronic METH abuse is associated with a 2-fold higher risk of human immunodeficiency virus infection and, possibly, additional infections, particularly those that enter through the respiratory tract or skin. *Cryptococcus neoformans* is an encapsulated opportunistic yeast-like fungus that is a relatively frequent cause of meningoencephalitis in immunocompromised patients, especially in individuals with AIDS. *C. neoformans* melanizes during mammalian infection in a process that presumably uses host-supplied compounds such as catecholamines. L-3,4-dihydroxyphenylalanine (L-DOPA) is a natural catecholamine that is frequently used to induce melanization in *C. neoformans* and L-DOPA-melanized cryptococci manifest resistance to radiation, phagocytosis, detergents and heavy metals. Using a systemic mouse model of infection and *in vitro* assays in order to critically assess the impact of METH on *C. neoformans* melanization and pathogenesis, we demonstrated that METH-treated mice infected with melanized yeast cells showed increased fungal burden in lungs, blood, and brain. Interestingly, cultures of METH-exposed cryptococci and supplemented with L-DOPA revealed that METH accelerates fungal melanization by increasing the expression of laccase, the enzyme responsible for this process, an event of adaptation to external stimuli that can be advantageous to the fungus during pathogenesis. Our findings provide novel evidence of the impact of METH abuse on host homeostasis and increased permissiveness to opportunistic microorganisms. This work was partially supported by NIH-NIAID 5K22A1087817-02 and LIU-Post Faculty Research Committee Awards.

Metabolic Reprogramming during Aging in *Drosophila melanogaster.* Mary Salim[1], Andrey Parkhitko[2] and Norbert Perrimon[2], [1]Montclair. State University, Montclair, NJ and [2]Harvard Medical School, Boston, MA.

The topic of aging has been a question that cannot be strictly targeted as the result of one specific biological process; rather it is due to numerous complex processes. In fact, nine hallmarks of aging have been identified as the following: stem cell exhaustion, altered intercellular communication, genomic instability, telomere attrition, epigenetic alterations, loss of proteostasis, deregulated nutrient sensing, mitochondrial dysfunction, and cellular senescence. Besides these hallmarks, aging is characterized by changes in activity of multiple metabolic pathways although their role has not yet been systematically studied. Therefore, the fruit fly is a good model system and powerful genetic tool to study the life cycle in parallel to the human life cycle in order to easily study its biology (1). Our first approach aims to determine the metabolic signature of aging in wild type and short/long-lived mutant flies. The second approach serves to identify how metabolic changes affect longevity. The enzymes involved in the pathways that promote lifespan will be screened for new genes that regulate lifespan. These findings can potentially target pathways involved in lifespan and be therapeutically translated to humans. Interestingly, during the aging process, transcription of metabolic genes is altered which suggests that metabolic changes play a key role in aging (2). Therefore, pivotal information about changes in metabolites during the life cycle can help us better understand their activity at times of high bodily functioning and at times of bodily deterioration. Hence, we hypothesize that lifespan and functional senescence are mediated by metabolic reprogramming. Furthermore, the enzymes associated with the metabolites can be identified in order to genetically and pharmacologically target the pathways to test whether these manipulations could prolong or shorten lifespan.

Toll Receptors on Human Mesenchymal Stem Cell-Derivrd Peptidergic Neurons in Neuronal Response to Antigen Challenge. Oleta Sandiford[1], Jacqueline Park[2], Steven Greco[2], Tammy A. Castro[1] and Pranela Rameshwar, [1]Bloomfield College, Bloomfield, NJ and [2]Rutgers-New Jersey Medical School and Graduate School of Biomedical Science. Newark, NJ.

Mesenchymal Stem Cells (MSCs) can differentiate into cells of all germ layers, making them attractive for use in models to study pathological disorders and for tissue regeneration. MSCs are also immune cells and can elicit both suppressor and enhancer activities, depending on the tissue milieu. Nerve endings are in contact with MSCs in the bone marrow, making it easy for neurotransmitters to regulate the immune responses of MSCs, thereby regulating inflammation in the bone marrow. The overarching hypothesis states that during infection the nerve fibers and MSCs interact via the neurotransmitter substance P (SP) to respond to the antigen while at the same time preventing an exacerbated immune response. This study asked how the neurons are activated by the foreign antigen. We hypothesize Toll-like Receptors (TLRs), which can interact with pathogen associated molecular patterns (PAMPs), to play a role in this activation. Hence we monitored the expression of TLRs in undifferentiated MSCs and during their development to neurons. The MSCs were induced with a defined induction protocol specific for the formation of peptidergic neurons that produce SP. TLR expression was checked at three endpoints; uninduced (D0), partially differentiated phenotype (D6) and fully differentiated phenotype (D12). Immunofluorescence labeling was performed for TLRs 1-10. Uninduced MSCs expressed TLR 3 and 4, partially differentiated TLRs 1, 4, 5 and 7, and fully differentiated expressed TLRs 3, 4 and 9. The findings of this study will be confirmed by methods of Western Blot and functional studies with a multi-chamber system. In summary, the results showed a development expression of the Toll receptors.

Methamphetamine Alters the Antimicrobial Efficacy of Phagocytic Cells during Methicillin-Resistant *Staphylococcus aureus* Skin Infection. Bhavikumar Shah[1], Mircea Radu Mihu[2], Jessica Roman-Sosa[3,4], Avanish K. Varshney[3,4], Eliseo A. Eugenin[5,6], Long N. Nguyen[7], Allan J. Guimaraes[8], Bettina C. Fries[3,4], Joshua D. Nosanchuk[3,4], and Luis R. Martinez[1,3,4], [1]Long Island University-Post, Brookville, NY, USA; [2]Montefiore Medical Center, Bronx; [3]Albert Einstein College of Medicine, Bronx; [5]Public Health Research Institute (PHRI), [6]UMDNJ, Newark, NJ; [7]Duke-NUS Graduate Medical School, Singapore and [8]Instituto Biomédico, Universidade Federal Fluminense, Rio de Janeiro, Brazil.

Methamphetamine (METH) is a major drug of abuse in the United States and worldwide. Furthermore, *Staphylococcus aureus* (*SA*) infections and METH use are emerging public health problems. *SA* is the single most important bacterial pathogen in infections among injection drug users, with skin and soft-tissue infections (SSTI) being extremely common. Notably, the incidence of SSTI, especially in the drug users, is difficult to estimate because such infections are often self-treated. Although there is substantial information on the behavioral and cognitive defects caused by METH in drug users there is a dearth of knowledge regarding its impact on bacterial infections and immunity. Therefore, we hypothesized that METH exacerbates *SA* skin infection. Using a murine model of METH administration and wound infection, we demonstrated that METH reduces wound healing and facilitates bacterial-mediated collagen degradation. Additionally, we showed that METH leads to detrimental effects on the functions of neutrophils and macrophages enhancing susceptibility to *SA* infection. Our findings provide empirical evidence of the impact of METH use on the antimicrobial efficacy of the cells that comprise the innate immunity, the initial host responders to combat microbial infection. This work was partially supported by NIH-NIAID 5K22A1087817-02 and LIU-Post Faculty Research Committee Awards.

Stimuli Responsive, Small Molecule Binding and Cellular Uptake of Engineered Protein Polymer•gold Nanoparticle Hybrids. Ekta Sharma[1], Min Dai[1], Raymond Chen[1] and Jin Kim Montclare[1,2], [1]Polytechnic Institute of NYU, Brooklyn, NY and [2]SUNY Downstate Medical Center, Brooklyn, NY.

The ability to deliver drugs to targeted destinations remains a significant challenge. Inspired by nature, we developed protein polymers, E1C and CE1, comprised of two self-assembling domains derived from elastin (E) and the coiled-coil domain of cartilage oligomeric matrix protein (C) capable of encapsulating therapeutic small molecules as smart biomaterials for drug delivery. In order to control the encapsulation and delivery of drug molecules, we have incorporated gold nanoparticles (GNPs). Our

studies demonstrate that GNP templation leads to a more ordered structure for both E1C and CE1 protein polymers as well as an increase in transition temperature. Both protein polymer-GNP complexes demonstrate improved binding to the small molecule curcumin, making them suitable for potential use in drug delivery.Further, proteins with or without templation were investigated for their effect on CCM uptake by cancer cell lines (MCF7) and their effect on CCM release. Both templated and non-templated exhibit significant uptake of CCM by cell compared to CCM. Our studies support the polymer-GNP complex to be used as drug delivery vehicle.

Factors Affecting Manganese Accumulations in Gill Mitochondria of *Crassostrea virginica*. *Temitope Shoneye, *Ahmed Nuhar, Margaret A. Carroll, and Edward J. Catapane, Medgar Evers College, Brooklyn, NY.

Manganese is a neurotoxin causing Manganism in people exposed to elevated levels in their environment. Oxidative stress is implicated as a factor underlying manganese toxicity and mitochondria play a role as both cause and target of oxidative stress damage. The mechanisms of the cellular damage is attributed to manganese's capacity to produce toxic levels of free radicals and induce mitochondrial dysfunction. Controversy exists to the extent of manganese accumulation within mitochondria and if this contributes to the cause of Manganism. We have been using the oyster, *Crassostrea virginica*, as a test animal to study manganese neurotoxicty. We found manganese disrupts the animals' dopaminergic system, impairs its mitochondrial respiration and manganese accumulates within mitochondria of gill cells of *C. virginica* . The mechanism of influx and efflux has not been well studied. Manganese is believed to utilize the mitochondrial Ca^{2+} uniporter and H^+ or Na^+/Ca^{2+} exchanger for these movement. We hypothesize Ca^{2+} channel blockers will alter mitochondrial manganese accumulations. We homogenized and centrifuged *C. virginica* gills to prepare mitochondria. Isolated mitochondria were treated with Ca^{2+} channel blockers prior to manganese exposure, pelleted and washed to remove non-accumulated manganese. Treated mitochondria were digested in HNO_3 in a microwave digester, then analyzed for manganese content with an atomic absorption spectrophotometer. Manganese (1-5 mM) treated mitochondria exhibited dose dependent accumulations up to 1000% compared to controls. The channels blockers, $LaCl_3$, diltiazem, verapamil and ruthenium red (0.25-2 mM) each significantly reduced the accumulations. $LaCl_3$ was the most effective in the doses we tested. The study shows isolated mitochondria readily accumulate manganese and the mechanism of influx and efflux can be affected by drugs that interact with the mitochondrial Ca^{2+} uniporter and the H^+ or Na^+/Ca^{2+} exchanger. This work was supported by grants 0516041171 of NYSDOE and 0622197 of the DUE Program of NSF.

Physiological Response of *Chlamydomonas* to Nickel Chloride. Anaika Singh, Jillian Cortese, *Jude Sanchez and Tin-Chun Chu. Seton Hall University, South Orange, NJ.

Algal blooms are currently becoming one of the greatest concerns of environmentalists and microbiologists. The ability of green alga (particularly *Chlamydomonas*) to cause eutrophication and grow in the presence of heavy metals poses a great threat to both underwater life and humans. The purpose of this study is to investigate the possible mechanisms of heavy metal resistance in environmental alga. In this study, *Chlamydomonas* was exposed to various concentrations of nickel chloride (0, 10, 25, and 50 mg/L $NiCl_2$), a toxic metal, to observe its resistance. Cell growth was monitored in various concentrations by using turbidity study and direct count technique. At 10 mg/L, the *Chlamydomonas* displayed prolonged lag phase and did not enter the log phase until after day 12. At 25 mg/L, the *Chlamydomonas* stayed at the lag phase and did not enter the log phase. These results suggested that 25-50mg/L $NiCl_2$ is lethal for the *Chlamydomonas*.

Genome Project of Plasmid and Stress Response of Plasmid in Cyanobacteria *Synechococcus* IU 625. Anna Slusarczyk and Lee H. Lee. Montclair State University, Montclair, NJ, USA.

The notorious cyanobacteria gained their interest after the discovery that they are responsible for the formation of Freshwater Harmful Algal Blooms (FHAB). Cyanotoxins produced by cyanobacteria influence aquatic biota, earthbound wildlife along with humans producing allergic reaction and cancer. *Synechococcus sp.* IU 625 (*SIU* 625) is one of the cyanobacteria that are responsible for the

production of algal blooms. Due to its simplicity and easy to culture, it has been used as a potential environmental pollution indicator, especially for heavy metal contamination. Many EPA targeted metals such as Hg, Cd, Pb, Zn and Cu etc. have been studied and published from our lab. In this study, large plasmid was identified and sequenced. Plasmid isolation of *SIU* 625 was carried out utilizing QIAPrep® Spin Miniprep Kit. Nano drop analyses were performed to check purity and quantity. OligoPerfect™ Designer was used to design primers based on closely related *S. elongatus PCC* 7942 sequence. The PCR based assay was carried out and the PCR products were sequenced and assembled. The near complete sequence of plasmid was obtained and annotated. BlastN and BlastX searches were carried out to identify homology with other plasmids. The results indicated that plasmid in *SIU* 625 has high similarity to the plasmid in *S. elongatus PCC* 7942. In addition, stress responses of plasmid were also studied using different concentrations of HgCl2 (0.1, 0.5 and 1.0 mg/L). The results indicated that in the presence of heavy metal the number of plasmids in the cell increased. This suggests that there are Hg tolerant or resistant genes on the plasmid to help the cells survive in the stress environment.

Inferring Biological Networks using Boolean-Sparse Network Inference Methods. Vladimir Solano, Wenwei Xiong and Chunguang Du, Montclair State University, NJ, USA.

Biological networks are the processes that occur within complex biological systems. It can be genetic, regulatory, signaling, metabolic, developmental or any other processes that applies to a living organism. To refine our knowledge of the cell, we integrate knowledge from diverse biological components and data into models of the system as a whole. Network inference is the reconstruction of biological networks from data, identifying the interconnections between the biological entities. There are many network inference methods available, generating different hypothesis about cell biology. Understanding biological networks can lead to a better understanding of biological mechanisms, from finding treatment of diseases to evolutionary processes. An important molecular mechanism in biological process is gene regulation and gene expression. Gene regulatory network inference is an intense studied problem for which many techniques have been developed. Genes interact with each other forming intricate networks that can be modeled and simulated using various approaches. We can infer gene regulatory network from high-throughput data from gene expression measurements like microarrays and RNA-seq. Here we present a fresh look on the inference of gene regulatory networks using Boolean logic and Sparse Linear Regression methods. Based on these methods, we developed a pseudocode that can be applied to microarray gene expression data.

Early Signs of DCA-Induced Apoptosis in Cancerous Cells. Alexandria Smith and Tammy A. Castro, Bloomfield College. Bloomfield, NJ.

Cancer cells have long been known to exhibit mitochondrial dysfunction that results in the predominant use of glycolysis over oxidative phosphorylation which in turn contributes to the development of an apoptosis resistant phenotype. Dichloroacetate (DCA) is a small molecule, and an orphan drug, that has been reported to normalize mitochondrial function and to promote apoptosis. The objective of this study is to identify the early signs of DCA-induced apoptosis by monitoring caspase levels in tumorigenic and non-tumorigenic cell lines. Preliminary data obtained using a luminescent assay to monitor the activity of Caspase-9 shows a DCA concentration-dependent increase in the activity of this initiator caspase. Caspase-9 was selected because it is activated by the mitochondrial death pathway. Future work will assess the state of other caspases by measuring their activity as well as mRNA levels.

Engineered Self-assembling Coiled-coil Protein Fibers. Jennifer Sun, Rudy Jacquet, Jasmin Hume and Jin Kim Montclare, Polytechnic Institute of New York University, Brooklyn, NY.

Research towards biomaterials has become increasingly popular, as scientists look for energy efficient alternatives to electronic components commonly used in medical and biological applications. Using protein-derived materials as electronic components, biological engineers are given design options that are easier and less expensive to achieve than using synthetic methods. In this project, our goal is to design and construct self-assembling protein fibers capable of metal nanoparticle templation. We have engineered two variants of the α-helical coiled-coil of cartilage oligomeric matrix protein (COMPcc) to self-assemble longitudinally. Characterizations of these protein fibers are conducted using circular dichroism (CD), transmission electron microscopy

(TEM) and fluorescence microscopy (FM). Additionally, confocal microscopy provides evidence that our protein fibers demonstrate small molecules binding capabilities, specifically to the small fluorescence molecule curcumin. The aim of our research is to functionalize protein nanowire materials as components of electronic devices with the ability to deliver the same level of functionality and effectiveness as their synthetic equivalents.

Effect of Green Tea Polyphenols and Modified Lipophilic Tea Polyphenols on Biofilm Formation in *Pseudomonas aeruginosa* and *Pseudomonas fluorescence*. Hassan Tahir, David Aponte, Michael Klotz and Lee Lee, Montclair State University, Montclair, NJ.

Green tea polyphenols are crude compounds that are isolated from green tea leaves in efforts to potentially benefit from their numerous attributes. The specific compounds being used within this study are Green Tea Polyphenol (GTP) and Modified Lipophilic Tea Polyphenol (LTP). Within the past decade the growing bacterial problem has been the formation of biofilm. *Pseudomonas aeruginosa* and *Pseudomonas fluorescence*, gram -negative biofilm forming bacteria, were used in this study. In this study, both bacteria were grown under various concentrations of GTP and LTP ranging from 10 μg/mL to 100 μg/mL that are well below the minimum inhibitory concentration (MIC) of 1% for *P. aeruginosa* and *P. fluorescence*. The microorganisms were placed in 24 and 6 well plates and incubated for 5 days to allow biofilm formation. The plates were removed and a crystal violet assay was performed to the adhered biofilm cells to find their relative concentration using a spectrophotometer at wavelength 495 nm. The 6 well plates containing a cover glass within each well for biofilm microscopic observation was also performed. Treatments with GTP and LTP were 30 μg/mL and 50 μg/mL for both bacteria. Results indicated that GTP is able to inhibit biofilm growth up to 100% with a concentration of 30 μg/mL for both bacteria while LTP is able to inhibit biofilm growth up to 81%, at a concentration of 30μg/mL with *P. fluorescence* and up to 100% with a similar concentration on *P. aeruginosa*. The results indicated that both GTP and LTP are good anti-biofilm forming agents.

Identifying Genetically Modified Organisms Among Typical Produces. Melody To, Nidhi Gadura, Queensborough Community College, Bayside, NY.

Plant engineering has led to the production of genetically modified (GM) foods. Some selective advantages that plant genetics can develop for GM plants are insecticidal resistance, herbicidal resistance, viral resistance, and fungal resistance. Genes that have been cloned and expressed in GM plants have enhanced the quality of crops, increased yields of harvests and added to the nutritional value of produces in order to fulfill commercial needs as well as provide better food to the population. Plasmids can be used to introduce new genetic information to plants such as antibiotic resistance. *Agrobacterium tumefaciens* possesses a bacterial plasmid; a tumor inducing (Ti) plasmid approximately 200kbp that can be used to introduce new genes but first must be disarmed of its virulence. A section of the Ti plasmid, T-DNA, can be integrated into the plant genome as a binary vector by being transformed and cloned into a small plasmid with sequences from viral vectors. The three viral vectors often used to incorporate genes of interest are the Califlower mosaic virus (CaMV), nopaline synthase (NOS) terminator, and the plant chloroplast genes. In this study, primers specific to these viral vectors typically found in GMOs were used to investigate if produces such as banana, corn, peas, kale, plum, carrot, and lemon were genetically modified or not. Basic techniques of gene analysis were utilized by extracting the DNA of these produces, performing a polymerase chain reaction (PCR) to amplify genetically modified DNA *in vitro*, and identify the GMOs with an agarose gel electrophoresis.

Effects of Urbanization on Water Quality of Two New Jersey Rivers. Paul Tomasula[1], Jewel Lipps[2], Myla Ramirez[3], Meiyin Wu[3], Josh Galster[3] and Gregory Pope[3], [1]Rutgers University, [2]Southern Methodist University and [3]Montclair State University.

Use of land by humans impacts the environmental characteristics of an area. As the number of people using the land increases, the impact also increases. In particular, heavily used land may lead to higher levels of nutrient pollution, which can cause eutrophication and decrease water quality. The purpose of this research is to study the effects of urbanization on water quality in two New Jersey rivers, the Passaic River and

the Flat Brook. This was accomplished by sampling water at test sites distributed along each of the rivers. Water samples were tested for species of nitrogen and phosphorus using flow injection analysis (FIA). Land use of each river's watershed was determined by using Geographic Information Systems (GIS), and riparian assessments were used to examine land use at the immediate site. This showed that the Flat Brook watershed is dominantly forest cover while the Passaic watershed is highly urbanized. By comparing the FIA results of water quality for the Passaic and the Flat Brook, it was determined that urbanization results in significantly lower water quality.

Towards the Synthesis of a Potent, Selective, and Covalent Inhibitor of Cysteine Cathepsin L. Viviana Torres[1] and Sanjai Kumar[2], [1]Queensborough Community College, Bayside, NY and [2]Queens College, Flushing, NY.

Cysteine cathepsins are an important class of enzymes that participate in the degradation of proteins, both within the living cell and the extracellular matrix. The endopeptidase cathepsin L, a dominant member of the cysteine cathepsin family, plays an essential role in the processing of antigens, proper bone resorption, and turnover of intracellular and secreted proteins. However, aberrant expression of the enzyme cathepsin L has been proven to provoke tumor cell invasion, tumor cell apoptosis, and resistance to therapies due to the catalytic degradation of the extracellular matrix and basement membranes. Therefore, the enzyme Cathepsin L has become an important therapeutic target for drug development. Unfortunately potent, selective, and cell permeable inhibitors of cathepsin L remain scarcely available to serve as lead compounds for therapeutic development. Herein, a library of aryl vinyl sulfonate compounds has been synthesized with a variety of substituted phenols, in the presence of 2-chloroethanesulfonyl chloride, anhydrous dichloromethane, and the base triethylamine. From the library of compounds, compound 8 has been identified as the lead covalent inhibitor of cathepsin L activity. Enzyme kinetics analysis demonstrates that the para-substituted bromine functional group in compound 8 plays a critical role in the binding affinity towards the putative S2' pocket of cathepsin L. Finally, a potent, selective, and cell preamble inhibitor of cathepsin L enzyme, will be developed utilizing compound 8 as the lead scaffold. Viviana is a participant in the NIH Bridges to the Baccalaureate Program at Queensborough Community College (R25 GM65096-11).

Wildlife Guardians Project: Improving Permeability of Wildlife Habitats in NJ. Kelly Triece[1], Natalie Sherwood, Meiyin Wu[1], Gretchen Fowles[2] and Brian Zarate[2], [1]Montclair State University, Montclair, NJ and [2]New Jersey Division of Fish and Wildlife, Endangered and Nongame Species Program, Clinton, NJ.

Human impacts are threatening biological systems that sustain populations on Earth, and its consequences are significant and extremely intricate. Habitat fragmentation has a large negative impact on biodiversity; animals need to be able to move through the landscape to find food, mates, and other resources. Human transportation roadways often intersect habitats and reduce wildlife habitat permeability. New Jersey's extensive road network has been shown to impact wildlife populations in multiple ways, including direct mortality of individuals and creating barriers to wildlife movement and genetic exchange. Wildlife Guardians Project aims to identify wildlife crossing and mortality hotspots by surveying selected road segments during Spring 2013. Evidence of wildlife crossing and road mortality will be recorded and photographed. Species found on selected road transects include Northern spring peeper (*Pseudacris crucifer crucifer*), green frog (*Rana clamitans melanota*), pickerel frog (*Rana palustris*), wood frog (*Rana sylvatica*), Northern gray treefrog (Hyla versicolor), bullfrog (Rana catesbeiana), spotted salamander (*Ambystoma maculatum*), red-spotted newt (*Notophthalmus viridescens viridescens*), common snapping turtle (*Chelydra serpentina*), Northern water snake (*Nerodia sipedon sipedon*), and Eastern garter snake (*Thamnophis sirtalis sirtalis*). Landscape assessments will be conducted at each surveyed road transect to determined potential habitat characteristics that may be associated with wildlife crossings. At the end of the project period, the results will be integrated into New Jersey's Habitat Connectivity Project and used to 1) identify and validate GIS-modeled movement corridors, 2) prioritize wildlife crossing hotspots for supplemental monitoring, 3) determine habitat characteristics associated with the mortality hotspots, 4) use significant landscape characteristics to predict other possible mortality hotspots and 5) when applicable, inform road infrastructure mitigation strategies to reduce future vehicle-wildlife conflicts.

Brain Awareness Video Contest Project: Multiple Sclerosis. Candice Valenzuela, Maria Didiego, Rachel Geylin, Daniela and Kursh, Maria Agapito Bergen Community College, Paramus, New Jersey, USA.

The society for neuroscience sponsors a brain awareness video contest every year. The aim is to provide an educational resource that is designed for a lay audience as an introduction to neuroscience. In the Fall of 2012, the students from the Anatomy and Physiology class at Bergen Community College submitted a video that provides a valuable educational resource for families that have been diagnose with Multiple Sclerosis (MS). Their audience target were children of families that were diagnosed with MS.

Classical Conditioning and Associative Learning with Auditory Stimuli and 3rd Instar *Drosophila melanogaster.* Jessyka Venchkoski, Adrianna, Krul, Alexa Gammo and Julian Paul Keenan, Montclair State University, Montclair, NJ.

Previous research indicates that *Drosophila* melanogaster 3rd instar larvae do have the capacity to learn association through classical conditioning with visual and olfactory cues. The current study was conducted to further extend the understanding of 3rd instar larvae associative learning with auditory cues. Tones of five different hertz levels (0, 50, 100, 250, and 500), were used as the conditioned stimuli. Fructose served as the gustatory unconditioned stimulus UCS+. Conditioning assays were performed in petri dishes on half agar-only, half agar and fructose. Five 3 minute conditioning trials paired the UCS+ with one level of hertz of the CS. Five separate assays were performed to keep the level of the CS controlled. Testing involved agar-only petri dishes in which only the tone was presented. More larvae were found on the tone side of the dish during the testing trials. These primary findings suggest that the use of auditory stimuli with gustatory reinforcement inspires learning. To extend our findings, we conducted a generational experiment to test whether auditory associative learning capacities could spread to successive offspring. We ran 30 larvae through five, 3 minute conditioning trials. Each conditioning trial paired the UCS+ to 250Hz level CS. The testing trial exposed the larvae to only the 250Hz tone. 33% of the larvae that spent a significant amount of the three minutes on the positive zone (tone side) were separated and bred. Further testing of the successive generations will provide insight about associative learning and inheritance.

GABA is an Inhibitory Neurotransmitter in Ganglia of the Bivalve Mollusc, *Crassostrea virginica*. Fatima Walden[1], *Sadchla Mathieu[2], *Darlene Sylvain[2], Edward J. Catapane[2] and Margaret A. Carroll[2], [1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY.

In most studied bivalves, beating rate of gill lateral cilia is controlled by serotonergic-dopaminergic innervations. GABA (γ-aminobutyric acid) is an inhibitory neurotransmitter in molluscs and other animals, but has not been well studied in bivalves. We previously showed GABA inhibited actions of serotonin on gill lateral cilia beating when applied to the cerebral ganglia of *C. virginica.* We hypothesize GABA also serves as an inhibitory neurotransmitter in the visceral ganglia and inhibits the excitatory serotonin neurons there as well. We studied this by examining effects of GABA at the visceral ganglia. Ciliary beating was measured by stroboscopic microscopy in animal preparations in which the innervation of the gill by the cerebral ganglia was cut, but the innervation of the gill by the visceral ganglia was intact. Superfusing serotonin (10^{-6}-10^{-3}M) onto visceral ganglia produced dose-dependent increases in beating from an average basal rates of 10 beats/min to 25. Superfusing GABA (10^{-6}-10^{-3}M) by itself did not alter beating rates. Superfusing serotonin in the presence of increasing concentrations of GABA resulted in a dose-dependent blockage of the serotonin induced response. This study in conjunction with our previous work demonstrates GABA is working centrally at both the cerebral and visceral ganglia as an inhibitory ganglionic neurotransmitter in *C. virginica* inhibiting serotonin neurons innervating gill and speeding up cilia beating. The bivalve mollusc gill is a useful model to study regulatory mechanisms of ciliary activity as well as the pharmacology of drugs affecting biogenic amines in nervous systems. This work was supported by grants 2R25GM0600309 of the Bridge Program of NIGMS, 0516041071 of NYSDOE and 0622197 of the DUE Program of NSF.

Presence of Inhibitory GABA Receptors on Serotonin Neurons in the Bivalve Mollusc *Crassostrea virginica*. *Christopher Welsh, A.C. Everard Saunders, Edward J. Catapane, and Margaret A. Carroll, Medgar Evers College, Brooklyn, NY.

GABA (γ-aminobutyric acid) is an inhibitory neurotransmitter in molluscs and other animals, but has not been well studied in bivalves. In several bivalves, including *Crassostrea virginica*, beating of gill lateral cilia is controlled by serotonergic-dopaminergic innervations. Serotonin increases beating rates, dopamine slows down beating. Earlier we showed GABA has no effects on beating of gill lateral cilia in *C. virginica* whether superfused to cerebral or visceral ganglia, or gill. GABA blocked the cilio-excitatory effects of serotonin on beating when both were applied to the cerebral ganglia, and the GABA antagonist bicuculline methchloride blocked this. We hypothesize cerebral and visceral ganglia contain GABA neurons and the cilio-excitatory serotonin neurons have inhibitory GABA receptors. To test this we used immunofluorescence to visualize GABA and serotonin neurons, and GABA receptors in cerebral and visceral ganglia of *C. virginica*. Tissues were dissected, snap-frozen, cryostat sectioned, fixed with paraformaldehyde, treated with blockers, and incubated with primary then secondary antibodies. Sections were viewed FITC and Texas Red excitation/emission filters. We found cerebral and visceral ganglia contained GABA neurons and some serotonin neurons had GABA receptors on their soma. This study confirms our pharmacological studies indicating GABA works centrally as an inhibitory ganglionic neurotransmitter in *C. virginica* to inhibit cilio-excitatory serotonin neurons that innervate the gill and helps to explain the ganglionic circuitry by which this could be done. This work was supported by grants 0516041071 of NYSDOE and 0622197 of the DUE Program of NSF.

Using Video to Monitor Captive Juvenile and Trilobites Atlantic Horseshoe Crabs (*Limulus polyphemus*) Activity and Movement Patterns. Paul White, Christina Colon and Arthur Zeitlin, Kingsborough Community College.

The aim of the investigation was to examine aspects of juvenile and trilobite (hatchling) Atlantic horseshoe crab's (*Limulus polyphemus*) activity levels, movement pattern, and to identify and quantify any correlations between the two age categories. It was hypothesized that juvenile and hatchling horseshoe crabs will exhibit non-random movement patterns during intervals of foraging or exploration and there will be no difference in the activity levels and movement patterns of trilobites and juveniles. It was also hypothesized that there would be a correlation between activity level and size among juvenile horseshoe crabs. A captive study was done shed some insight into this unknown area of research. Using a high resolution video camera, movement patterns of captive juvenile and trilobites were continuously recorded for one hour in a shallow seawater pool under laboratory conditions. Activity level data were analyzed and compared. The mean activity level per hour of the trilobites was not significantly lower than that of the juveniles. The movement patterns of each cohort were categorized as turns (left, right) and spiraling (constricting, expanding), with trilobites producing more spiraling/turning patterns, with juveniles activity being predominantly linear. Trilobites spent their time swimming with frequent rest intervals while juveniles spent their time walking, and showed fewer rest intervals. Gratitude is extended to Dr. Mark Botton and Dr. Yumiko Iwasaki, Kang Lee, Richard Ramsundar of Fordham University, New York City Audubon, NY Sea Grant, NYC Parks, NY State DEC, National Park Services and the Army Corps of Engineers. This work was supported by grant 2R25GM0600309 of the Bridge Program of NIGMS and grant 0537121091 of the CSTEP Program of NYSED. The authors would also like to thank Jeff Crysral and Voltaics Systems for providing the equipment used in this study.

HelitronScanner: A Two-layered Local Combinational Variable Approach to Generalized Helitron Identification. Wenwei Xiong[1], Limei He[2], Hugo K. Dooner[2], Chunguang Du[1] [1]Montclair State University, Montclair, NJ and [2]Rutgers University, Piscataway, NJ.

Helitrons, new rolling-circle eukaryotic transposons discovered in plant and animal species, have been implicated in processes of great evolutionary significance, such as gene duplication, exon shuffling, and horizontal transfer. Identifying *Helitrons* is a challenge because, unlike other DNA transposable elements, *Helitrons* have no terminal repeats and do not create target site duplications. Here we present a two-layered Local Combinational Variable (LCV) approach (HelitronScanner) for generalized *Helitron*

identification. LCV represents either patterns of nucleotide sequences or the combinations/ associations of such sequence patterns. The first layer extracts location-nonspecific LCVs (n-LCV) in a known *Helitron* set and then creates a distribution matrix of these n-LCVs matching against *Helitrons*. The second layer draws location -specific LCVs (s-LCV) from the distribution matrix. This two-layered procedure is applied to new sequences comparably. In HelitronScanner, n -LCVs represent sequence patterns shared by *Helitrons* and s-LCVs constitute the associations of these patterns within *Helitrons*. Both dry lab and wet lab verifications were conducted to reduce the false positive rate. We first compared *Helitrons* identified by both HelitronScanner and HelitronFinder (one of our previous algorithms for *Helitron* detection). HelitronScanner detected more *Helitrons*, including those also identified by HelitronFinder. *Helitron* insertion polymorphisms were identified by (i) matching flanking sequences against genome sequence data of 6 maize inbred lines and (ii) PCR assays of *Helitron* vacant sites in multiple maize inbred lines. These verification feedbacks allow HelitronScanner to be iteratively improved in order to achieve high accuracy and convenience in genome-wide *Helitron* identification. HelitronScanner has been run successfully on a wide array of plant genomes.

InsertionMapper: A Pipeline Tool for the Identification of *Ds*-targeted Sequences from Next-generation Sequencing Data Using Multi-dimensional Pooling Strategy. Wenwei Xiong[1], Limei He[2], Hugo K. Dooner[2], Chunguang Du[1], [1]Montclair State University, Montclair, NJ and [2]Rutgers University, Piscataway, NJ.

Next-generation sequencing (NGS) technology is an unprecedented high throughput and cost-effective way of sequencing genomes. In our NSF-PGRP-funded project, we developed a pipeline tool for the analysis of NGS data to identify *Ds*-targeted sequences and, thus, generate a sequence-indexed *Ds* library. Our transgenic *Dsg* element is marked with the jellyfish green fluorescence proteins (GFP), allowing amplification of *Dsg*-adjacent sequences with nested PCR primers based on GFP and a 5-bp region at the end of *Ds* (also known as the *Ds* identifier). DNA samples are sheared and amplified in multiple phases so as to enrich for *Dsg*'s and their adjacent insertion sites. A 3-D pooling strategy is adopted to further increase throughput. Each sample is placed in a 3-D well, where every dimension is barcoded before sequencing starts. Our raw data consist of reads assigned to different libraries according to their barcodes. The pipeline aims to: map reads back to their original wells (i.e., deconvolute the 3-D pool); and localize *Dsg* insertion sites in the maize genome. First, in each library, the pipeline filters out reads unrelated to *Ds*-adjacent sequences by checking accordance between reads and the sequence of the PCR primer plus the *Ds* identifier. Retained reads are imported into MySQL database, with each database table linked to one library. Reads are merged according to well coordinates from related 3-D libraries and ranked by their copy number after grouping by sequence. Ideally, the top ranked sequence in a specific well should correspond to the real *Dsg*. However, due to the presence of endogenous *Ds* elements and possible sequencing errors, top-ranked candidates have to be carefully inspected to identify the real *Dsg*. An alternative to 3-D merging is to rank reads in individual libraries and pick reads with top ranks in all three dimensions, which complement the merging method yet requires empirical thresholds. Last, *Ds* insertion site junction sequences are mapped to the maize genome using a local version of BLAST. This pipeline tool is suitable for massive NGS data manipulation in similar scenarios.

Loss of GSK3β in Epithelial Ovarian Cancer Leads to Chemoresistance by Epigenetic Regulation and Suppression of Apoptosis. Mena Yacoub[1], Noelle Cutter[1], Robert Lucito[2], Doug Levine[3], Kazimierz Wrzeszczynski[4]. [1]Molloy College, Rockville Centre, NY, [2]Hofstra North Shore LIJ, Hempstead, NY, [3]Memorial Sloan Kettering Cancer Center, New York, NY, [4]Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

Epithelial ovarian cancer is the leading cause of death from gynecological malignancies. Currently platinum-based chemotherapy, coupled with a taxane based drug, and debulking surgery are the primary treatment for ovarian cancer. Approximately 25% of patients either present with or rapidly develop resistance to platinum based chemotherapy and all recurrent tumors ultimately become resistant. Epigenetic modifications have been associated with tumor formation and progression and may contribute to therapy response. We performed a methylation screen on a set of tumors and have found a number of genes and family members differentially methylated between resistant patients and sensitive patients. Here we suggest that loss of expression of

GSK3β, a proline-directed serine threonine kinase, causes increased resistance to platinum chemotherapy drugs. Additionally, ovarian cell lines transcriptionally silenced for GSK3β are more invasive and display a decrease in apoptosis. Taken together, we suggest a role for GSK3β as an important epigenetic regulator of chemo-resistance in ovarian cancer and hypothesize evading apoptosis as one of the underlying mechanisms. Furthermore, GSK3β expression might represent a therapy response predictor and could be a future therapeutic target for ovarian cancer.

Relative Contributions of Pol II CTD Phoshporylation and Histone Methylation to NuA4 Occupancy in Coding Sequences. Kalpana Yadamakanti and Daniel S. Ginsburg LIU Post Brookville, NY.

NuA4 is the only essential lysine acetyltransferase (KAT) complex in S. cerevisiae, acetylating histones H4 and H2A. During transcription, NuA4 is recruited to promoters and stimulates transcription initiation. NuA4 is also recruited to coding sequences through interaction with the RNA polymerase II (Pol II) C-terminal domain (CTD) where it interacts with methylated nucleosomes and stimulates transcription elongation. We aimed to investigate the relative contributions of Pol II CTD phosphorylation and histone methylation in recruiting NuA4 to coding sequences. We are generating double and triple mutants lacking CTD serine 5 phosphorylation (Ser5p) and methylation of histone H3 lysines 4 and 36. We show here that loss of CTD Ser5p in a kin28ts mutant reduces NuA4 occupancy at coding sequences. Our data suggests that the loss of occupancy is due to decreased NuA4 interaction with Pol II. We have also shown that H4 acetylation is decreased in a bur2? mutant suggesting that phosphorylation of CTD serines 2 and 5 may stimulate NuA4-mediated histone acetylation. Many coactivator complexes are recruited to coding sequences and then must act on nucleosomes. This work sheds light on what may be a general mechanism in which both the Pol II CTD and nucleosmes stimulate occupancy in coding sequences. This research was supported by a grant from the LIU Post Research Committee. We thank Hongfang Qiu for technical assistance.

Preliminary Microsatellite Analysis Suggests that *Thalassia testudinum* in Separated Bays of St. John Virgin Island May Have Greater Genetic Diversity than Previously Believed. Nadia Zaben[1], Mohamedhakim Elakhrass[1], Paul A.X. Bologna[1], Robert W. Meredith[1], John V. Smalley[2], James J. Campanella[1], [1]Montclair State University, Montclair, NJ and [2]Bergen Community College, Paramus, NJ.

We have conducted previous studies examining the genetic diversity and population genetics of the marine turtle grass *Thalassia testudinum,* employing polymorphic mitochondrial and nuclear DNA sequences. These data suggested that several geographically separated populations (Hurricane Hole, Little Lameshur Bay, Great Lameshur Bay, and Reef Bay) of the sea grass from around the island of St. John in the Virgin Islands were clonal with little or no genetic variation between them. Since this result seemed unusual, we further employed polymorphic, genomic microsatellite alleles to determine if our first analyses represented the true level of genetic diversity in these plants. When the study is completed we will have analyzed 25-30 plants per population and utilized 7-8 microsatellite loci. Our preliminary data, with only four loci analyzed and 16-23 plants employed per population, strongly indicate that the St. John *T. testudinum* populations are 1) not clonal, 2) have a reasonable level of genetic diversity, and 3) have microsatellites that are evolving at a faster rate than their mitochondrial and sampled nuclear DNA regions.

Auxin Conjugate Hydrolases of Two Gymnosperms and Evolutionary Implications. Nadia Zaben[1], Dalma Enriquez[1], John V. Smalley[2], Jutta Ludwig Müller[3] and James J. Campanella[1], [1]Montclair State University, Montclair, NJ, [2]Bergen Community College, Paramus, NJ and [3]Institute of Botany, Technische Universität Dresden, Zellescher Weg 20b, 01062 Dresden, Germany.

We have examined how the ILR1□like auxin conjugate hydrolase gene family has functionally evolved in the gymnosperm species Sitka spruce (*Picea sitchensis*) and Loblolly pine (*Pinus taeda)*. We have isolated and cloned two orthologues from spruce (PsIAR31, PsIAR32) and one from pine (PtIAR31) that are homologous to the *Arabidopsis thaliana* AtIAR3 auxin amidohydrolase. We have previously examined the enzymatic activity of PsIAR31 using a thin layer chromatography

method. Using more sensitive HPLC methods, we have re□investigated the hydrolytic activity and substrate recognition of both PsIAR31 and PsIAR32. Neither PsIAR31nor PsIAR32 appears to hydrolyze IBA or IPA conjugates. Additionally, we have found that PsIAR31 and □32 recognize several IAA conjugates (including IAA□Alanine, IAA□Aspartate, IAA□Glucose, and IAA□Isoleucine). The PtIAR31 enzyme seems to primarily recognize IBA□Alanine as a substrate. Using phylogenetic analysis, we also found a family of five putative paralogue hydrolases in both the pine (PtIAR31□35) and the spruce (PsIAR31□35) genomes. This result supports the hypothesis that multiple copies of auxin conjugate hydrolase genes have been present since gymnosperms evolved, and that this redundancy did not arise later in angiosperms.

Flourinated Cartilage Oligomeric Matrix Protein Fiber Design and Assembly. Kevin Zhang, Haresh More and Jospeh Frezzo, Polytechnic Institute of NYU, Brooklyn, NY.

Rationally designed proteins are gradually becoming more commonplace. Proteins are incredibly varied and diverse in their chemistry, allowing the assembly of rationally designed proteins to be fine-tuned at a molecular level. Over the past decade, considerable efforts have been made to develop protein and peptide based self-assembled systems. The α-helix based coiled -coil proteins systems have been successfully engineered to develop structurally defined fibrils with potential application in nanoelectronics and biomedical field. The α-helical coiled-coil consists of two or more α-helices bound together by non-covalent interaction with a repetitive sequence of hydrophobic and polar residues designated as heptad repeat *abcdefg*. The two rationally designed peptides CC and Q54, derived from Cartilage Oligomeric Matrix Protein, were designed to self-assemble longitudinally based on sticky ends. To improve the thermal and chemical stability of proteins and assembly of fibers we replaced leucine from hydrophobic core with 5,5,5 -trifluroro-D-L-leucine (TFL) by residue incorporation. Circular dichroism results indicate that the proteins exhibit a strong α-helical structure in the presence of TFL. Fluorescence microscopy shows the formation of protein fibers in the presence of salt and the small molecule curcumin. The fibers seen in fluorescence microscopy were approximately 600 nm. Transmission electron microscopy (TEM) showed fibers that were 12.6 microns in length and 152.9 nm in width. The incorporation of TFL into alpha-helical proteins provides a larger insight into the mechanism behind the formation self-assembling nanofibers.

Behavioral Analysis of *Drosophila melanogaster* Speed Based on Generational Olfactory Perception. **Alina Zhyvotovska, Michelle Batchu, Mamuna Faizi, Alexander Braun and Kathleen Nolan, St. Francis College, Brooklyn Heights, NY.**

Drosophila melanogaster is a widely utilized model organism for many areas of research. Behavioral experiments were performed characterizing olfactory response of wild-type fruit fly larvae to a specific scent. Larvae were placed in petri dishes with the scent (cinnamon) placed in the center and the time required for them to reach the food was recorded. Cinnamon scents were used due to a previous study that identified cinnamon as a preferred scent among *Drosophila melanogaster* larvae. Larvae were separated into "slow" and "fast" categories based on the time it took them to reach the center from the edge. These were placed in separate "fast and "slow" fresh vials and hatched out adults were self-bred. The speed test was then performed on the F1, F2, F3 and F4 generations. In total, 43 trials were conducted using wild-type fruit fly larvae. There was no significant difference in speed among subsequent generations from the first generation of ether "slow" or 'fast" flies. This indicates that there may be a genetic component to speed in fruit flies. [1]

Latitudinal Gradient of Reproductive Investment in the Marine Snail *Nucella lapillus.* Halvor Adams and Aaren Freeman, Adelphi University, NY.

Nucella lapillus is a species of marine snail with a distribution from Long Island to Greenland/ Iceland, and across the rocky coast of Europe. They are found on exposed and sheltered shores throughout the intertidal zone, feed on barnacles and mussels, and are eaten by small fish and crabs. *N. lapillus* lay vase-shaped egg masses (about 10 mm x 3-4 mm) on rocks and under stones in the intertidal zone along the coast. The number of capsules laid varies with abiotic conditions and the female's size and nutritional state. The purpose of this experiment was to investigate the influence of latitudinal gradient on reproductive investment of *N. lapillus*. Egg masses and mature snails were collected over the summers of 2012 and 2013 from sites with different wave exposures ranging from Connecticut to southeastern Maine. The egg masses and mature snails were brought back to Adelphi along with additional *N. lapillus* population data collected from each site. Egg capsules were then photographed and the eggs removed and immediately photographed. Photographs of capsules and egg masses were measured using ImageJ software to compare the surface area between egg masses from populations of differing latitudes. I hypothesized that the egg capsules from regions of lower latitudes would be larger and would contain more embryos. Results are discussed in terms of energy expenditure and climatic influences.

"Meet the Expert" Student Outreach, An Integrative Learning Experience at Bergen Community College. B. D. Davis, M. Flannery, M. Lowe and J. Payne, Bergen Community College, Paramus, NJ

Integrative learning is a non-compartmentalized approach to learning that extends beyond traditional academic boundaries and is an essential learning outcome for college students. The goals of the "Meet the Expert" outreach series were to encourage students to integrate learning; apply skills to different situations and to see Microbiology and Anatomy & Physiology as related subjects. In the "Meet the Expert" outreach series Biology students met virtually with scientists and authors of scientific papers and interviewed the professionals remotely. Microbiology and Anatomy & Physiology Professors and students participated in the projects. In the first "Meet the Expert" series students discussed an interdisciplinary case study with a clinical microbiologist. Discussions with the clinical microbiologist provided students with a unique look at real life problems. The interviews were conducted using Skype for the first interview followed by an online webinar format in a second project. The "Meet the Expert Interviews" outreach project was created to enhance student understanding of topics in current scientific literature. In this project students interviewed authors of research papers remotely, thus integrating their learning via outreach to professionals and encouraging students to make connections with complex, real world problems presented in the literature. The projects were assessed by student surveys. Student evaluations of the "Meet the Expert" series were very positive and will be presented. The projects were engaging for students and faculty and provided a unique method of professional outreach for Biology students. The project is an innovative example of an integrative method to enhance student learning through interaction with professional scientists. We gratefully acknowledge the support of the BCC Departments of Biology and Horticulture, Media Technologies and CITL.

Retention of Basic Chemical and Cellular Concepts in Anatomy and Physiology. Maureen N. Gannon, Bronx Community College, Bronx, NY.

As in other disciplines, student retention of concepts learned in the introductory sequence of Anatomy & Physiology (A&P I) and their application in subsequent course, such as A&P II, often appears problematic. A pilot study to determine which concepts covered in A&P I, if any, were retained in A&P II was conducted. Questions were designed at both basic and higher levels of Bloom's taxonomy. Comparing pre- and post-test scores in A&P I demonstrated a significant increase in overall student performance. In A&P II, both pre- and post-test scores were not significantly different to post-test scores in A&P I, suggesting that what students learned in A&P I was, in fact, retained. However, overall scores in both A&P I & A&P II were poor. Individual question analysis suggested that some basic concepts were mastered and retained, while others were never learned. In addition, no significant changes in the students' ability to answer questions designed to be at a higher level of Bloom's taxonomy was observed. Overall the results suggest that students retain some basic concepts learned in A&P I, but they do not learn enough to demonstrate proficiency.

GLT-1 Trafficking in Alexander Disease Astrocytes, as Shown by Total Internal Reflection Fluorescence Microscopy. Rujin Tian[1], Kameka Deans[2] and Xiaoping Wu[3], [1]Bronx Community College, CUNY, NY, [2]Lehman College, CUNY and [3]Columbia University, NY.

Mutations in the gene for glial fibrillary acidic protien GFAP, which encodes the major intermediate filament protein of astrocytes, result in Alexander Disease (AxD), a fatal neurological disorder in which myelin and neurons are lost. The uptake of glutamate (Glu) via the major glutamate transporter (GLT-1) of astrocytes is important for controlling the extracellular concentrations of Glu, thus limiting Glu-mediated toxicity to other cell types. Previous work has defined a loss of GLT-1 in AxD and in mouse models of AxD effective Glu uptake requires a high density of GLT-1 transporters localized to the plasma membrane, but the direct visualization of GLT-1 trafficking in astrocytes has been a major challenge. Here, we describe an optical imaging approach, based on total internal reflection fluorescence, to examine the dynamic remodeling of RFP-GLT-1 fusion protein at the cell surface of live astrocytes on a timescale of minutes. Quantification of the density, size and morphogenesis of RFP-GLT-1 proteins in astrocytes expressing the R239C GFAP mutant revealed a significantly reduced number, size and motile redistribution of GLT-1 proteins compared to the wild type, particularly at transient, spine-like membrane protrusions of the R239C astrocytes. This suggests dysfunctional Glu transport may be due, in part, to a defective membrane organization of GLT-1. Our study provides the first structural insights into the intercellular mechanism underlying an astrocytic encephalopathy caused by a mutation in GFAP that compromises survival of their neighbors.

Some Ecological Observations of Old Growth Trees at 50 Home Sites in Montvale New Jersey. Richard Stalter[1], Katherine Archila[1], Kevin Argune[1], Adriana Largotto[1], Jasmine Molina[1], Grace Nesheiwal[1], Alberto Rameriz[1], Joseph Renda[1], Gillian Richardson[1], Stephanie Sfiroudis[1] and Michael O'Donovan[2], [1]St. John's University znd [2]Bergen County Community College.

The objective of the present study was to identify, map, determine tree dominance, and frequency of occurrence of trees and colonizing tree seedlings and saplings at 50 home sites at Powhatan Park, Montvale New Jersey. Powhatan Park (41.05, 74.05) includes Waverly, Forest and Westmoreland Avenues and was developed as a summer resort complete with bungalows and a club house in the 1920's. Whiteoak, (*Quercus alba)*, Red oak (*Quercus rubra*), and Black oak (*Quercus velutina*) were the most frequently encountered old growth trees. The three trees with the highest relative dominance were *Q. velutina*, *Q. alba* and *Q. rubra* with relative dominance values of 25.4, 18.9 and 17.4 respectively. Scarlet oak (*Q. coccinea*) and Black oak were the largest trees encountered in our survey both with trunk diameters of 49 inches. Twenty eight tree species have colonized the home sites mostly occupying property borders where they have escaped extirpation. White ash (*Fraxinus americana*), red oak (*Q. rubra*), white mulberry (*Morus alba*), and yellow poplar (*Liriodendron tulipifera* L.) were the most frequently encountered colonists, found at 42, 30, 28, and 28 percent of the home sites. Tree mapping, tree sampling, land use history, and anecdotal information from individual home owners regarding tree loss will be covered in our presentation. Most tree loss was due to selective cutting to prevent potential home damage due to tree fall. Hurricanes and wind microbursts were also cited by home owners for tree loss. Tree replacement in yards was primarily by non-native trees notably crab apple (*Pyrus baccata*) flowering cherry (*Prunus serrulata*), Japanese red maple (*Acer palmatum*) and native dogwood, (*Cornus florida* L.). Hedge borders were composed primarily by arborvitae (*Thuga occidentalis*), Canadian hemlock (*Tsuga canadensis*), and white pine (*Pinus strobus*).

An integrated network study. Wenwei Xiong and Chunguang Du, Montclair State University, Montclair, NJ.

Biological network inference has been a long-standing challenge in molecular and computational biology. It aims to reverse engineer the complex regulatory relationships among a group of interested genes or gene products, by applying computer models to gene or protein expression profiles, which are measured under different circumstances including genomic variation, gene mutation, perturbation and environmental stimulation. Recent advance in high-throughput sequencing technology such as microarray and RNA sequencing has brought unprecedented tremendous data, which requires further computational approaches to reveal biological meanings. Here we present an integrated network study to tackle this problem. First we create cross-referencing procedures for gene/protein expression profiles to exploit existing resources for gene annotation, transcription factor binding site, microRNA targets and well-studied metabolic pathways. When we applied it to microarray data from salt-treated *Populus euphratica* in two concentrations, a full-view of interactions related to plant hormone transduction was generated, clearly showing the interplay among up/down regulated genes, transcription factors, microRNA, and metabolites. To discover even new gene interactions, we have developed two model-based methods, based on Boolean logic dynamics and mutual information. Three basic Boolean operations AND, OR and NOT combined with genes as operands can model the relationship between target gene and its potential activators and inhibitors. Expression profiles in time series dictate the way to build up connections among genes. Meanwhile, in mutual information method, we calculate the conditional independence of gene pairs, remove those irrational connections, and construct networks with weight edges for confidence levels of prediction, based on information content. High-throughput RNA sequencing data and protein quantification data from four maize inbred lines were tested with the two models. Predicted networks help us focus on highly probable gene/protein candidates, and shed light on the regulatory mechanisms of interested genes.


Conference Highlights

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To provide investigative research support for undergraduate students working under the supervision of faculty who are current members of MACUB. Awards Applications will be evaluated and awards granted based on the scientific merit and overall quality of the proposed research experience.

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Application

On-line proposal requires:
Student contact information
Faculty advisor contact information
Faculty reference letter from the research advisor
This letter must include a statement of institutional support for the project
Proposal title
Proposal (maximum of 500 words)
The proposal should provide a brief background on the project with reference, a statement of the proposed question or hypothesis to be tested, and a description of the experimental approach.
References
Basic budget justification.
Include discipline. For example, molecular biology, cell biology, genetics, etc.
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