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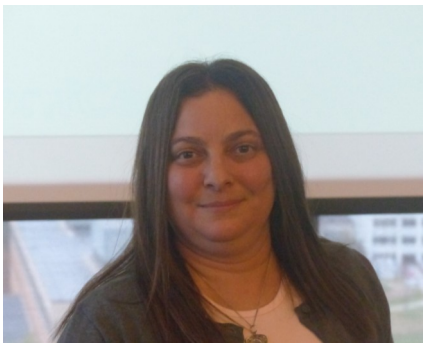

Instructions for Authors

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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The 2016 MACUB Conference will be at SUNY at Old Westbury
Oct. 29, 2016

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MACUB 2015 Conference

Poster Presentation Award Winners

COMMUNITY COLLEGE

Biochemistry, Biophysics and Biotechnology

First Place

Kervens Hector, Veronika Yakovishina, Tirandai Hemraj-Benny and Regina Sullivan
Cytotoxic and Cytostatic Effects of Single Walled Carbon Nanotubes on Triple Negative Breast Cancer Cells
Queensborough Community College of CUNY, Bayside, NY

Second Place

Chanele Rodriguez[1], Sharon Lall-Ramnarine[1], Suraj Shiman[2], James F. Wishart[2], Nicole Zmich[2] and Edward W. Castner, Jr.[3]
Synthesis of Pyrrolidinium Ionic Liquids
[1]Queensborough Community College, Bayside, NY; [2]Brookhaven National Laboratory, Upton, NY and [3]Rutgers University, Piscataway, NJ

Developmental Biology and Genetics

First Place (Tie)

Joey Costanzo and George Proteasa
Extract from Plantago Lanceolata has an Important Mucolytic Effect on the Respiratory Tract Mucus
Queensborough Community College, CUNY, New York, NY

Haseeb Shah and Nidhi Gadura
Determining the Genetic Pathways Involved in Cell Death of Copper Treated Saccharomyces cerevisiae
,Queensborough Community College, Bayside, NY

Second Place

Irene Sun[1], Elaine Lin[2], Yuanyuan Wu[2] and Andrew Van Nguyen[1]
Examining the Effect of Anti-Phospholipid Antibody on MicroRNA Regulation of Tissue Factor in Breast Cancer Tumor Progression
[1]Queensborough Community College CUNY, Bayside, NY and [2]Albert Einstein College of Medicine, Bronx, NY

Environmental Biology and Ecology

First Place

Grace Loussakou[1,2], Michael Llano[1,3], Lalitha Jayant[1] and Christine Priano[1]
Salinity Tolerance of a Marine Ciliate Co-Isolated with Eggs of the Sea Urchin Lytechinus variegatus
[1]Borough of Manhattan Community College, New York, NY; [2]Rutgers University, Camden, Camden, NJ and [3]The City College of New York, New York, NY

Second Place

Elhizeh Hydara and Catarina Mata
The Effect of Lead on the Growth of Phaseolus vulgaris (Beans)
Borough of Manhattan Community College, New York, NY

Microbiology and Immunology

First Place (Tie)

Karla M. Cerrato, Mary T. Ortiz and Loretta Brancaccio-Taras
The Effectiveness of Essential Oils as Possible Treatment for Upper Respiratory Tract Infections
Kingsborough Community College, Brooklyn, NY

Bharti Kumari and Nidhi Gadura
Comparison of Copper Surface Mediated Toxicity in Gram-Positive, Gram-Negative Bacteria and *Saccharomyces cerevisiae*
Queensborough Community College, Queens, NY

Second Place

Sherwayne Morrison, Patricia Schneider[1], Raji Subramaniam[1] and Olga Calderon[2]
Cellulolytic and Xylanolytic Bacteria Associated with Bark Beetles in Fallen Logs
[1]Queensborough Community College, Bayside, NY and [2]LaGuardia Community College, Long Island City, NY

Third Place

Wilson Nieves, Naydu Carmona, Peter Novick and Monica Trujillo
Elucidation of the Role of Rhomboid Proteins in Streptomyces
Queensborough Community College, Bayside NY

Physiology, Neuroscience and Clinical

First Place

Kimone Marrett[1], Danellie Semple[2], Edward J. Catapane[2] and Margaret A. Carroll[2]
Histamine Mediates the Response to Light in the Sensory Motor Integration of Gill Lateral Cell Cilia in the Bivalve Mollusc, Crassostrea virginica
[1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY

Second Place

Maria Villa and Susan McLaughlin
The PKD2 Activator Triptolide Stimulates Cnidocyte Discharge in Hydra
Queensborough Community College, Bayside, NY

MACUB 2015 Conference

Poster Presentation Award Winners

SENIOR COLLEGE

Biochemistry, Biophysics and Biotechnology

First Place

Zayna King[1], Kevin D. Walker[2] and Tyler Walter[2]
Stereochemical and Mechanistic Studies of a Tyrosine Aminomutase in Oryza sativa
[1]Medgar Evers College, Brooklyn, NY and [2]Michigan State University, East Lansing, MI

Second Place

Oluwadamilola Lawal[1,2], Christian Schenkelberg[2], Shounak Banerjee[2], Benjamin Walcott[2] and Christopher Bystroff[2]
Scoring Sequence for Modelled Folding Conformation in InteractiveROSETTA Using HMMSTR
[1]Medgar Evers College, Brooklyn, NY and [2] Rensselaer Polytechnic Institute, Troy, NY

Developmental Biology and Genetics

First Place

Imari Patel, Martin J. Hicks, Dennis G. Urbaniak and Diane E. Urbaniak
Genetic Delivery of a miRNA Cluster with Polycistronic siRNAs Reduces mRNA Expression of Epidermal Growth Factor Receptor in Human Glioblastoma Cells
Monmouth University, West Long Branch,, NJ

Second Place (Tie)

Kerianne Fuoco and Martin J. Hicks
Synthesis of Mini-Reporter Construct to Test Gene Transfer of RNA Therapeutics
Monmouth University, West Long Branch, NJ

Sarah Falotico[1], Peter Nekrasov[2], Nicole Sivetz[1] and Martin J. Hicks
Design of a Pre-Trans-Splicing Molecule to Generate a Soluble Extracellular Peptide Decoy to Block Activation of the EGFR Pathway in Human Glioblastoma Cells
[1]Monmouth University and [2]Biotechnology High School, West Long Branch, NY

Third Place (Tie)

Sachin Parikh and Martin J. Hicks
Design of a Gene Transfer Vector to Deliver a Stabilized Anti-EGFR RNA Aptamer to the Glioblastoma Microenvironment
Monmouth University, West Long Branch, NJ

Jermaine Wilson, Ligny Lugo and Chiyedza Small
Effects of Dietary Supplements on Blood Cell Tumors in Drosophila
Medgar Evers College, Brooklyn, NY

Madeleine Maas, Gabe Makar and Joost Monen
Investigating the Role of CPAR-1 in Cell division in the Nematode C. elegans
Ramapo College of New Jersey, Mahwah, NJ

Environmental Biology and Ecology

First Place

Rachelle Carino, Thomas J. Daniels, Richard Falco, Mark Green and James Ciaccio
The Efficacy of Catnip Oil as a Botanic Tick Repellant
St. Francis College and Fordham University Louis Calder Center Biological Field Station

Second Place

Sally Tarabey, Ruchit Patel, Robert Newby Jr., Jose L. Perez and Tin-Chun Chu
Molecular Approaches in Detecting Cyanobacteria and Their Toxins in Greenwood Lake
Seton Hall University, South Orange, NJ

Third Place

Kaylee Saltos[1], Naysha Angellucci[1], Allison M. Fitzgerald[1], Jon Miller[2] and Andrew Rella[2]
The Effects of Invertebrate Colonization on Water Flow Around Pier Pilings: Implications on Homeland Security
[1]New Jersey City University, Jersey City, NJ and
[2]Stevens Institute of Technology, Hoboken, NJ

Microbiology and Immunology

First Place (Tie)

Monique Salmon and Jill Callahan
The Effects of Salvadora persica (Miswak) on Biofilm Formation in Cariogenic Species Streptococcus mutans
Saint Peter's University, Jersey City, NJ

Richa Rana, Megha Rana, Shivani Rana, Priya Patel and Lee H. Lee
Study the Inhibitory Effects of EGCG, EGCE-S and PEGCG on Sporulation of Spore Forming Bacilli
Montclair State University, NJ

Second Place

Yasmeen Abboud, Emma Seidman and Lee H. Lee
Effect of Time and Temperature on EGCG and EGCG-S's Stability as Antimicrobial Agents
Montclair State University, NJ

Third Place

Mitchell I. Parker and Michael A. Palladino
Post-Transcriptional Control of Gene Expression by microRNAs Following Lipopolysaccharide-Induced Inflammation of Rat Testis
Monmouth University, West Long Branch, NJ

Physiology, Neuroscience and Clinical

First Place

Kehinde Cole, Chisom Ogbuagu, Edgar Tello and Reed C. Carroll
The Colocalization of CaMKIIα with GRIP and Inhibitory Synapses Using NMDA and Glutamate as a Stimulus to Mimic Brain Activity
New Jersey City University, Jersey City, NJ

Second Place

Alix Duarte, Christina Faltas, Jan Osea and Natalia Coleman
NMDA Receptors as a New Therapeutic Target for Cancer
New Jersey City University, Jersey City, NJ

Third Place

Margaret Massett, Mina Youssef, Jan Osea, Wayne Eby and Natalia Coleman
Mathematical Model of Cancer Cell Viability After Different Regimes of Treatment with Doxorubicin
New Jersey City University, Jersey City, NJ

MACUB 2015 Conference

Poster Presentation Award Winners

MASTERS/DOCTORIAL

Developmental Biology and Genetics

Mohammed Almish and Daniel S. Ginsburg
NuA4 Interaction with RNA Polymerase II is Stimulated by Phosphorylation of CTD Serines 2 and 5*
Long Island University Post, Brookville, NY

Biochemistry, Biophysics and Biotechnology

Joseph Bulatowicz, Dina Edani, Rossara Nunez and Carlos Molina
Lysine Knockouts of Inducible cAMP Early Repressor (ICER) are Strongly Localized to the Nucleus of Transfected PAC2 Zebrafish Fibroblasts
Montclair State University, Montclair, NJ

Environmental Biology and Ecology

Alessandra Rossi, Kevin Olsen and Meiyin S. Wu
A Phosphorus Sediment Storage Assessment of Lake Hopatcong (NJ)
Montclair State University, Montclair, NJ

Ruchit Patel, Robert Newby and Tin-Chun Chu
Flow Cytometric and Microscopic Analysis of Cyanobacteria and Their Toxins in Greenwood Lake
Seton Hall University, South Orange, NJ

Microbiology and Immunology

Robert Newby, Jr. and Tin-Chun Chu
Potential Zinc Stress Response Mechanisms in Synechococcus sp. IU 625
Seton Hall University, South Orange, NJ

Siti Ayuni Mohmaemed Yussof, Chris Chen, Amy Melok and Lee H Lee
Green Tea Polyphenols as Synergistic Agents to Enhance Antibiotic Erythromycin Activity on Bacteria
Montclair State University, NJ

Christopher Chen, Siti Ayuni Mohamed Yussof, Amy Melok, Yasmeen Abboud and Lee H. Lee
Targeting Orthopedic Infections Using Tea Polyphenols
Montclair State University, Montclair, NJ


Conference Highlights


Conference Highlights

Effect of Time and Temperature on EGCG and EGCG-S's Stability as Antimicrobial Agents. **Yasmeen Abboud, Emma Seidman and Lee H. Lee, Montclair State University, NJ.**

EGCG is a water-soluble green tea polyphenol that is derived from the plant *Camellia sinensis* and EGCG-S is a modified lipophilic green tea polyphenol. Both polyphenols are potent antioxidants, which possess chemo preventive, anti-apoptotic, anti-inflammatory activities, and most recently, anti-microbial properties. Stability tests have been conducted in order to formulate these green tea derivatives into therapeutic preparations. In this study, stock solutions (2mg/ml) of EGCG and EGCG-S were prepared and stored at 4°C, 25°C and 37° C for durations of 2 hours, 5 days, 2 weeks and 4 weeks, consecutively. At every time point, EGCG and EGCG-S were added to the bacterial culture *Streptococcus mutans* at a final concentration of 200 μg/ml and treated for 1 hour. In order to evaluate the effect of time and temperature on the antimicrobial activity of these polyphenols, three methods were used. The turbidity study of the culture was monitored at OD 650 after 1 hour and 24 hours of treatment. The viable count was determined by the quantification of colony forming units (CFU). Cell death was assessed by using live/dead bacterial staining kits in combination with fluorescence microscopy. The results indicated that incubation for 2 hours at all the temperatures did not affect EGCG and EGCG-S's antimicrobial activity. EGCG-S incubated for longer periods (5 days, 1 week and 2 weeks) at 25°C and 37°C, yielded results similar to the control. However, EGCG exposed to the same conditions was determined unstable, the antimicrobial activity was significantly reduced. The results suggested that modified EGCG-S is structurally and functionally more stable, and as a result a better molecule to be used as a potential therapeutic agent to combat bacterial infection.

Determination of Whether Oysters in the Tappan Zee Area of New York are from a Long Island Oyster Farm. Precious I. Aduware, Craig S. Hinkley and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.

The eastern oyster, *Crassostrea virginica*, was abundant in bays along the east coast of the United States. As a result of overharvesting and habitat destruction, oysters have disappeared in these bays including Jamaica Bay (JB) in New York. Our goal is to determine which oysters are best to repopulate JB. We previously showed that oysters from Frank M. Flower & Sons (Flower's) oyster farm could survive and reproduce in JB and might be a good choice for repopulating the bay. Genetic analysis of these oysters revealed a "G" polymorphism in the cytochrome-c-oxidase I (COXI) gene that is a good marker for oysters from Flower's farm. Oysters from the Tappen Zee (TZ) area of New York are another possible source of oysters for repopulating the bay. By comparing the genetic diversity between the oysters from the TZ area and the Flower's farm, we can determine their genetic relationship. My hypothesis is that the oysters from the TZ area will not have the "G" polymorphism found in oysters from Flower's farm. I tested my hypothesis by extracting DNA of oysters from the TZ area. The polymerase chain reaction was used to amplify a 700-bp region of the COXI gene. Gel electrophoresis was performed to make sure the DNA was the correct size before sending it to ELIM Biopharmaceuticals for sequencing. BLAST searches were used to make sure each sequence was from the COXI gene. Alignment of the sequences of the TZ oysters showed they all had an "A" polymorphism compared to the oysters from the farm which had a "G" polymorphism. These results support my hypothesis and suggest that the oysters from the TZ area are not from Flower's farm. In the future, we would like to test whether oysters from the TZ area are able to survive and reproduce in JB.

Lipophilic Green Tea Polyphenol, EGCG-S, as a Potential Anti-Endospore Agent in Food and Milk. Bushra Ali, Hassan Tahir and Lee H. Lee, Montclair State University, NJ.

Like many gram positive bacteria, Bacilli possess the ability to form endospores when placed under unfavorable environmental conditions. Thus, they pose high concern when found in various environments such as the food and medical industries. Due to supportive and promising results from a preliminary study, green tea polyphenols have shown to work in inhibiting the germination of *Bacillus cereus* endospores. Therefore, the first goal of this experiment was to test what minimal treatment time was necessary to result in a 95%-100% rate of inhibition. *B. cereus* endospores were first harvested over a ten-day period, purified and boiled at 100°C for 20 minutes, and treated with two types of lipophilic green tea polyphenols: LTP and EGCG-S at 1% and 5% concentrations for 5-, 10 -, 15-, and 30-minutes. Non-boiled and boiled cells without treatment were designated as controls. Three repeats were set up; each sample was serially diluted, plated onto nutrient agar plates, and subsequently incubated at 37°C for 24 hours. The colony forming unit and the percent of inhibition were then determined. The average inhibition rate for the 15-minute treatment time was 98.7% for 1% LTP, 99.6% for 1% EGCG-S, 99.9% for 5% LTP and 100% for 5% EGCG-S. The second goal

of this experiment was to test the effect of the lipophilic green tea polyphenol in food and milk. *B. cereus* is one of the most prevalent bacterial species found in contaminating food and beverages. That is why it is important to analyze whether or not EGCG-S can inhibit the bacteria and endospores in the food and milk. Overall, these results suggest that LTP and EGCG-S play a significant role in inhibiting endospore germination best at a 5% concentration and at a 15-minute minimal treatment time.

The Effects of Garlic, Turmeric and Lemon Marinades on Growth Inhibition of *Salmonella enteritidis* on Chicken Breast and Chicken Skin. Gabriella Ali and Kathleen Bobbitt, Wagner College, Staten Island, NY.

Bacterial enteric pathogens are a major cause of foodborne disease. Animals raised for consumption such as chickens are a major reservoir for these pathogens, such as *Salmonella enteritidis*. There has been an increased interest in using natural antibacterial substances to inhibit the growth of these pathogens and minimize foodborne illness. Garlic, turmeric and lemon are known to have antimicrobial properties. This study was conducted to test the antimicrobial effects of garlic, turmeric and lemon extracts when applied as a marinade to chicken fillets and chicken skin on growth inhibition of *Salmonella enteritidis*. Prepared plant extracts were added to chicken breast fillets and chicken skin both singly and in combination. The fillets and skin were then incubated at 4°C. Cell counts were made at 1, 24 and 48 hours. Lemon juice was found to be the most effective against *Salmonella enteritidis* on chicken breast and skin within 1 hour of incubation. Furthermore, turmeric and a combination of lemon and turmeric inhibited growth within 24 hours of incubation of chicken meat. Moreover, a combination of lemon and turmeric in addition to, a combination of garlic, turmeric and lemon inhibited growth within 1 hour of incubation on chicken skin. After, 24 hours all growth was inhibited on chicken skin except those marinated in garlic. This study shows that lemon and turmeric extracts when applied singly and in combination to chicken meat and skin as well as, a combination of garlic, turmeric and lemon when applied to chicken skin extracts have bactericidal effects when used as marinade on chicken meat and skin. The data suggests that these plant extracts can be used as marinades to eliminate *Salmonella* and foodborne illness associated with poultry.

NuA4 Interaction with RNA Polymerase II is Stimulated by Phosphorylation of CTD Serines 2 and 5. Mohammed Almish and Daniel S. Ginsburg. LIU Post, Brookville, NY.

Transcription of protein-coding genes is carried out by RNA polymerase II (Pol II). Pol II is made up of 12 subunits, the largest of which (Rpb1) has a long C-terminal domain (CTD). The CTD in yeast is composed of 26 repeats of the heptapeptide $Y_1S_2P_3T_4S_5P_6S_7$. Post-translational modification of the CTD is important for recruiting protein complexes involved in transcription and RNA processing to gene bodies. We investigated the importance of serine 2 and serine 5 phosphorylation (Ser2p/Ser5p) for interaction between the CTD and the lysine acetyltransferase (KAT) complex NuA4. NuA4 is the only essential KAT in yeast and has been shown to be important for both transcription initiation and elongation. We have previously proposed that NuA4 occupancy in gene bodies is stimulated by interaction with the CTD phosphorylated on serine 5, but were not able to observe binding to Ser5p peptides *in vitro*. In this study, we examined NuA4 binding to Pol II and chromatin in mutants affecting the CTD kinases Kin28, Bur1, and Ctk1. Kin28 phosphorylates serines 5 and 7, while Bur1 and Ctk1 phosphorylate serine 2. We found that NuA4 interaction with both Pol II and chromatin as measured by coimmunoprecipitation was reduced in *kin28* mutant cells. Consistent with this, NuA4 occupancy at the ADH1 3' ORF was also reduced in *kin28* cells. Interestingly, loss of Ser2p in either *bur2Δ* (the cyclin for Bur1) or *ctk1Δ* led to reduced NuA4 binding to Pol II as well as decreased occupancy across *GAL1*. These results provide the first evidence that NuA4 may be able to bind both the Ser2p and Ser5p forms of the Pol II CTD.

Testing the Succession of Marine Invertebrates on Various Settlement Plates. Naysha Angelucci, Kaylee Santos, Christian Bojorquez, Na'Vonna Turner and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

The focus of this study is based on the biofouling communities on piers, and how they impact infrastructure. As sessile organisms settle onto permanent structures, their community will change over time which may impact the underwater infrastructure and the surrounding aquatic ecosystem. The succession (change in community over time) of the community may vary with the type of substrate material used. It was hypothesized there will be a change of species and abundance, based on varying habitat parameters such as salinity, temperature, and light. To study the succession of the settlement plates we used fiberglass, ecological concrete, wood and shell settlement plates. A subsample of each type was removed from the water biweekly for 10 weeks. Image analysis software (Image J) was used to calculate percent coverage of sessile organisms, and mobile organisms were identified to the lowest possible taxon using field guides and dissecting microscopes. Our results show there were less species, but higher abundances after 2 weeks. Over time, the amount of species increased and key species abundances increased as well. The most abundant organisms were amphipods and barnacles, native to the site.

World's Most Valuable Living Fossils: Density of Horseshoe Crab Eggs (*Limulus polyphemus*) on an Undisturbed Spawning Habitat on Plumb Beach, Brooklyn New York. Kelvin Arhire-Thomas and Christina Colon, Kingsborough Community College, Brooklyn, NY.

Horseshoe crabs (*Limulus polyphemus*) are a prehistoric marine invertebrate that creep ashore in the spring to spawn on sandy beaches during the full moon and high tides. It plays an essential role in protecting human lives by insuring the safety of agricultural and medical products. The goal of this research was to continue surveying eggs on a critical spawning beach which has been heavily impacted by storms and restored by the Army Corps of Engineers. Plumb beach is an important beach because it's the most suitable habitat in New York for the Atlantic Horseshoe crabs to spawn. It was hypothesized that the number of spawning crabs would continue a trend of decline, observed in 3 of the past 4 years. Surveys were done based on spawning peaks after which sand samples which were collected with the aid of GPS and landmarks to relocate six quadrats along the beach. Results showed that the number of eggs found in 2015 was close to twice the number from 2014 on the eastern side of the beach while on the western restored side of the beach, zero eggs were found in 2015, despite a count of 342 eggs found in 2014. Results show that the Horseshoe crab population is recovering, although the western side of the beach has declined despite re-nourishment of that area. While egg counts are up, there were zero juveniles or hatchlings found on either side of the beach, which could be due to observed variability in grain size, maybe due to SuperStorm Sandy. A mixture of larger and finer grains is suitable for spawning crabs and egg development, but smaller grain size is optimal for small juveniles. If this proves to be the cause, it may be necessary to further modify the beach to ensure survival of the next generation.

Identification and Characterization of Endogenous Plasmids from Marine Bacteria Isolated from the Sea Urchin *Lytechinus varieagatus.* Drew Ballard, Cristian Acevedo, Jing ran Chen, Christine Priano and Lalitha Jayant, Borough of Manhattan Community College, New York, NY.

Bacterial flora that coexist on the surface and test of the sea urchin Lytechinus variegatus were screened for the presence of cryptic plasmids. Several bacterial strains were isolated from the test, spines, mouth, and gonads of fifteen different urchins by gently swabbing these regions with a sterile tip and plating them onto marine agar plates. Strains were also isolated from the water samples in which the urchins arrived. Gram staining of more than sixty isolated bacteria revealed that all were gram negative rods. Isolated bacteria were tested for the presence of plasmids using a Bio Rad Aurum plasmid mini kit. Results indicated that at least two out of the sixty bacterial samples contained plasmid DNA. One of these bacterial isolates DU9 was taken from a spine that had been shed from an urchin. A red area at the base of the spine was used for the initial streaking. The second bacterial isolate WU12 was obtained from the water sample in which the urchin was shipped. Both bacteria test negative for lactose fermentation and show resistance to specific antibiotics. Plasmids isolated from both bacteria are small, about 2.0 to 3.0 kb in size. Bacteria WU12 shows presence of at least three plasmids. These plasmids were isolated from the agarose gel using Qiagen gel extraction kit. Restriction mapping and DNA sequence analysis will be performed to characterize and identify unique elements of the isolated plasmids. Bacteria hosting these plasmids will be classified using biochemical tests and 16S rRNA sequencing. The biological role of the plasmids in the bacteria, and the symbiotic relationship between the bacteria and the urchins will be examined by genome mapping and biochemical testing.

The Fight Against Food Waste: Is Food Recovery a Sustainable Option? Deborah Balthazar[1], Jamie Harding[2], Roni Neff[2], Carrie Fisher[2], Caitlin Fisher[2] and Amanda Buczynski[2]. [1]Caldwell University, Caldwell, NJ, [2]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD.

Food waste is a significant problem in the United States, at the same time there are many Americans who experience food insecurity and hunger. Food recovery – the process of reclaiming good food that would otherwise be wasted and redirecting it to people in need – may be a way to reduce both food waste and food insecurity. Through primary research and interviews (e. g., email and phone) a qualitative approach was taken to holistically catalogue the many different organizations (farms, food businesses, universities and communities) who take part in furthering food recovery throughout the state of Maryland. Although a statewide plan was developed to curb the amount of food and other waste throughout Maryland, it is not enforced or tracked, nor did it expressly include food recovery. Most of the food recovery was taking place in central Maryland, specifically in Montgomery County and Baltimore City. The results reflect only a small portion of the food recovery movement in Maryland, due to research conducted during a limited amount of time. Although it was found that there is a sense of urgency to curb food waste, not everyone is tracking the impact regarding the reduction of food waste or food recovery. This research was funded by Caldwell University through the Diversity Summer Internship Program at Johns Hopkins Bloomberg School of Public Health.

Regulation of Nicotinic Acetylcholine Receptors (nAChR) Expression and Localization by the Actin Cytoskeleton. Mike Berrios, Jennifer Morillo, Hilda Manson and Juan Brusés, Mercy College, Dobbs Ferry, NY.

Nicotinic acetylcholine receptors (nAChR) are ligand-gated ion channels that mediate excitatory cholinergic transmission in the central and peripheral nervous systems. Neuronal nAChRs are comprised of five homologous subunits forming homo (α subunits) or hetero (α and β subunits) pentamers. All nAChR subunits have similar structures comprised of an N-terminal extracellular domain containing the acetylcholine binding site, four transmembrane domains (TM1 - 4), a large cytosolic loop between TM3 and TM4, and a short extracellular C-terminal tail. nAChRs participate in a variety of physiological functions including cognition, autonomic regulation, and neuromuscular coupling. nAChR function is affected in various human conditions including Alzheimer's disease, depression, epilepsy, drug addiction, and myasthenia. Efficient cholinergic transmission relays on the expression and localization of nAChR at particular sites of the cell surface, which is regulated by cell membrane composition, protein sequence motifs, and the actin cytoskeleton. However, the mechanisms regulating the localization of nAChRs in distinct domains of the cell membrane are not completely understood. The goal of this study is to examine whether the actin cytoskeleton and actin-myosin contractility regulates the expression levels and localization of α3β4 nAChRs on the cell membrane. Heterologous expression α3β4 nAChR C-terminally fused to a myc tag epitope in CACO2A and Madin-Darby Canis Kidney (MDCK) epithelial cells is used to examine nAChR expression levels by immunofluorescence and confocal microscopy. By exposing stably transfected MDCK cells expressing myc-tagged α3β4 nAChR to chemicals that disrupt actin dynamics, we aim at determining the role of filamentous actin (F-actin) in nAChR expression and localization on the cell surface.

The Chick Embryo Astrocyte-Neuron CoCulture Model Is an Ideal Tool for Studying Astrocytic Neuroprotection. Christina Boetang, Samie Jules, Esther Yoon and Renée E. Haskew-Layton Mercy College, Dobbs Ferry, NY.

Astrocytes, a glial cell type in the central nervous system, play a critical role in maintaining neuronal survival and astrocyte-neuron cocultures provide an ideal model to study astrocyte-neuron interactions. In addition to supplying vital growth factors and energy substrates, astrocytes provide antioxidant support to neurons in the form of precursors of the antioxidant molecule glutathione (GSH). The brain, which consumes 20% of the body's oxygen, is highly vulnerable to the effects of reactive oxygen species (ROS): oxygen containing molecules (e.g. superoxide, hydrogen peroxide, and the hydroxyl radical) that readily remove electrons from nucleophilic molecules. Although ROS have numerous physiological roles in the brain – such as the facilitation of neuronal communication – accumulation of ROS during aging and in neurodegenerative conditions (e.g. Parkinson's disease, Alzheimer's disease, Huntington's disease) leads to neuronal death. Therefore, understanding the specific mechanisms by which astrocytes protect neurons from oxidative stress is of paramount importance in developing novel neuroprotective therapeutics. One such potential therapeutic avenue is the inhibition of protein tyrosine phosphatases (PTP) in astrocytes which, based on our previous data, leads to the robust protection of neurons from oxidative stress. Our long-term goal is to identify the specific PTP and PTP-downstream target involved in this astrocytic neuroprotective response. Our current candidate PTP is PTEN – as such we hypothesize that PTEN and its downstream target Akt promote astrocyte-dependent neuroprotection. To study the potential involvement of PTEN and its target Akt, we subcloned the Akt gene downstream of the astrocyte-specific promoter GFAP. To study astrocytic neuroprotection, we are optimizing an astrocyte-neuron coculture model derived from E8 chick embryo optic tectum brain region. Future plans are to express Akt specifically in the chick astrocytes followed by induction of oxidative stress in the coculture induced via glutathione depletion.

How Does Cultivating Oyster Reefs Revive Invertebrate Diversity In The Bronx River? Christian Bojorquez, Naysha Angelucci, Kaylee Saltos, Navonna Turner and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

The Hudson Raritan Estuary was previously home to an abundance of oysters. However, due to unsustainable harvesting and mistreatment of aquatic ecosystems, they are now considered 'ecologically extinct' in the estuary. Efforts have been made to help the wild oyster population flourish, including creating artificial reefs as a place for wild oysters to settle. By studying the differences in invertebrate diversity of the oyster reefs and sediment found in the Bronx River, we can gain a better understanding of how oyster reefs affect other invertebrates. We hypothesized that the artificial oyster reefs would be home to a far more diverse ecosystem of invertebrates when compared to the sediment bottom of the Bronx River. Each month, nine sediment cores were collected and taken back to the lab for analyzation. In addition, nine net passes were collected from the sediment site and three net passes were collected from oyster reef for comparison. Also, 3 baskets from the artificial oyster reef were collected, sorted through, measured, and analyzed. Once the baskets were sorted through and analyzed, 20 oysters were collected to perform conditioning index and the rest were returned to the reef. Over the course of three months, we found that the artificial oyster reef was host to a more diverse and larger population of invertebrates.

Is Rolling Behavior in the Isopod *Armadillidium vulgare* Influenced by the Presence of a Predator? Emily Brodkin[1], Christina Campana[2] and Scott L. Kight[3], [1]Tufts University, Medford, MA, [2]University of Delaware, Newark, DE and [3]Montclair State University, Montclair, NJ.

Terrestrial isopods, *Armadillidium vulgare* (Isopoda: Oniscidea), can position the body into a seamless, protective ball through a process called conglobation. This behavior is thought to function in defense from predators, but may also minimize desiccation in arid conditions. We examined the conglobation response of *Armadillidium vulgare* in the absence versus the presence of an arachnid predator. In order to test the behaviors, we manipulated the isopods in two different trials by gently stimulating the subjects with a pencil eraser- first, in the absence of a predatory spider, and second, in the presence of a predator. We then recorded the presence or absence of the conglobation reaction. We observed that the isopods were significantly more likely to exhibit rolling behavior in the presence of a predator than they were in the absence of a predator. We then rejected the null hypothesis that there is no difference in rolling behavior of *Armadillidium vulgare* between the presence and absence of a predator. These results demonstrate that *Armadillidium vulgare* are able to detect the presence of a predator in their environment and to initiate a defense mechanism of rolling up into a defensive ball.

Lysine Knockouts of Inducible cAMP Early Repressor (ICER) are Strongly Localized to the Nucleus of Transfected PAC2 Zebrafish Fibroblasts. Joseph Bulatowicz, Dina Edani, Rossara Nunez and Carlos Molina, Montclair State University, Montclair, NJ.

Inducible cAMP Early Repressor (ICER) is a transcriptional repressor that regulates the expression of cAMP inducible genes. ICER has recently garnered attention because of cAMP's implication in oncogensis. ICER is shown to be downregulated in melanomas by the means of the ubiquitin-proteasome pathway. It is marked for degradation on its lysine residues. By rescuing ICER levels in cancer cells, it is hypothesized that it may be possible to reverse the adverse progression of tumor growth. One possible way of rescuing ICER is by making it unavailable for ubiquitination by altering its ubiquitination sites. Special mutant ICERs that have their lysines mutated may offer the answer. However, in order for these ICERs to function properly they need to be localized in the nucleus. Through immunocytochemistry, cell fractionation, and Western blot analysis of PAC2 Zebrafish fibroblast lysine knockout mutants, we were able to show strong nuclear subcellular localization of our mutant ICERs. This positive step could potentially open the door to further study on ICER as a melanoma treatment.

Capturing Full Length Candidate Genes by *Helitrons.* Nico Carbone, Kaitlyn Socha, Wenwei Xiong and Chunguang Du, Montclair State University, Montclair, NJ.

Helitrons transposable elements have been reported in numerous species of plants and animals. *Helitrons* are unique from other types of transposable elements because they have the capability to capture gene fragments and carry them throughout the genome. However they are difficult to identify because they lack the classic characteristics found in other types of transposable elements. Many characteristics of *Helitrons* are still unknown due to their relatively recent discovery and the difficulty of locating and identifying them within genomes. It has been documented that *Helitrons* can capture pseudo genes and partial gene fragments within their structures, and these fragments can be highly varied. We are looking for a correlation between full length genes and *Helitron* sequences. We annotated sequences that have been found to be *Helitrons* by HelitronScanner software. This was done predominantly with the aid of Phytozome's genome browser. The process by which it was done was to check the region of the genome where there is a potential *Helitron*. Any full length genes in the area are then recorded. The areas before and after the gene are also noted and recorded, as it is important that these spaces are either unannotated or characterized on the genome browser as a *Helitron* sequence. If anything else is in this space, it is unlikely that the region has a *Helitron* sequence.

The Efficacy of Catnip Oil as a Botanic Tick Repellent. Rachelle Cariño[1], Thomas J. Daniels[2], Richard Falco[2], Mark Green[2] and James Ciaccio[2]. [1]St. Francis College, Brooklyn, NY and [2]Fordham University, Louis Calder Center Biological Field Station, Armonk, NY.

The blacklegged tick, *Ixodes scapularis*, is a vector for many tick-borne diseases and applying repellents can prevent the spread of these pathogens. Three different catnip oils: Catnip oil C, Berjé and MG, were evaluated based on how effective they repel the *I. scapularis* nymph. Horizontal assays were conducted in a plastic petri dish where a filter paper, which contained two sides: treated with catnip oil, and untreated with no catnip oil. On top of the filter paper was an O-ring and the assay was conducted over a grid. A series of concentrations were tested and the main ones that were focused on were: 100 µL, 200 µL, 300 µL, and 1000 µL. A total of five nymphs were used per assay and three assays were conducted per concentration. Each assay lasted for a total of twenty minutes. To quantify tick movement over time photos would be taken every two minutes. For catnip oil C, Berjé and MG, there were significant differences in the mean number of ticks on both the treated and untreated sides at 100 µL-1000 µL. A series of comparisons were conducted between the concentrations of Catnip oil C, Berjé, MG, and DEET. There were no significant differences among the four concentrations. A final comparison between the three catnip oils and DEET indicated that there was no significant difference between DEET and catnip oil as an effective repellent at six to twenty minutes.

The Effectiveness of Essential Oils as Possible Treatment for Upper Respiratory Tract Infections. Karla M. Cerrato, Mary T. Ortiz and Loretta Brancaccio -Taras, Kingsborough Community College, Brooklyn, NY.

Herbal remedies are common practice throughout the world, but widespread use of these treatments has been limited. With bacterial drug resistance, new antibacterial agents are needed. This study compared the effectiveness of essential oils to traditional agents in killing bacteria that cause upper respiratory tract infections (URTI). The hypothesis was: essential oils would be as effective as the antibiotics prescribed to treat URTI. The procedure was a standard agar diffusion assay using brain heart infusion agar plates inoculated with *Corynebacterium pseudodiptheriticum*, *Staphylococcus aureus*, *Staphylococcus epider*midis, and Streptococcus mutans. Disks of colloidal silver and oils (castor, eucalyptus, sandalwood, mineral, oregano, diluted oregano, tea tree (TTO)), and sensi-disks of clindamycin (CC), doxycycline (D), and vancomycin (Va) were placed on the inoculated plates. After incubation (24hr, 37o C), zones of inhibition were measured (mm). Mean zone sizes and standard error of the mean (X+SEM) for 10-13 trials were calculated. Zones sizes between test agents and antibiotics were compared using the Mann-Whitney U-test (p=.05). For *S. mutans* oregano oil was statistically more effective than all 3 antibiotics; the oregano oil mean zone was 47.71± 2.10mm versus zones of D (37.58±1.06mm), CC (40.71±1.34mm) and Va (20.57±0.61mm). TTO (18.78 ± 0.98mm) was equally effective as Va (20.57 ± 0.61mm). For *S. epidermidis*, oregano oil (37.75±1.55mm) was statistically better than D (10.66 ± 0.30mm), CC (32.50 ± 0.77 mm) and Va (15.25 ± 0.37mm). TTO (17.66 ± 1.70mm) was more effective than D (10.66 ± 0.30mm); TTO is equally as effective as Va (15.25 ± 0.37mm). For *S. aureus*, oregano oil (29.76 ± 0.42mm) was equally effective as D (27.23 ± 0.16mm) and CC (26.23 ± 0.10mm). For *C. pseudodiphtheriticum*, TTO (25.54 ± 3.47mm) was as effective as Va (19.25 ± 0.44mm). Oregano oil (55 ± 2.98mm) was significantly better than D (34.09 ± 1.56), CC (34.66 ± 1.05) and Va (19.25 ± 0.44mm). The hypothesis is accepted for TTO and oregano oil. Oil combinations will next be tested. Grant support: NIH Bridges #2R25GM06200313, NYSDOE CSTEP #0537151091.

The Use of the Macaulay Library of Natural Sounds to Supplement Labs and Field Studies. Kwun Chan, Afia Azaah, Kristy Biolsi, Allen Burdowski and Kathleen A. Nolan, St. Francis College, Brooklyn, NY.

Our students have been playing recordings from the Macaulay Library of Cornell University of natural sounds and videos (http:macaulaylibrary.org) while simultaneously recording with the sound recording program Audacity. In this way they can analyze number of vocalizations per a certain time period, the range of frequency of the sounds, as well as other parameters. This data has been used for compare/contrast scenarios in their own live recordings of vocalizations of sea lions from zoos and aquaria. The students have been able to hear recordings of animals (including sea lions) from places such as New Zealand and the Galapagos that are currently inaccessible to them in person.

Targeting Orthopedic Infections Using Tea Polyphenols. Christopher Chen, Siti Ayuni Mohamed Yussof, Amy Melok, Yasmeen Abboud and Lee H. Lee, Montclair State University, Montclair, NJ.

Orthopedic infections can be detrimental for patient's rehabilitation process. Such infections may require further surgical repair which increases the risk of complication due to higher exposure to anesthetics, an increase risk of blood loss, and other surgical complications. Approximately 77% of all medical device infections in orthopedic surgeries are due to common opportunistic pathogens such as *Staphylococcus aureus, Staphylococcus epidermidis,* and *Pseudomonas aeruginosa.* A distinctive property that makes these pathogens difficult to treat is its ability to form biofilm. Biofilm allows bacteria to become more resilient under stressful conditions. It increases cell-to-cell communication, adhesion, and virulence factors between cells. Our study looks to overcome this problem by using green tea polyphenols from *Camellia sinensis* to analyze the antimicrobial and anti-biofilm properties. Crude lipophilic tea polyphenol (LTP) and epigallocatechin gallate -sterate (EGCG-S) were examined to understand their potential effects on causes to infections. Qualitative and quantitative studies of the polyphenols at different concentrations range from 100 ug/ml to 250 ug/ml on *Staphylococcus aureus, Staphylococcus epidermidis,* and *Pseudomonas aeruginosa* were used. We looked to determine if microbial population density, cell morphology, biofilm production and cell viability were effected by our treatments. Crystal violet assay showed dosed dependent results from EGCG-S and LTP in biofilm reduction properties after treatment. Colony forming unit count revealed significant reduction in population density after exposure to various concentrations of polyphenols. Live and dead microscopic observation revealed significant reduction in cell viability with exposure to polyphenols. Cell morphology was also altered after the treatment through scanning electron microscopy observation. The overall study shows potential for a novel surgical solution to prevent acute infections and potential usage in therapeutic agents to eradicate biofilm accumulation that leads to chronic infections.

Electricity Generation Using Microbial Communities from New Jersey Soils. Tina Choe, Margarita Kulko, Ryan Kim, Therande Jashari, Isabella Canal Delgado and Luis Jimenez, Bergen Community College, Paramus, NJ.

Microbial fuel cells (MFCs) are bioelectrical devices that harness the natural metabolism of microbes to produce electrical power. Within the MFC, microbes munch up the sugars and other nutrients in their surrounding environment and release a portion of the energy contained within that food in the form of electricity. Once the electron has been transferred to the anode; it then travels to the cathode, where it reacts with an oxygen molecule and a proton, a byproduct of electrogenic metabolism, to form water. Thus electrical current is generated, from which one can extract power by simply placing a load (such as an LED light) between the two electrodes. Samples from soils were used to generate a mud suspension. The suspensions were used to inoculate MudWatt™ cells with the Anode buried with the mud, while the Cathode rested on top. Electricity generation and bacterial numbers were measured using an app downloaded into an iPhone 6. The best MFC generated a maximum of 73 microwatts with 1.52×10^7 electrogenic microorganisms. MFC incubated at 37ºC generated faster and more electricity than MFC incubated at 25ºC. MFCs provided a clean and environmentally friendly generation of electrical power.

The Colocalization of CaMKIIα with GRIP and Inhibitory Synapses Using NMDA and Glutamate as a Stimulus to Mimic Brain Activity. Kehinde Cole, Chisom Ogbuagu, Edgar Tello, Reed C. Carroll, New Jersey City University, Jersey City, NJ.

As we experience events throughout our lives, our brain responds and is modified in a long-term manner. Synaptic plasticity represents the ability of our brain to respond to stimuli in the world around us by altering the strength of the connections between neurons. One form of synaptic plasticity seen in inhibitory synapses involves Ca2+ /calmodulin protein kinase IIα (CaMKIIα). With increased activity in neurons, CaMKIIα redistributes to inhibitory synapses and increases the strength of signaling at those sites. The signaling pathways and conditions necessary to allow CaMKIIα to modulate inhibitory synapses remain poorly understood. Here, we examine the effects of two stimuli on the levels of calcium in cortical neurons and their effects on the localization of CaMKIIα in those cells. Immunocytochemical analysis of cortical neurons isolated from rat brains demonstrated that stimuli coupled to moderate, but not high elevations in calcium levels caused an increase in the colocalization of CaMKIIα at inhibitory synapses. Additional experiments examined the colocalization of CaMKIIα and Glutamate Receptor Interacting Protein (GRIP), a possible CaMKIIα interacting protein found at inhibitory synapses. Moderate calcium elevations strongly increased the colocalization of CaMKIIα and GRIP. Results suggest that in cortical neurons, stimuli coupled to moderate, but not large calcium elevations induce CaMKIIα to move to inhibitory synapses and possibly interact with GRIP. As studies have shown, various disorders are the result of imbalance between excitation and inhibition in the brain. Understanding regulation of inhibitory synapses can aid in providing insight into possible therapies for the treatment of diseases associated with altered inhibition. This work was supported by National Science Foundation Louis Stokes Alliance for Minority Participation in Science (LSAMP) grant #NSF-0902132 and US Department of Education Title V HSI-STEM grant #P031C110067. We also thank Charles Ta for his contributions to the calcium imaging experiments.

Molecular and Phylogenic Analysis of the Long Distance Developmental Signaling Gene *FT* (FLOWERING LOCUS T). Kevin Colon and Terry L. Kamps, New Jersey City University, Jersey City, NJ.

Prior to transitioning to mature flowering and fruiting, citrus tree development proceeds through a juvenile period lasting up to 10 years. The small globular protein encoded by orthologs of the Arabidopsis Flowering Locus T (*FT*) gene, have been shown to have a vital role in initiating floral transition. This graft transmissible protein delivers the signal to produce flowers when it is transported from phloem companion cells in leaves to shoot apical meristems to trigger expression of homeotic genes. The *FT* gene is one member of a family of genes including *TSF*, *TFL*, and *BFT* affecting flowering induction in response to environmental cues. BLAST results from querying the assembled *Citrus sinensis* genome revealed four regions of significant sequence similarity to a genomic *ciFT3* clone which clustered on chromosome 6. Two of these regions contain poor quality sequence as indicted by long lengths of N sequence, whereas another region appears to contain only partial sequence of an *FT*-like gene. This research investigation will improve sequence quality of four *FT*-like sequence containing regions of citrus chromosome 6 and clarify the copy number of *FT* related genes in citrus. This study is also investigating the effects of ectopic expression of three distinct genomic clones from *C. sinensis* using tobacco as a model system. The combined information from the assembled genome and our new sequencing results are expected to ascertain whether our current three genomic clones (*ciFT1*, *ciFT2*, and *ciFT3*) are one, two, or three distinct genes in citrus. Using the information of the assembled *C. sinensis* genome, the additional citrus sequenced genomes, and BLAST data obtained from querying these genomes, and new sequencing data, we expect to answer questions about evolution of the *FT* ortholog and its paralogs in citrus.

Extract from *Plantago Lanceolata* has an Important Mucolytic Effect on the Respiratory Tract Mucus. Joey Costanzo and George Proteasa, Queensborough Community College, CUNY, New York, NY.

Mucous is typically produced from cells found in mucous glands. This mucus serves to protect epithelial cells (the lining of the ducts) in the respiratory, gastrointestinal, urogenital, visual, and auditory systems of the human body. A major function of mucus is to protect against pathogens such as fungi, bacteria and viruses. The average human body produces about two pints of mucus per day. In the human respiratory system, mucus aids in the protection of the lungs by trapping foreign particles that enter it, in particular, through the nose, during normal breathing. This explains why coughing often occurs in those who smoke filtered cigarettes or have respiratory diseases. The body's natural reaction to inflammation and infection is to increase mucus production as in chronic bronchitis or in COPD (Chronic Obstructive Pulmonary Disease).Increased mucus production in the respiratory tract is also a symptom of many common illnesses, such as the common cold and influenza. In the case of a viral infection such as cold or flu, the first stage and also the last stage of the infection cause the increase production of mucus in the respiratory tract. As the body begins to react to the virus, mucus thickens and may turn yellow or green. Cystic fibrosis is an inherited disease that affects the entire body, but symptoms begin mostly in the lungs with extremely viscous (thick) production of mucus that is difficult to expel. Our research focuses on the use of an extract from *Plantago Lanceolata* to fluidify the thick mucus secreted during respiratory inflammatory diseases.

Effects of Nano-Selenium on the Growth and Antioxidant Activity of *Nasturtium Officinale*. Ariel Crawford and Tetyana Delaney. St. Joseph's College, Brooklyn, NY.

Selenium is a nonmetal that is widely considered as a trace element for human and animal nutrition. One of its benefits includes being a component of antioxidant enzymes that combat the reactive oxygen species in humans. Plants tend to be one of the carriers of selenium. However, there are barely any studies that focus on nano-selenium's effect on plants. This study used *Nasturtium officinale* (Watercress) to analyze whether selenium can be a possible fertilizer for plants, and to examine the effects of selenium on its morphology, chlorophyll content, and antioxidant activity. *Nasturtium officinale* sprouts were grown under four different Selenium treatments: 0g (control), 0.500g, 0.750g, and 1g. For results, the stems of the sprouts were measured to observe differences in their morphology. Later, changes in chlorophyll content were determined by chloroplast isolation. Its antioxidant activity was tested by introducing 2,2-diphenyl-1-picrylhydrazyl (DPPH), a free radical, to the leaf extracts. There were hardly any changes in stem length, for the stems were around 3 cm. As the selenium concentration increased, chlorophyll concentration in *Nasturtium officinale* increased as well. Finally, its DPPH activity decreased as antioxidant activity of the plant increased. Thus, we demonstrated that the antioxidant activity of *Nasturtium officinale* could be stimulated by introducing selenium nanoparticles as fertilizer.

Induction of Chondrogenesis in Mesenchymal Cells Isolated from Limb Buds of Early Chicken Embryos. Amanda Cripriana, Conor Gallagher Jacinta Marshall, Matt Murphy, Alysia Pemberton, and Anthony Tolvo. Molloy College, Rockville Centre, NY.

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 for use in future studies. We report the ability of chick mesenchymal cells to undergo chondrogenic 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 chondrogenic induction. Cells were initially plated in 100 mm dishes (experimental and control) at 1 x 10^6 cells/ml in α-MEM with 10% FBS, high glucose and 1% antibiotic-antimycotic solution. For differentiation, cells were trypsinized and centrifuged, then suspended in α-MEM medium containing 50 μg/ml L-ascorbic acid-2-phosphate and 40 μg/ml proline at 10^7 cells/ml. 25 μl aliquots of cells were taken for micro mass cultures. Control cells were cultured in α-MEM without inducers. Both control and experimental cells were cultured for at least 14 additional days. After removing the medium, cells were fixed with 4% paraformaldehyde and stained for the presence of cartilage mucopolysaccharides with Alcian Blue stain. The cells were photographed using bright field phase 1 microscopy. Results showed that treatment of the mesenchymal cells with the induction medium caused a dramatic increase in the deposition of cartilage matrix in the induced cells over controls. The results indicate that chick embryonic limb bud mesenchymal cells can undergo differentiation into chondrogenic cells at this stage of embryonic development and validate the avian embryonic model for such differentiation studies. Future studies include using immunohistochemical techniques to check for specific collagen type deposition and calcified cartilage development.

Does Social Context Influence Positional, Feeding and Aggressive Behavior in Turkestan Cockroach Nymphs, *Blatta lateralis*? Peter Cruz and Scott L. Kight, Montclair State University, Montclair, NJ.

The invasive Turkestan cockroach, *Blatta lateralis*, is presently undergoing range expansion across the southern United States, and appears to be displacing other species of cockroaches. We examined the interactive behavior between *B. lateralis* nymphs and American cockroach nymphs, *Periplaneta americana*, to investigate potential competition between the two species. Turkestan cockroach nymphs were examined in choice chambers under three social conditions: isolation, presence of a conspecific nymph, or presence of a *P. americana* nymph. We found that *B. lateralis* nymphs were significantly more likely to move throughout the chamber in the presence of the other species. There was also a trend for *B. lateralis* to spend more time in the center of the chamber (near a food source) in the presence of a conspecific nymph. Turkestan cockroach nymphs were also statistically less likely to feed when isolated than when in the presence of another cockroach, regardless of species. Although there were no statistical differences in aggressive behavior between treatments, we interpret the heightened activity in opposite-species trials as avoidance behavior that potentially minimized aggressive encounters. Indeed, *P. americana* nymphs defended places where food was located. We discuss apparent ecological competition between invasive populations of Turkestan roaches and other cockroach species. This work was supported by the LSAMP program at Montclair State University.

HEXIM1 Mediates Changes in Expression of miRNA 143 and the PI3 Kinase Pathway in Prostate Cancer Cells. A Novel Mechanism of Metastasis. Deodate Davis,Yuvraj Singh and Manya Mascareno, SUNY, College at Old Westbury, Old Westbury, NY.

Previous studies have shown that Hexim-1 plays an important role in prostate cancer plasticity and progression. The TGF-β pathway associated with epithelial-mesenchymal transition has been linked to Hexim-1 protein expression levels in prostate cancer models. The aim of our research was to study the effects that reduced Hexim-1 expression would have in the progression of prostate cancer in vivo using two transgenic adenocarcinoma of the mouse prostate (TRAMP) derived cell lines, a wild type and a Hexim-1 heterozygous (HT) TRAMP cell line that expresses reduced levels of Hexim-1 protein. Wound healing assays were performed as in vitro models of cell migration. We investigated the changes in the expression of miR143 during the prostate cancer progression. We also studied the effect of Hexim-1 levels on the signaling by the AKT pathway. Our studies indicate that Hexim regulates the expression of miRNA143 and phosphorylation of AKT during the wound healing process. Acknowledgements: National Cancer Institute at the National Institutes of Health Award # R15CA169984.

Antibacterial and Anti-Herpes Simplex Virus Activity of Black Tea Polyphenols. Aline de Oliveira, Gabriella Appice and Tin-Chun Chu, Seton Hall University, South Orange, NJ.

Black tea originates from the leaves of *Camellia Sinensis* plant and contains large amounts of theaflavin polyphenols, in particular theaflavin (TF1), theaflavin-3-monogallate (TF2A), theaflavin-3′-monogallate (TF2B), and theaflavin-3,3′-digallate (TF3). In this study, the anti-Herpes Simplex Virus (HSV) effect of purified black tea theaflavins was investigated in both A549 and Vero cells. Results indicated that all three theaflavins are effective in inhibiting HSV in both cell lines, with TF3 being the most efficient. Flow cytometric assay, fluorescence microscopy and real-time PCR demonstrated that a concentration of 50 μM TF3 and above was sufficient to inhibit >99% of herpes simplex virions. The antibacterial effect of theaflavins was assessed using microplate bioassay. Serial concentrations of theaflavins (1.0, 2.5, 5.0, and 10.0 mg/ml) were used in order to determine the minimum inhibitory concentration (MIC) in three gram-negative and three gram-positive bacteria. Black tea theaflavins showed antibacterial activity against all bacteria tested in this study and the MIC was of 2.5 mg/ml for most bacteria. The results indicated that black tea polyphenols may serve as a promising natural alternative for current antibacterial and anti-HSV medications.

Inhibition of C-SRC Activity in Primary Bone Marrow Cells Mimics the Decreased Expression of the Osteoblast Phenotype Seen in Tumor Cells. Ashley Dinkel, Joseph Tarr, Dana Branch, Joshua Luster and Thomas Owen. Ramapo College of New Jersey, Mahwah, NJ.

Deletion of the c-src gene results in decreased osteoclast and increased osteoblast activity. PP2 is a c-src inhibitor and PP3 is a structurally similar inactive compound. To further investigate the mechanisms through which c-src inhibition drives differentiation, we tested PP2 and PP3 on ROS 17/2.8 osteosarcoma cells. C -src inhibition by PP2 beginning at plating decreased alkaline phosphatase (AP) activity at days 4 and 8. In order to address whether this unexpected observation was due to the tumor-derived nature of ROS cells, primary rat bone marrow cells (BMC) were also tested. BMCs were treated with a single dose of PP2 or PP3 at plating or at the first or second media change or the compounds were added beginning at plating or at the first or second media change and continuing until harvest. BMCs were stained for AP activity and mineralized nodules on day 25 and showed that treatment with PP2 resulted in less differentiation. A single dose of PP2 at plating resulted in a 50-70% decrease in AP positive and mineralized nodule area, whereas a single dose of PP2 at days 3 or 7 had no effect as compared to PP3-treated cells. With continuous treatment, a similar decrease was seen when cells were dosed beginning at plating or day 3, however, if dosing was initiated at day 7, a smaller decrease of ~25% in AP activity was seen. These data suggest that c-src is

involved in the commitment of BMCs to becoming osteoblasts as well as in their initial differentiation. This work was supported in part by a grant from the Ramapo College Foundation. The authors would also like to acknowledge the support of the School of Theoretical and Applied Science and the TAS Research Honors program at Ramapo College.

Beating of Gill Lateral Cell Cilia of *Crassostrea virginica* Involves Neuronal Innervation and the Presence of Gap Junctions. Nicole Dobey[1], Reniece Buchanan[2], Dane Frank[3], Margaret A. Carroll[2] and Edward J. Catapane[2], [1]Kingsborough Community College, Brooklyn, NY, [2]Medgar Evers College, Brooklyn, NY, and [3]Behavioral Instruments, Hillsborough, NJ.

Suspension feeding bivalves use ciliary pumps driven by gill lateral cell (LC) cilia, producing water currents for feeding, respiration and waste elimination. LC in *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervation via the branchial nerve. The cellular mechanism regulating LC cilia is not fully explained. Second messengers are involved. It is not known if each LC is individually innervated. LC have gap junctions (GJ) and questions arise if GJ are involved in controlling coordination or rate of beating. We hypothesize GJ are involved in cellular mechanisms regulating LC cilia beating rate and/or coordination. We studied this with immunohistological preparations using antibodies to visualize GP, and the Sihler Whole Mount method to visualize nerves in gill filaments. We also used preparations in which filaments were divided into proximal and distal sections by petroleum jelly barriers, which prevented drug diffusion from side to side. We stimulated the branchial nerve entering proximal ends with suction electrodes, which releases serotonin increasing beating rates. We used stroboscopic microscopy to measure beating rates. Drugs were applied to distal ends and beating rates of both ends compared. Procaine, a local anesthetic, prevented stimulations from increasing rates at distal ends, showing nerve impulse propagation is necessary for ciliary response. Similarly, we tested 3 GJ blockers each with different mechanisms of action: lindane, diphenylborinic anhydride and mefloquine. Mefloquine did not affect beating. Lindane and diphenylborinic anhydride produced statistically significant reductions in beating. Lindane was stronger, causing dose -dependent (10^{-7} – 10^{-4}M) blockage of beating. Diphenylborinic anhydride only blocked at 10^{-4}M. Results show neuronal innervation to filaments along with functioning GJ are necessary to increase cilia beating rates. Disrupting either one interfered with normal responses. Lindane is reported to reduce GJ permeability and increase intracellular Ca^{2+} levels; either one or both of these actions may be responsible for the results we obtained.

NMDA Receptors as a New Therapeutic Target for Cancer. Alix Duarte, Christina Faltas, Jan Osea, and Natalia Coleman, NJCU, Jersey City, NJ.

Despite intensive research efforts and promising discoveries, cancer remains the leading cause of death in the US. There is growing evidence of the importance of glutamate signal transduction in cancer. N-methyl-D-aspartic (NMDA) receptors are one of the three glutamate receptors found in the mammalian central nervous system. While it is common knowledge that NMDA receptors are essential for spatial learning and memory, little is known about its function in cancer. We previously showed that human prostate, breast and lung cancer cells express NMDA receptors. The aim of the current study is to evaluate the NMDA receptor antagonists memantine and MK-801 as potential targets for cancer treatment. The cancer cells growth inhibition was determined by using a 3 -(4,5-dimeththylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. Our results suggest that NMDA receptors show anti-proliferative effects in some cancers. We would like to thank the National Science Foundation Louis Stokes Alliance for Minority Participation in Science (LSAMP) grant #NSF-0902132 and US Department of Education Title V HSI-STEM grant #P031C110067 for funding this research.

The Neurotoxic Effects of Manganese on Dopamine Post-Synaptic Receptors are Reversed By p-Aminosalicylic Acid (PAS). Loren Dubose, Kurt Loney-Walsh, Edward J. Catapane and Margaret A. Carroll, Medgar Evers College, Brooklyn, NY.

Manganese, a neurotoxin causing the human disease Manganism, disrupts dopamine neurotransmission in brain. The neurotoxic mechanism of action is not resolved. There is no effective clinical treatment. Literature reports postulate manganese toxicity is related to dysfunction of post-synaptic dopamine receptors (D2DR) rather than degeneration of dopamine neurons. Our previous work showed gill lateral cells (GLC) of *Crassostrea virginica* are innervated by cilio-inhibitory dopamine fibers and have D2DR post-synaptic receptors. We found manganese treatments blocked cilio-inhibitory effects of dopamine on GLC and treatments with manganese in the presence of p-aminosalicylic acid (PAS) prevented toxicity. Our immunofluorescence work with 1° antibodies against D2DR and FITC-linked 2° antibodies showed treatments with manganese reduced fluorescent intensity in GLC, suggesting manganese caused a loss of D2DR number or disrupted their structural integrity. We hypothesize PAS would reverse neurotoxic effects of manganese on D2DR when applied after manganese. To test this we treated *C. virginia* for 3 days with manganese (500 μM) followed by 5 days with PAS (500 μM). Gills were excised, fixed, exposed to 1° antibodies against D2DR, FITC-linked 2° antibodies, embedded, sectioned and visualized on a fluorescence microscope. Fluorescence intensity was quantified using ImageJ software from NSF. Results

showed fluorescence intensity in animals treated with manganese had statistically significant progressive decreases in fluorescence compared to controls. Animals treated with PAS after manganese or PAS alone did not show reduced fluorescence, indicating PAS reversed manganese induced loss of post-synaptic D2DR fluorescence. This immunohistological study shows positive correlation between losses of D2DR fluorescence in manganese treated animals vs controls. It also shows PAS reversed toxic effects of manganese on D2DR after 3 days of manganese treatments. The actions of PAS are likely due to chelation. Results suggest manganese chelating agents like PAS that can penetrate human blood -brain barrier might be effective therapeutic agents for Manganism.

The Efficacy of LifeStraw® Water Filters in Filtering *Enterococci* from Various Water Samples. William Echavarria[1], Mauricio Gonzalez[2], Nazish Nawaz[1] and Kathleen Nolan[1], [1]St. Francis College, Brooklyn, NY and [2]New York Harbor School, Governors Island, NY.

Enterococci, contained in normal human fecal flora, can be dangerous to humans if ingested in large quantities. LifeStraw® water filters (by Vestergaard) have been shown to filter water that might be contaminated with *Enterococci* and other bacteria. In this study, samples of undiluted marine and fresh water were filtered using a LifeStraw® water filter in an attempt to test the efficacy of these filters.. Tap water was used as a negative control. Test samples included brackish water from the Brooklyn Bridge Park (East River) and a fresh water sample from the Spuyten Duyvil Pond in the Bronx. Unfiltered samples tested positive with an Enterolert® detection kit. Samples filtered through the LifeStraw® water filter yielded the same results as the negative control, as did water from an aquarium containing zebrafish. Therefore, we have shown that LifeStraw® water filters are an efficacious way to filter water contaminated with *Enterococci*. Next steps include testing additional water samples from various locations with the LifeStraw®.

Design of a Pre-*Trans*-Splicing Molecule to Generate a Soluble Extracellular Peptide Decoy to Block Activation of the EGFR Pathway in Human Glioblastoma Cells. Sarah Falotico[1], Peter Nekrasov[2], Nicole Sivetz[1] and Martin J. Hicks, [1]Monmouth University and [2]Biotechnology High School, West Long Branch, NY.

Glioblastoma multiforme (GBM) is the most common central nervous system malignancy. The current standard of care allows patients to survive approximately 14 months. In addition, systemic therapies targeting the brain tumor are limited by the blood-brain barrier. Tyrosine kinase receptors (TKRs), such as epidermal growth factor receptor (EGFR), are often overexpressed in GBM and drive cell proliferation. The beginning of the EGFR pre-mRNA transcript corresponds to the extracellular domain of the EGFR protein, followed by the sequence coding for the transmembrane domain. In the strategy presented, we have designed a pre-*trans*-splicing molecule (PTM) with a poly-adenylation (poly-A) signal engineered to splice into the portion of the EGFR pre-mRNA transcript corresponding to the extracellular region. This shortened transcript with a poly-A tail would translate into a soluble extracellular peptide decoy and inhibit activation of the EGFR pathway. The PTM was engineered with a target pre-mRNA transcript binding domain, intronic region, 3' splice site (3'SS), coding region, and poly-A signal. Potential target regions of the pre-mRNA transcript were ranked according to splice site strength, presence of splicing motifs, and intronic length in order to design the optimal binding region to block the natural 3'SS. Crucial for recognition of the PTM by the spliceosome, a strong 3'SS and an intronic region devoid of competing splicing elements were designed. Distinct elements of known poly-A signals were characterized, and the simian vacuolating virus 40 late poly-A signal was selected for the design of this PTM due to its high efficiency *in vivo*. In addition, the mouse U7 snRNA with SmOpt was added to the 5' end due to its stabilizing structure and localization signal in order to retain the PTM in the spliceosome of the nucleus.

Lead Toxicity in the Blood Brain Barrier. Christina Faltas, Alix Duarte, Jan Osea and Natalia Coleman, New Jersey City University, Jersey City, NJ.

The blood-brain barrier (BBB) protects the brain from harm by controlling the influx and efflux of transport. Breakdown of the barrier can result in neuroinflammation and neurodegeneration. While it is common knowledge that lead and other heavy metals cause neurological toxicity, little is known about how these elements influence BBB viability and integrity. Here, we study the effects of Pb on BBB survival and function using Madin-Darby canine kidney (MDCK) cells. MDCK cells display morphological, enzymatic and antigenic cell markers that are commonly found in cerebral endothelial cells and are widely used to mimic the BBB. To assess cell viability, we detected the number of metabolically active cells using the MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay. Our results have shown dose-dependent MDCK cell deterioration. This work was supported by LSAMP-NSF grant.

A Quest for a Custom-Made Mesenchymal Stem Cell in the Treatment of Inflammatory Diseases. Natalie Fernandez, Caroline Winters, Maria Barandica, Abi Ocava, Michael Delsignore, Kristina Coppola and Jodi Evans, Molloy College, Rockville Centre, NY.

Mesenchymal stem cells (MSC) are multipotent cells that can differentiate into adipocytes, osteoblasts and chondrocytes. These cells are widely studied in tissue regeneration and for their therapeutic effects in inflammatory disease. MSC interact with cells of the innate and adaptive immunity to promote or suppress the inflammatory response. MSC from the bone marrow (D1 MSC) decrease inflammatory responses by lowering macrophage (Mϕ) secretion of soluble factors such as nitric oxide (NO), interleukin-12 (IL-12) and tumor necrosis factor--α (TNF-α). Aorta-derived MSC (mAo MSC) support the macrophage inflammatory response by contributing to NO secretion and enhancing secretion of TNF-α by Mϕ. Previous studies have isolated and enriched MSC populations using one or two specific cell surface markers and subsequently tested their functional properties in the regulation of immune cells. In this study we took a different approach. Using two populations of MSC with opposing immune regulatory function, we examined differences in their MSC-associated gene expression using PCR array. We sought to identify sets of MSC-associated genes that correlate with either suppression or support of the Mϕ inflammatory response. Our results revealed that the mAo MSC express genes that potentiate chondrogenic differentiation, while the D1 MSC express genes that potentiate adipogenic and osteogenic differentiation. Our unique approach identified MSC populations that have greater propensity to develop into osteogenic and adipogenic lineages are immunosuppressive, while those with greater propensity to develop into chondrocytes are immuno-supportive. We have identified lineage potential as a way to select MSC populations for use in cell-based therapies of inflammatory disease.

A Study of Marine Biology in the New York/New Jersey Harbor Estuary: A Multi-Pronged Approach. D'Angelo Fletcher[1], William Echavarria[1], Nazish Nawaz[1], Mauricio Gonzalez[2], and Kathleen A. Nolan[1], [1]St. Francis College, Brooklyn, NY, and [2]Harbor School, Governor's Island, NY.

Water quality sampling, seining, and restoration ecology are three of the ways that we have been studying and analyzing various waters of the New York/New Jersey Harbor estuary (Hudson and East Rivers, Fire Island, Fort Tilden, and Orchard Beach). Water has been tested for various parameters, including pH, salinity, dissolved oxygen (DO), nitrates, phosphates, and others. These water samples were compared and contrasted with water collected from places such as Maine and Vermont. We seined with school groups in the East and Hudson Rivers. We assisted with a restoration project that is currently underway at the esplanade on the East River near 125th street in New York City, and are helping draft an environmental impact statement for this project. We participated in New York State Department of Environmental Conservation projects such as The Great Fish Count (in which texting pictures for ID to exports was incorporated for the first time) and a Day in the Life of the Hudson River in an effort to contribute to a monitoring of the estuary databases. In preparation for the latter event, we participated in an invertebrate identification workshop at the Great Kills National Park in Staten Island. This holistic approach of sampling mixed with education should enhance our motivation to learn and discern more about the New York/New Jersey Harbor Estuary and other waterways.

Using Next Generation Sequencing Technology to Elucidate the Microorganism Diversity in Different Water Sites in Brooklyn. Fabiola Fontaine[1], Jeremy Seto[1] and Davida S. Smyth[1,2], [1]New York City College of Technology, Brooklyn, NY and [2]Mercy College, Dobbs Ferry, NY.

There is much interest in examining the effects of human activities on water sites in urban areas. Many studies have utilized classical microbiology techniques to examine the abundance of microbes in the water. More recently, next generation sequencing has been used to examine prevalence of microbes in a variety of sites and has led to great insights. Our project is examining three sites in Brooklyn, one with little human activity, Greenwood Cemetery and two with extensive human activity, Newtown Creek and the Gowanus canal. To date, examination of the three sites in Brooklyn, Green-Wood Cemetery has been performed using 16S rRNA sequencing. Within each site multiple samples were taken. Visual surveys of the biodiversity were done as well as taking into account the location of human activities such as sewage outflows. The flora and fauna were assessed. Water samples were filtered through 0.2um and 0.45 um filters and the DNA extracted. Extracted DNA was sent to a company for PCR amplification and DNA sequencing. The results have been analyzed using QIIME, STAMP and PiCRUST. Significant differences in the samples from the sites were observed both from site to site and from season to season. Several notable organisms were identified that could be used as potential makers for the health of the water bodies. Our future work will examine samples from the remaining seasons. We hope that our project will generate data that could be used to develop non-culture based methods of testing water quality.

Testing the Efficacy of Two RNAi Strategies in *C. elegans*. JJ Fritsch and Matthew Von Bargen, Ramapo College of New Jersey, Mahwah, NJ.

RNA-mediated interference (RNAi) is a process by which RNA molecules inhibit gene expression via specific degradation of mRNA transcripts. Since its discovery nearly 20 years ago, researchers have utilized this understanding to specifically knock-down genes of interest. In the nematode *C. elegans,* several RNAi techniques have been developed, including injection of double stranded RNA (dsRNA) and feeding of bacteria expressing dsRNA. In this study, we will test both approaches to knock-down an essential mitotic protein HCP-3, and assess the effectiveness of both strategies for use in future studies. Knock-down effectiveness will be measured by western blot analysis and immunofluorescence, and the phenotypic consequences will be assayed by live-imaging of cell division in mCherry:Histone-H2B & GFP:□-tubulin transgenic worms. Currently, we have synthesized the dsRNA and have begun to establish an effective injection and feeding protocol, which will be subsequently used to rigorously test the efficacy of both approaches.

Synthesis of Mini-Reporter Construct to Test Gene Transfer of RNA Therapeutics. Kerianne Fuoco and Martin J. Hicks, Monmouth University, West Long Branch, NJ.

Glioblastoma multiforme (GBM), a grade IV tumor of the central nervous system, is the most common malignant primary brain tumor in adults. Individuals diagnosed with GBM have a poor life expectancy of approximately 12 months. The poor survival rate is due to a lack of efficacy in current therapies, including chemotherapy and radiation, which are limited by the blood-brain barrier. We are creating novel strategies to bypass these barriers by developing gene transfer vectors to deliver the genetic sequences of RNA therapy molecules to alter the splicing pattern and expression of tyrosine kinase receptors (TKR), creating soluble TKR decoys. In this approach, we expect to modify GBM and CNS cells to deliver the therapeutic anti-cancer molecule into the local milieu. To test this approach, we are creating an *in vivo* tissue culture model. We have designed mini-reporter gene constructs that contain the targeted regulatory elements, including the 5' and 3' splices sites as well as the intronic region of interest of the TKR, vascular endothelial growth factor receptor 2, VEGFR2 (KDR). This mini-reporter construct will test the efficacy of RNA anti-sense therapeutics to block the pre-mRNA splicing event leading to intron retention and alternative polyadenylation signal recognition. Using fluorophores as visual markers, eukaryotic green fluorescent protein (eGFP) will be used to detect the natural exon splicing product, whereas the monomeric red fluorescent protein, mCherry will detect RNA anti-sense mediated intron retention. In this manner, the mini-reporter construct provides a quick and visually measurable test to optimize RNA anti-sense therapies against VEGFR2. In addition to VEGFR2, we will use this mini-reporter design to test the efficacy of RNA therapies directed toward alternative TKRs known to be upregulated in cancer.

Analysis of Sea Lion and Fur Seal Vocalizations Using Audacity and the Macaulay Sound Library. Joanna Garcia, Nilufer Demirkan, Ashley Treharne, Jacchione Volpe, Valerie Rodriguez, Kristy Biolsi, Allen Burdowski and Kathleen Nolan, St. Francis College, Brooklyn, NY.

St. Francis College students have been visiting local zoos and aquaria for the past two years and recording and analyzing vocalization of California sea lions. We decided to supplement and expand our work by recording vocalizations in the Cornell University Macaulay Sound Library, and analyzing those with the free-downloadable program Audacity. In this way we have recorded sea lions that we would not normally have access to, such as South American and Galapagos sea lions and Antipodean, Northern, and Antarctic fur seals, in addition to California sea lions. Patterns in the vocalizations, such as seasonal, sexual, age cohort and evidence of bonding differences have been noted, and comparisons of vocalizations of animals found in the wild have been made with animals in captivity. Sea lions produce a variety of vocalizations and sounds such as growls, barks, a braying type sound and large expulsion of breath sounds. Each sound produces a unique spectrogram with Audacity. The number of vocalizations per a set time, duration of vocalization, and maximum and minimum frequencies have been recorded. We would like to continue with additional recordings of marine mammals from the Macaulay Sound Library and their analysis.

***In situ* Identification of Proteins Using Micro-proteomic Approaches and Top-down Approach. Kendra Getaw[1], Vivian Delcourt[2], Julien Franck[2], Isabelle Fournier[2], Michel Salzet[2] and Fernando Nieto[1], [1]Suny Old Westbury, Old Westbury, NY and [2]University of Science and Technology of Lille1, Lille, France.**

Early detection of cancer improves substantially patient outcome. Discovery of early detection markers on biopsy samples is critical. Proteomics coupled to Matrix Assisted Laser Desorption/Ionization Time of Flight (MALDI-TOF) can be applied to the detection of small size protein markers for cancer. Larger proteins found in the sample can obscure the detection of small size protein markers. Development of an extraction method that enhances detection of small size proteins is germane to the early detection of cancer. The purpose of this study was to determine the most efficient extraction method for the detection of small size proteins. Two different tissue sources were used, frozen rat brains and rat brain that had

been sliced and parafilm embedded. In both instances the tissues were homogenized using 50 mM DTT and 1% SDS and diluted to different concentrations. The proteins were extracted, filtered, and then washed extensively before they were tested using MALDI-TOF coupled to proteomics. It is found that improving the wash method after the extraction of proteins contributes to the improvement of proteins detection. This improvement was accomplished by the addition of 20% Acetonitrile to multiple washes. Though using a larger sample size improves protein detection, it is possible to detect proteins from a smaller area of the brain sample. This experiment shows that it is possible to detect small molecular weight proteins from both fresh and parafilm embedded tissues using various top-down proteomics and micro-proteomic approaches. These results may lead to many potential applications in various research areas from immunology and infectious diseases, to cancer research (this project was funded by a NIMHD-MHIRT grant, MD001429).

Are Hand-Sanitizing Stations Reservoirs of Microbial Contamination? Tricia Griffith[1], Marie Joseph[1], Cheryl Meddles-Torres[2] and James A. Timbilla[1]. [1]Queensborough Community College, CUNY, Bayside, NY and [2]Stony Brook University, Stony Brook, NY.

A study was conducted at the campus of Queensborough Community College, Bayside, N.Y. in 2013 and 2014 to determine whether hand-sanitizing stations could be a source of microbial contamination. Samples were collected from hand-sanitizing stations in 10 campus buildings. Aseptic techniques were used to collect samples, which were streaked onto Tryptic Soy Agar plates divided into four quadrants. The samples were incubated at 37^{o}C and observed after 48 hours for microbial growth. Samples from eight of the 10 buildings showed microbial growth in the first trial and samples from nine of the 10 buildings showed microbial growth in the second trial. On a 0-4.0 point scale the degree of microbial growth ranged from 0.3-2.0 in the first trial and 1.0-2.7 in the second trial. Two of the 10 sampled buildings showed higher microbial growth than the other buildings. Our analyses of the results found no correlation between the observed degree of microbial growth and whether or not the containers at the hand-sanitizing stations were full or empty. The present study though preliminary shows that hand-sanitizing stations can be a source of microorganisms that may cause infection.

Assessing the Role of Adhesion-GPCRs in Visual System Axon Guidance. Christopher Guevara, Joanna Garcia, Joseph Pagnotta and Alison Dell. St. Francis College, Brooklyn, NY.

How do axons form the correct connections during development? Using the zebrafish retinotectal projection as a model system, we previously showed that G-protein coupled receptor (GPCR) signaling is required for axon guidance during normal development. Retinal ganglion cell (RGC) axons that express a dominant negative G-protein subunit GaS fail to cross the midline and misproject to the ipsilateral tectum. GaS promotes expression of the axon guidance receptors Nrp1a and Nrp1b, helping retinal axons cross the midline, likely via cAMP-dependent signaling. This suggests a mechanism by which advancing growth cones can respond to local signals that upregulate cAMP and thereby ready themselves for the next guidance cue they encounter. However which GPCRs and ligands contribute to this process is still unknown. We hypothesize that adhesion GPCRs (ADGRs) direct growing axons. To test our hypothesis, we first looked for candidate receptors. We assessed the expression pattern of ADGR family members by analysis of GEO datasets and the literature, and designed probes for in situ hybridization. We focused on CELSR3 as our first candidate, due to its expression pattern. CELSR3 is a member of the adhesion-GPCR family with a characteristic a long n-terminal tail decorated with adhesion motifs including EGF-, leucine-rich, and cadherin repeats as well as Ig domains. In the zebrafish retina, CELSR3 is expressed in amacrine cells as well as RGCs. CELSR3 mutants fail to carry out a visually evoked behavior (OKR) but have not been analyzed for guidance defects. We find that CELSR3$^{-/-}$ retinal axons can cross the midline but are defasiculated (4/30 projections p=0.03). This result suggests that CELSR3 may primarily function as an adhesion molecule to maintain axonal bundling during neuronal tract formation.

A Rat Model to Simulate Seizure-Induced Laryngospasm. Lissette Guzman[1]; Ko Nakase[2], Richard Kollmar[2], Jason Lazar[2], Krishnamurthi Sundaram[2], Joshua B. Silverman[2] and Mark Stewart[2], [1]Medgar Evers College, Brooklyn, NY and [2]SUNY Downstate Medical Center, Brooklyn, NY.

An epileptic seizure is characterized by abnormally synchronous brain activity in cortical regions that can spread to brain stem areas controlling respiration and cardiac activity. The most severe consequence of an epileptic seizure is death, but the mechanisms by which seizures cause or contribute to death remain largely unknown. Laryngospasm, a spastic closure of the airway by muscles of the larynx, has been observed in epileptic patients and in our rat model. We have seen that laryngospasm can completely prevent breathing (obstructive apnea), and this can be fatal. To better understand the time course of changes in respiration and cardiac function, we studied rats with a simulated laryngospasm produced by capping a tracheal tube to close the airway. We hypothesized that the sudden airway occlusion would produce cardiac and respiratory changes that resemble those in our epileptic rats and allowed us to accurately study the relative timing of changes in respiration and cardiac function. We conclude that the rapid loss of systemic oxygen, complete respiratory arrest, and severe cardiac dysfunction caused by sudden complete airway closure can model seizure-induced laryngospasm and defines a narrow time window for resuscitation efforts.

Utilizing CRISPR-Cas9 Gene Editing Technique to Eliminate Target Sequence from ICER Promoter in Zebrafish (*Danio rerio*). Cory Haluska and Carlos Molina, Montclair State University Montclair, NJ.

The recent emergence of RNA-guided CRISPR-Cas9 gene editing system adapted from the natural defense mechanism found in bacteria and archaea has made the manipulation of genetic loci more feasible than ever. Using this technique we attempted to eliminate a target sequence of about 20 nucleotides from the promoter of the protein ICER (Inducible cAMP Early Repressor) located just upstream of the start sequence. ICER is a small transcription factor and supposed tumor suppressor protein that comes from the CREM (cAMP Responsive Element) gene. ICER has been found to be absent in tumor cells, marked for degradation by the ubiquitin-proteasomal pathway. By eliminating the target sequence we hope to knockout functional ICER protein in order to observe any possible effects this could have. Essentially it is believed that the elimination of ICER would lead to the generation or acceleration of tumor development. To achieve this we are using the well-characterized zebrafish (*Danio rerio*) melanoma model as a paradigm. Two types of methods are being utilized to insert our Cas9/gRNA construct into zebrafish: transfection via PAC2 cells and direct injection into one-cell stage embryos. In addition, we are using a number of techniques including PCR amplification, Sequencing, T7 endonuclease assay, and TOPO cloning in order to provide evidence of target sequence manipulation. The purpose of this study will be to determine whether eradication of ICER will affect the tumorigenesity of wild-type (EK) zebrafish in comparison to the established zebrafish model for melanoma.

Horseshoe Crabs Along the South Shore of Long Island Have No Variation in a 700-bp Region of the Cytochrome c Oxidase I Gene. Jonathan Hanna, Craig S. Hinkley and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.

Atlantic horseshoe crab (*Limulus polyphemus*) populations along the northeastern United States have declined in numbers in recent years. This decline has negatively impacted the pharmaceutical industry and the survivability of other species. Between the months of May to June, horseshoe crabs return to the same location to spawn. Two locations that are frequented for spawning, Plumb Beach (PB) and Spring Creek (SC), lie along the south shore of Long Island and are approximately eight miles apart. These two sites were chosen because they have notable population sizes and are a significant distance from each other. We hypothesize that due to the distance apart of these two sites that the PB and SC crabs represent two different populations. To test this hypothesis, we obtained tissue samples of six crabs from each site, extracted the DNA from these samples, and used the polymerase chain reaction (PCR) to amplify a 700 base-pair region of the cytochrome-c-oxidase I (COXI) gene. We used gel electrophoresis to compare the PCR products to ensure they were the correct size and then sent the DNA to ELIM Biopharmaceuticals for sequencing. The DNA sequences were subjected to BLAST searches to ensure they were from the COXI gene of *Limulus polyphemus*. A multiple sequence alignment determined that there were no polymorphisms present between any of the twelve crabs. These results do not support our hypothesis. When compared to COXI sequences of twelve crabs taken from Fire Island, approximately 40 miles from Plumb beach, there were also no polymorphisms. This suggests there is little genetic diversity among *Limulus polyphemus* along the south shore of Long Island which could be a factor contributing to the decline in their numbers. In the future, we would like to test more samples from the south shore as well as other sites including Long Island Sound.

Cytotoxic and Cytostatic Effects of Single Walled Carbon Nanotubes on Triple Negative Breast Cancer Cells. Kervens Hector, Veronika Yakovishina, Tirandai Hemraj-Benny and Regina Sullivan, Queensborough Community College of CUNY, Bayside, NY.

Single-walled carbon nanotubes (SWCNTs) are sp^2 hybridized carbon structures that possess unique chemical and physical properties. Since their identification in 1991, numerous biomedical applications including drug delivery and photodynamic therapy have been proposed. However, the data on cytotoxic effects of unfunctionalized single walled carbon nanotubes varies with exposure time and cell type as well as other variables. In this study we used the triple negative breast cancer cell line, 468 to investigate the cytotoxic and cytostatic effects of SWCNT treatment. Triple negative breast cancer cells serve as a model to study triple negative breast cancer, a disease in the treatment options are limited due to a lack of cell surface hormonal receptors. Therefore there is a great need for novel therapies including carbon nanotube based therapies. Several assays were employed namely trypan blue exclusion assay to (determine the number of viable cells), MTT, a colorimetric assay to (assess cell metabolic activity) and Hoechst nuclear staining (an indicator for apoptotic cell death). Our trypan blue data revealed little to no effect on cell viability in concentrations 2.5-200 μg after a 24 hour exposure. The MTT results show that cell viability decreases at concentrations as low as 2.5 μg suggesting an effect on the aerobic respiratory metabolism. Further Hoechst staining indicates an increase in apoptotic death. The results show that although the trypan blue assays show little or no effect on cytotoxicity, SWCNT treatment may be affecting 468 metabolic pathways. Further studies will investigate the changes in 468 cellular oxidative stress after single walled carbon nanotube treatment.

Evidence that Eastern oysters *(Crassostrea virginica)* of Wellfleet, Massachusetts Are a Separate Population From Oysters South of Cape Hatteras, North Carolina. Tamara Hernandez, Craig S. Hinkley and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.

Crassostrea virginica, eastern oysters, are bivalve mollusks, which are ecologically and economically beneficial. They filter water, make reefs that serve as habitats for other marine organisms and buffer ocean waters that have become increasingly acidic. Also there is an oyster industry, which grows, harvests and sells oysters. However, eastern oyster populations have decreased significantly in many regions due to disease and destruction of their habitats. Our lab has been studying the genetic structure of eastern oyster populations with the overall goal of reestablishing oysters within depleted areas. Prior research by our lab looking at the oyster populations along the east coast of the United States discovered an "A" polymorphism in the mitochondrial cytochrome c oxidase I (mtCOXI) gene that was only present in oysters south of Swansboro, North Carolina. We have since been examining oysters from many different regions along the east coast to determine if this polymorphism is indeed restricted to the south. We hypothesized that oysters from Wellfleet, Massachusetts, will not have the "A" polymorphism in the mtCOXI gene. To test our hypothesis, we extracted DNA from gill and mantle tissues of a twelve oysters from Wellfleet, MA and then amplified a 700-basepair region of the mtCOXI using the polymerase chain reaction. The amplified DNA was separated by agarose gel electrophoresis to verify the correct size and was then sequenced by ELIM Biopharmaceuticals. A BLAST was performed to confirm that the DNA sequences were of the *Crassostrea virginica* mtCOXI gene. Afterward, we performed a multiple sequence alignment of the mtCOXI gene sequences obtained from the twelve Wellfleet oysters and the "A" was not present in any of them. These results support our hypothesis. For future research we would like to examine more oysters from the different areas in Massachusetts and compare them to the oysters from Wellfleet.

Effects of mTOR Upregulation on Neural Development. Jamie Himmelreich, Emily Lucas and Cathryn Kubera, Monmouth University, West Long Branch, NJ.

The mammalian target of rapamycin (mTOR) is an atypical serine/threonine kinase that is the central controller of many cellular activities including translation, cell growth, homeostasis and proliferation. When mTOR is activated by a small GTPase signaling molecule (Rheb), Phospho S6 ribosomal protein is produced which is used to indicate high mTOR activity. Preliminary data has shown that upregulation of mTOR activity in cultured primary cerebellar Granule Cell Precursors increases neurite length and complexity. It is also known that process outgrowth in neurons is regulated by elevations in cytosolic calcium levels. Hence, we will examine whether there is a connection between dysregulated mTOR and cellular calcium signals. Through the introduction of constitively activated Rheb, we will manipulate mTOR in Neuro 2a cells to determine how mTOR impacts intrinsic calcium signaling.

Akt Signaling in Cells Defective in DNA Repair. Britni Hinderhofer, Lauren Diaz, Stephanie Meyer, Anthony Mangelli and Maureen Sanz, Molloy College, Rockville Centre, NY.

Bloom's syndrome (BSyn) is a rare genetically-determined growth disorder characterized by proportional small size. One clinical complication of BSyn is insulin resistance in the form of non-insulin dependent diabetes mellitus. The primary defect in BSyn is absence of functional BLM protein. BLM functions as part of a protein complex that is active in DNA repair via homologous recombination. Absence of functional BLM protein results in hypermutability and hyperrecombinability, a specific genomic instability featured by BSyn cells. BSyn cells can be used as a model system to obtain basic biological information concerning mechanisms by which cells respond to the accumulation of somatic mutations using energy for maintenance rather than growth, repair and proliferation. The Akt signaling pathway is common to regulation of cell growth and carbohydrate metabolism, both of which are affected in persons with BSyn. Identification of a defect in the insulin-like growth factor-1 (IGF-1)/insulin signaling cascade to growth factors and glucose transport may be a first step in explaining the short stature and glucose metabolism abnormalities seen in BSyn. Cultures of exponentially growing SV40-transformed cells were incubated for 24 hours in serum free medium. Following serum starvation, cultures were stimulated with IGF-1 for 0, 10, 20, 40, and 60 minutes. Phosphorylation of proteins in the Akt signaling network was analyzed by immunofluorescence, western blot analysis, antibody array analysis, and RNA array analysis. Immunofluorescence studies revealed similar patterns of subcellular localization and onset of Akt phosphorylation in both cell lines. Western blot analysis confirmed the observations made by immunofluorescence. Antibody array analysis was performed to compare phosphorylation of 16 proteins in the Akt signaling pathway activated by IGF-1 in unaffected and BSyn cell lines to identify defects in the post receptor Akt network in BSyn cells. Preliminary analysis of the arrays revealed similar patterns of protein phosphorylation in both cell lines.

Microbiology of the Built Environment: The Changing Microbiome of New York City College of Technology. Manuela Hoyos[1] and Davida S. Smyth[1,2], New York City College of Technology, Brooklyn, NY and [2]Mercy College, Dobbs Ferry, NY.

Staphylococci are recognized as a serious threat by the CDC, responsible for 80000 infections and 11000 deaths annually. About one in three people carry Staphylococci asymptomatically in their noses. The bacteria can often be found on the hands and survive on surfaces for prolonged periods of time. Worryingly, few new drugs are in the pipeline and community-associated Staphylococcal infections are on the rise. Newer technologies like DNA sequencing have not yet been leveraged to determine transmission of Staphylococci from surface to surface. Our study is using DNA sequencing to identify species of Staphylococci that are present on our model surface, elevator buttons. Using agar selective for Staphylococci and DNA sequencing we are identifying which members and genetic subtypes of Staphylococci prevail on the surfaces and we are attempting to identify putatively transmitting types. We are also examining the ability of the organisms to express a biofilm, a survival mechanism also used by bacteria in the host. To date we have collected over 300 staphylococci and identified several members of the coagulase negative Staphylococci, most notably, *S. epidermidis*, and *S. capitis*. We've also identified the presence of many novel, as yet unidentified types of resistance genes. Lastly, many of our strains have the ability to form a robust biofilm. Our preliminary findings indicate that many potentially pathogenic organisms are readily colonizing surfaces in our college and indicate that at present, decontamination methods are not succeeding. We conclude that our campus is a suitable model system for studying the transmission of bacteria.

The Effect of Lead on the Growth of *Phaseolus vulgaris* (Beans). Elhizeh Hydara and Catarina Mata, Borough of Manhattan Community College, New York, NY.

The purpose of this research is to determine the effects of lead (ll) nitrate ($Pb(NO_3)_2$) on the growth of *Phaseolus vulgaris* (red kidney beans). Lead (ll) nitrate is a white powder or crystalline inorganic salt that is soluble in water and highly toxic. It is a byproduct of formerly industrial areas and their surroundings, and as a result, it poses a risk to the environment and human health. It inhibits photosynthesis in plants and therefore may affect the proper growth of plants like *Phaseolus vulgaris.* To determine this, red kidney beans were planted on potting soil and the test plants were given 1200ppm of $Pb(NO_3)_2$ weekly and the length and diameter of the shoot and the width of the leaves were measured and recorded over a time period of 30days. The $Pb(NO_3)_2$ treated test plants germinated faster than the controls and grew better than the controls over the period of the experiment. The number of bean pods produced was also greater on the test plants than on the control plants by the end of the experiment. The small amount of nitrate found in $Pb(NO_3)_2$ may have provided the plants with extra nutrition and as a result, grew better than the control plants. This work was funded by CSTEP of the NYSED. My special thanks also goes to the Borough of Manhattan Community College Academic Affairs for the award to attend this conference.

Development of MULA, a Novel Multicolor Cell Labeling System in *Drosophila melanogaster*. Nataly Jara[1], Chris Roblodowski[1] and Qi He [2], [1] Queensborough Community College, Bayside, NY and [2]Brooklyn College, Brooklyn, NY.

How neural circuits process information to control animal behavior is a fundamental issue in neuroscience. Neural circuitry formation during development consists of many steps including cell type specification, lineage differentiation, neural connectivity, synapse formation and production of different neurotransmitters. A better understanding of neural circuitry is critical for analyzing the onset and progression of neural degenerative diseases such as the Parkinson's. An obstacle in disease related research is a lack of more efficient cell marking methods to enable the tracing of cell lineage and neural cell-cell interaction. We have proposed a strategy for the development of a new multicolor cell labeling system (MULA) for detecting neural cell lineage and cell interaction. It uses the highly efficient recombination system of PhiC31 and attB/attP coupled with fluorescent proteins of many colors. We have completed the construction of vectors for colors mcherry, gfp, and cerulean as well as integrase PhiC31. The availability of this method and the coupling of this method with other existing ones such as MARCM will offer a new investigative route for probing lineage and cell-cell interactions, which in turn will provide essential knowledge for deciphering neurological changes associated with various nervous system disorders such as the Parkinson's. Nataly Jara is a participant in the NIH Bridges to Baccalaureate Program at Queensborough Community College.

Direct PCR Detection, Cloning, and Characterization of Bacterial β-Glucosidase Genes from Soils. Theranda Jashari, Isabella Canal Delgado, Elyssa Barron, Stephanie Zapata, Tina Choe, Satenik Melkonyan and Luis Jimenez, Bergen Community College, Paramus, NJ.

β-glucosidases are cellulases responsible for the final transformation of cellobiose to glucose. Cellobiose is a by -product of cellulose digestion by endoglucanases and exoglucanases. Microbial DNA was extracted from temperate soils using the Zymo Microbe DNA MiniPrep protocol. β-glucosidase gene sequences were amplified by PCR using degenerate primers βgluF2 and βgluR4.

DNA fragments of approximately 200 base pair were detected in all positive soil samples. The amplified DNA fragments were purified and ligated to vector pCR®4-TOPO. Transformations were performed using competent Mix and Go *Escherichia coli* cells. Plasmids were isolated from each clone and inserts were screened by PCR. DNA sequencing and BLAST analysis determined the identity of the cloned fragments. DNA sequencing of clone libraries showed the predominant presence of Proteobacteria (80%), Actinobacteria (16%) and Deinococcus-Thermus (4%). *Rhodanobacter* sp. was found to be the most frequently detected bacterial species carrying β-glucosidase genes. Direct PCR detection and cloning of β-glucosidase genes from soils provided a more comprehensive assessment of the different bacterial species potential to degrade cellobiose to glucose.

Magnetic Nanoparticle-Functionalized Protein Biomaterials. Teeba Jihad[1], Sumayya Vawda[1], Lindsay K. Hill[2] and Jin Kim, Montclare[1,2,3], [1]NYU Tandon School of Engineering, Brooklyn, NY, [2]SUNY Downstate Medical Center, Brooklyn, NY and [3]New York University, New York, NY.

In this work, we aim to synthesize proteins capable of magnetic iron oxide templation for monitored drug-delivery applications for cancer treatment. Our system is based on the pentameric coiled-coil domain of the Cartilage Oligomeric Matrix Protein, COMPcc. This non-collagenous extracellular matrix protein is composed of a hydrophobic pore capable of carrying small hydrophobic molecules, such as chemotherapeutic agents. One variant of this protein, dubbed Q, further self-assembles into nanofibers under acidic conditions, and has been shown to subsequently assemble into microfibers in the presence of a small hydrophobic molecule. Here we synthesized an azide-functionalized protein Q via residue-specific incorporation of an unnatural methionine analog, azidohomoalanine (AHA). The methionine auxotrophic cell line M15MA permitted the complete replacement of methionine with AHA in the protein Q. The azide group of this residue is capable of [3+2] alkyne-azide cycloaddition for covalent linkage to an alkyne moiety. Here we aim to assess the cycloaddition of the azide-functionalized protein Q to an alkyne-functionalized iron oxide-templating peptide CMms6, or the C-terminus of the protein Mms6. Mms6 is found in magnetotatic bacteria and is capable of binding and organizing iron oxide nanoparticles. In particular, the hydrophilic C-terminus plays a key role in iron binding. By performing click chemistry between our protein Q and alkyne-functionalized CMms6, we aim to create a magnetically functionalized protein for monitored drug delivery. This research was supported by the New York University Polytechnic School of Engineering Undergraduate Summer Research Program, ARO (W911NF-11− 1− 0449), NSF MRSEC Program under award number DMR-0820341 and the 2015 Wechsler Summer Internship.

Comparison of Bacterial Communities in Caterpillar Fecal Material, Compost, and Soil Using Next Generation Sequencing. Luis Jimenez, Isabella Canal Delgado, John Smalley, Elena Tartaglia and Stephanie Zapata, Bergen Community College, Paramus, NJ.

16S rDNA clone libraries were analyzed using next generation sequencing (Next-Gen) to describe and compare the bacterial community diversity of luna moth (*Actias luna*) caterpillar fecal samples, compost, and soil samples. Microbial DNA was extracted from all samples types using the Zymo Microbe DNA MiniPrep protocol. Eubacterial 16S rDNA genes were amplified by PCR and the resulting 465 base pair amplicons were sequenced using an Illumina protocol. The Next-Gen results showed that the bacterial community of the fecal material showed less diversity than those of soil and compost. Only 3 bacterial phyla were detected in fecal material with Actinobacterial sequences accounting for 54% of the clones. However, compost was found to have 11 different bacterial phyla, the most abundant (56%) being the Firmicutes. Soil was found to have the most diverse bacterial community with 15 phyla detected in the clone libraries. Most of the sequences isolated from soil belonged to the Proteobacteria (33%). The majority of bacteria were identified under the order Actinomycetales in fecal material and soil while the order Bacillales was more abundant in compost. The numbers of different bacterial orders found were 81 in soil, 39 in compost, and 5 in caterpillar samples. At higher than species taxonomic levels, next generation sequencing allowed for a better understanding of the diversity of bacterial communities in environmental samples that achieved using more traditional library construction and screening based methods.

The Effectiveness of Essential Oils as Possible Treatments for *Mycobacterial* Infections. Luana Johnston, Mary T. Ortiz and Loretta Brancaccio-Taras. Kingsborough Community College, Brooklyn, NY.

Mycobacterium infections are a health issue with multidrug resistant strains prevalent. Treatment alternatives available worldwide are critical. This study compared the effectiveness of essential oils to traditional agents in killing *Mycobacterium* species. The hypothesis was: essential oils are as effective as currently prescribed antibiotics in killing *Mycobacterium species*. Tryptic soy agar plates were inoculated with *M. phlei*, *M. smegmatis, and M. nonchromogenicum*. Disks saturated with colloidal silver and oils (castor, eucalyptus, sandalwood, mineral, oregano, diluted oregano and tea tree), and sensi-disks of rifampin, ethambutol, and isoniazid, were placed on the inoculated plates. After incubation (24hr,37^{o}C), zones of inhibition were measured (mm); mean sizes±standard error of the mean (X±SEM) of 6-10 trials were calculated. Zone sizes between test agents and antibiotics were compared using the Mann-Whitney U-test (p=.05). Ethambutol, tea tree oil, diluted and undiluted oregano oil

killed the three test organisms. Tea tree oil was statistically as effective as ethambutol against all three bacteria. Results were: for *M. phlei*, average zone size of 40.00± 2.89mm compared to 47.92±1.79 mm for ethambutol; for *M. smegmatis*, tea tree oil zone was 51.91±7.13mm compared to 48.25±1.16mm for ethambutol; for *M. nonchromogenicum*, tea tree oil zone was 62.69±7.28mm compared to 47.10±1.46mm for ethambutol. Diluted oregano oil was statistically less effective than ethambutol for all tested bacteria. Oregano oil was equally effective as ethambutol against *M. phlei* and statistically more effective than ethambutol against *M. smegmatis* and *M. nonchromogenicum. For M. phlei*, the average oregano oil zone was 51.38±5.11mm versus 47.92±1.79mm for ethambutol; for *M. smegmatis,* oregano oil zone was 76.00±5.98mm versus 48.25±1.16mm for ethambutol; for *M. nonchromogenicum,* oregano oil zone was 64.69±4.78mm compared to 47.10±1.46mm for ethambutol. The hypothesis is accepted for tea tree and oregano oils. Future work will test essential oil combinations. Grant support: NIH Bridges #2R25GM062003-13, NYSDOE CSTEP #0537151091.

Comparison and Contrast of Sea Lion Vocalizations in Captivity and in the Wild. Khadija Khan, Kwun Chan, Kristy Biolsi, Allen Burdowski and Kathleen A. Nolan, St. Francis College, Brooklyn, NY.

Sea lion vocalizations were recorded at the Prospect Park Zoo, the Queens Zoo, the New York Aquarium, the Central Park Zoo, the Bronx Zoo and the Aquarium at Niagara. The Queens Zoo and the Bronx Zoo revealed the greatest number and variety of vocalizations. The program Audacity was used, and total number of sounds, barks, duration of sounds, and pitch were recorded. Comparisons and contrasts were also made between captive (our own recordings) and wild California sea lions (*Zalophus californianus*) vocalization recordings found in the MacCaulay Sound Library (Cornell University).

The Oyster Drill (*Urosalpinx cinerea*) Does Not Appear to Be an Intermediate Host for Dermo (*Perkinsus marinus*). Thamina Khanam, Gary Sarinsky and Craig Hinkley, Kingsborough Community College, Brooklyn NY.

Dermo (*Perkinsus marinus*) is a pathogenic protozoan that is considered to be one of the main reasons for the significant decline of the Eastern Oyster (*Crassostrea virginica*) population from Jamaica Bay in the 1920s. Today, there are no known oyster beds observed in the Bay. Experiments conducted in 2004 testing for dermo in two year old oysters grown from dermo- free oyster spats in Jamaica Bay resulted in a few of the oysters testing positive. Studies suggest the parasite is transmitted from oyster to oyster, which prompts the question, "How did the oysters get infected if they were dermo-free as spats and there are no known oysters in the Bay?" We hypothesize that the Atlantic Oyster Drill (*Urosalpinx cinerea*),a species living in close proximity to the oyster is a vector for the parasite. Tissue was excised from 13 oyster drills and DNA was extracted from the tissues using a DNeasy Blood and Tissue Kit. The polymerase chain reaction (PCR) was used to amplify the Mitochondrial Cytochrome Oxidase 1 (CO1) gene using Folmer's primer. The PCR product was subjected to gel electrophoresis and from the gel results, we verified DNA was extracted from 12 of the samples. Amplified DNA was sent to Elim Biopharmaceuticals for sequencing and was subjected to a NCBI Blast search to confirm that the CO1 DNA was extracted from *Urosalpinx cinerea*. Extracted DNA plus a sample known to be positive for dermo was amplified by using a PCR reaction with a Dermo-specific primer, and subjected to gel electrophoresis to determine if the oyster drills were positive for dermo. No dermo DNA was amplified from the oyster drills tested. However we were able to demonstrate the amplification of a positive dermo sample under the conditions used. The results of this experiment did not support our hypothesis.

The Use of an *in Vitro* Isolated Brainstem-Spinal Cord Preparation in a Multilevel Analysis of Breathing Behavior in the Serotonin-Deficient Pet-1 Knockout Mouse. Shota Kikozashvili, Anshu Patel and Jeffery T. Erickson, The College of New Jersey, Ewing, NJ.

Pet-1 is a transcription factor that is required for the production of a full complement of central serotonin neurons. Targeted "knockout" of the *Pet-1* gene results in a selective 70% loss of central serotonin neurons that is associated with detectable breathing abnormalities in intact neonatal mice. These abnormalities include a decreased breathing frequency, an increased incidence of spontaneous apneas, and delayed autoresuscitation responses to experimentally induced apnea, compared to wild type littermates. However, the underlying mechanism(s) by which the severe loss of central serotonin neurons produces these breathing deficits is not yet known. To begin to address this issue we have assembled an *in vitro* electrophysiology recording system to measure neural output from the central respiratory rhythm generator in the medulla oblongata. Neonatal mice (postnatal day 4.5-5.5) are deeply anesthetized and the brainstem and upper spinal cord are rapidly dissected into ice-cold artificial cerebrospinal fluid. The brainstem is then transected at the ponto-medullary border and transferred to a recording dish where the tissue is superfused with artificial cerebrospinal fluid (pH 7.4, 25°C) that is bubbled with 95% O_2/5% CO_2). Suction electrodes are used to record neural discharges from the fourth cervical nerve rootlet and the hypoglossal nerve, both of which provide a measure of central respiratory drive. We are currently using this system to compare baseline "fictive" breathing from wild-type and Pet-1 knockout mice. However, the system will be instrumental for future pharmacological studies aimed at more clearly defining the role of serotonin neurons in the development and maturation of breathing behavior in neonatal mice during the early postnatal period. Supported by a TCNJ Support for Scholarly Activity (SOSA) award (JTE) and a grant from the CJ Foundation for SIDS Research.

Effect of a Shelter Environment Versus Ownership on Domestic Dogs' (*Canis familiaris*) Responses to Human Imperative Gestures. Kelley Kilpatrick and Brian Palestis, Wagner College, Staten Island NY.

Canis familiaris, better known as the domestic dog has been a part of humans' lives for over 10,000 years. After all these years of domestication, dogs have been found able to understand human gestures and human language. In prior research, using a test first developed to analyze chimpanzees' (*Pan troglodytes*) social intelligence, the cognitive ability of both domestic dogs and chimpanzees (our closest living relatives) were evaluated and found that domestic dogs were able to understand imperative human gestures (pointing at an object) as means to retrieve or go to that object better than chimpanzees. This same simple test was used in the following research on both pet dogs and shelter dogs to assess whether the human-dog bond has a significant impact on its ability to perform the test successfully. In addition to recording the results of the test, either the owner or a shelter worker was asked to complete a questionnaire about the tested dog, which was then analyzed by a Pearson correlation coefficient for each group and then for all dogs. Sixteen pet dogs and 12 shelter dogs of varying ages, breeds, sizes, temperaments, and sexes were subjected to the test and it was found that the pet dogs performed at significantly higher than chance levels and significantly better than the shelter dogs. Previous shelter dogs living as pets were able to complete the object-choice test significantly better than the current shelter dogs.

Stereochemical and Mechanistic Studies of a Tyrosine Aminomutase in *Oryza sativa.* Zayna King[1], Kevin D. Walker[2] and Tyler Walter[2], [1]Medgar Evers College, Brooklyn, NY and [2]Michigan State University, East Lansing, MI.

β-Amino acids serve as building blocks for biologically active compounds and important metabolites. A unique family of aminomutase enzymes contain a methylideneimidazol-4-one (MIO) prosthetic group that aids in the isomerization of α- to β-amino acids. Recently, an MIO-dependent tyrosine aminomutase (*Os*TAM) isolated from Japanese rice *Oryza sativa* was discovered. This is the first aminomutase from a cash crop and the first TAM isolated from a plant. The reaction catalyzed by OsTAM produced (3R)-β-tyrosine. We hypothesize that the mode of migration proceeds via retention of configuration (R.O.C). The R.O.C pathway was assessed by ^{2}H-NMR analysis of a [^{2}H]-labeled β-tyrosine product which showed that *Os*TAM removed the *pro*-(*S*) hydrogen and moved it to C_α. The β-product catalyzed by *Os*TAM was derivatized as the *N*-(2-(*S*)-methylbutyramide) methyl ester to assess the stereochemistry as (3*R*) by gas chromatography/mass spectrometry (GC/EIMS). Deuterium-labeled α-tyrosines were incubated with *Os*TAM to assess the stereochemistry of the hydrogen abstraction at C_β and rebound at C_α. The β-tyrosines from the deuterium labeling studies were derivatized as ethyl formamide methyl esters and analyzed by GC/EIMS. Overall, we found that *Os*TAM retains the configuration of each migration terminus. Further, like other TAMs, *Os*TAM makes a mixture of 3*R*- and 3*S*-β-tyrosine with a K_M = 600 μM and a $k_{cat} \simeq 4\ s^{-1}$. However, by contrast, long incubation time (24 h) and changes in pH did not affect the stereoselectivity of *Os*TAM like other bacterial TAMs.

Do NuA4 and Rpd3C(S) Compete for Binding to Chromatin? Maethinee Koonvisal and Daniel S. Ginsburg, LIU Post, Brookville, NY.

Gene expression is regulated in large part by chromatin, the DNA-protein complex that makes up eukaryotic chromosomes. Chromatin must be disassembled for transcription to take place. One important step in the disassembly of chromatin is histone acetylation. Acetylation weakens the interactions between histones and DNA and stimulates recruitment of chromatin remodeling complexes that remove the histones from chromatin. Acetylation is dynamically regulated by lysine acetyltransferase (KAT) and histone deacetylase complexes (HDACs). The NuA4 KAT complex and Rpd3C (S) HDAC complex have both been shown to bind di- and trimethylated H3K36. This work tested the hypothesis that one mechanism by which acetylation is regulated is by physical competition between NuA4 and Rpd3C(S) for binding to chromatin. We analyzed Rpd3C(S) mutants that affect complex binding to chromatin (*rco1*Δ) or deacetylase activity (*rpd3Δ*). We expected that loss of Rpd3C(S) binding to chromatin would lead to increased NuA4 binding and more histone acetylation. The increased NuA4 binding should then be reduced by eliminating H3K36 methylation in a *set2Δ* mutant. Consistent with our model we found that *rpd3Δset2Δ* cells had a more severe stress response phenotype than *rpd3Δ* cells. Unfortunately, *set2Δ* did not repress the stress response defects in *rco1Δ* cells, as we had expected. Histone H4 acetylation in *rco1Δset2Δ* cells was lower than in *rco1Δ* cells as expected, but we also observed less H4 acetylation in *rpd3Δset2Δ* as compared to *rpd3Δ* cells. Neither NuA4-nucleosome binding nor occupancy at *GAL1* were affected by the loss of Rpd3(S) complex in *rco1Δ* cells. Taken together, our results suggest that NuA4 and Rpd3C(S) do not physically compete for binding to di- and trimethylated H3K36. This suggests that some other factor helps regulate the chromatin binding of these complexes.

Direct PCR Detection, Cloning, and Characterization of Bacterial RubisCO Genes from New Jersey Soils. Margarita Kulko, Ryan Kim, Stephanie Zapata, Theranda Jashari, Aidan Holwerda, Anna Gonzalez, Tina Choe and Luis Jimenez, Bergen Community College, Paramus, NJ.

Ribulose-1,5-bisphosphate carboxylase/oxygenase, commonly known by the abbreviation RubisCO, is an enzyme involved in the first major step of carbon fixation, a process by which atmospheric carbon dioxide is converted by bacteria to energy-rich molecules such as glucose. Microbial DNA was extracted from temperate soils using the Zymo Microbe DNA MiniPrep protocol. RubisCo gene sequences were amplified by PCR using degenerate primers *cbbL*G1F and *cbbL*G1R. DNA fragments of approximately 800 base pair were detected in all positive soil samples. Clone libraries were constructed with the amplified DNA fragments by ligating the detected fragments with vector pCR®4-TOPO. Transformations were performed using competent Mix and Go *Escherichia coli* cells. Plasmids were isolated from each clone using the Zyppy Plasmid Miniprep and inserts were screened by PCR using M13 DNA primers. DNA sequencing and BLAST analysis determined the identity of the cloned fragments. DNA sequencing of clone libraries showed that 87% of the sequences were related to Proteobacteria and 13% to Actinobacteria. Some of the species detected were *Variovorax paradoxus, Bradyrhizobium elkanii, Pseudonocardia dioxanivorans, Rhodopseudomonas palustris,* and *Starkeya novella.*

Comparison of Copper Surface Mediated Toxicity in Gram-Positive, Gram-Negative Bacteria and *Saccharomyces cerevisiae*. Bharti Kumari and Nidhi Gadura, Queensborough Community College, Queens, NY.

Copper alloy surfaces are known as antimicrobial sanitizing agents that have the ability to kill microorganisms. However, the mechanism by which cell death occurs still remains unclear. The aim of our project is to determine the relationship between exposure to copper alloy surfaces or copper ions, lipid peroxidation, and killing of Gram positive, Gram negative bacteria and yeast. We hypothesize that we might see differences in the mode of copper mediated cell death in different bacterial and fungal species. Using Gram positive (*Staphylococcus aureus*), Gram negative (*Pseudomonas aeruginosa*) bacteria and *Saccharomyces cerevisiae* strain BY4741 quantitative dilutions series was performed to test for bacterial and yeast cell death. Our results indicate a biphasic killing curve for Gram positive, Gram negative and *Saccharomyces cerevisiae* when exposed to copper chips. TBARS assay was used to measure the amount of lipid peroxidation that occurred. The bacterial and yeast killing rate upon exposure to copper surfaces also correlates to increased levels of lipid peroxidation. There are some differences seen in the kinetics of cell death that correlates with the levels of lipid peroxidation between the two bacterial strains and yeast. Genomic DNA extraction indicates that the mode of cell death seems to be necrotic in all cases. This project was funded by PSC-CUNY and Copper Development Association grant to Dr. Gadura. Bharti Kumari is funded by QCC MSEIP grant.

Construction of a *Streptomyces coelicolor* Rhomboid Knockout. Liliana Lara, Naydu Carmona and Monica Trujillo, Queensborough Community College, CUNY, New York, NY.

Rhomboids are intramembrane proteases present in all forms of life. They have 6 to 7 membrane domains and their active site contains a serine and a histidine that are buried in the intramembrane space. There are many questions about the role of these proteases; they have diverse functions, all of them loosely associated to signaling, but it is not clear how they work or how they are regulated. In particular, very little is known about bacterial rhomboid proteases. We aim to elucidate the biological function of rhomboids in *Streptomycetes*. We focus on these bacteria because they produce the majority of antibiotics used in medicine and agriculture. This production relies on a complex developmental cycle and a signaling system not fully characterized. We hypothesize that rhomboid proteases play a role in the signaling pathways of *Streptomyces* species. Our preliminary genomic analysis identified four putative rhomboid homologues in *Streptomyces coelicolor* (the model species for the study of this genus).The aim of this project is to construct and characterize the SCO3855 knockout (KO), a gene that codes for a 7 membrane domain rhomboid protease from *S. coelicolor*. Our group has shown that this rhomboid protease can rescue the phenotype of a well characterized bacterial rhomboid mutant (□aarA) from *P. stuartii* (Nieves et al, unpublished results) suggesting this rhomboid recognizes the same substrate as ΔaarA. We used the recently described, clustered, regularly interspaced, short palindromic repeat (CRISPR) technology to build the pCRIPOmyces-SCO3855 knockout plasmid and we are currently conjugating it into *S. coelicolor*. Preliminary results obtained from a single disruption of SCO3855 suggest the sporulation pathway could be affected (Lara *et al*, unpublished results). We expect that the comparison between the wild-type and the mutant *S. coelicolor* SCO3855KO will provide further insight into the biological role of rhomboid proteases

Scoring Sequence for Modelled Folding Conformation in InteractiveROSETTA Using HMMSTR. Oluwadamilola Lawal[1,2], Christian Schenkelberg[2], Shounak Banerjee[2], Benjamin Walcott[2] and Christopher Bystroff[2], [1]Medgar Evers College, Brooklyn, NY and [2] Rensselaer Polytechnic Institute, Troy, NY.

Mutations introduced to an amino acid sequence during protein design may alter folding initiation sites thereby leading to folding inefficiency. I-sites (initiation sites) are short sequence-structure motifs used to predict local structures of a protein. HMMSTR is a hidden Markov model created using I-sites. Given backbone angles, HMMSTR can generate an amino acid probability profile at each position showing the propensity to maintain local structural conformations. The current study seeks to use HMMSTR in InteractiveROSETTA (a graphical user interface for ROSETTA protein modeling suite) to determine the probability for residues at each position for local protein folding. The HMMSTR program source code was remodeled for compatibility with InteractiveROSETTA and imported as a shared object. Backbone atomic coordinates of a particular protein were passed to HMMSTR to generate an amino acid probability profile for folding using the forward-backward algorithm. These probabilities were used to calculate the log-likelihood ratio (LLR) for folding, which were represented from high as green to low as red. HMMSTR in InteractiveROSETTA was tested on Green Fluorescent Protein sequence (2AWJ.pdb) that research has shown to not fold when the glycine is substituted for the tryptophan residue at position 57. A color change from green to yellow was observed at position 57 following the glycine substitution, indicating a reduction in folding probability. This added functionality to InteractiveROSETTA will facilitate protein design by helping the user to discern and avoid non-folding (and presumably non-functional) mutations in an intuitive manner. This project was funded by Rosetta Commons, NSF grant #1541278, and NIH grant R01 GM099827.

Adipogenic Differentiation of Rat Bone Marrow Mesenchymal Stem Cells. Sophia Lazar, Alisha Malla and Thomas Owen, Ramapo College of New Jersey, Mahwah. NJ.

Bone marrow mesenchymal stem cells (MSCs) are multipotent cells that have the capacity to differentiate into an assortment of cell types including osteoblasts, chondrocytes, myocytes, and adipocytes. Prostaglandins are small lipid compounds derived from arachadonic acid in the cell membrane. The E-series prostaglandins (PGE1 and PGE2) stimulate cellular responses through four cell surface receptors and they increase MSC differentiation into osteoblasts. The question remains as to whether PGE1 or PGE2 cause increased commitment of MSCs to osteoblasts directly or whether they simply prime MSCs to respond to whichever environmental differentiation cues they subsequently experience. In our work, primary rat bone marrow cells were initially plated in MEMa with 15% FCS. At the first media change, the cells were fed with MEMa supplemented with 10% FCIII in order to encourage differentiation. Various combinations of concentrations of insulin, dexamethasone, and isobutyl-methylxanthine (IBMX) were also added assess which would lead to optimal adipocyte differentiation. Insulin is known to induce differentiation of MSCs to adipocytes in a concentration-dependent manner and was tested at 0 uM, 5 uM, and 50 uM. Dexamethasone is an anti-inflammatory steroid which promotes adipogenesis and was used at a constant 1 uM concentration. IBMX is a nonselective phosphodiesterase inhibitor that raises the levels of cAMP within cells. It is required for adipogenesis in some cell lines and was tested here at 500 uM. Optimal adipogenesis was found to occur using 5 uM insulin and 1 uM dexamethasone with IBMX actually blocking adipocyte formation. MSCs were then cultured as above except that PGE1, PGE2 or vehicle were added at plating and the optimal adipogenic factors were added at the first feeding. Both visual observation and quantitative analysis of Oil Red O Staining showed no difference in adipogenic differentiation of MSCs exposed to either PGE1 or PGE2.

A Genetic Screen to Identify Regulators of Collective Cell Migration. Dheveline Louis, Jamal Mattis, Andreas Mavrommatis and Monn Monn Myat, Medgar Evers College, Brooklyn NY.

Cell migration is key for the proper location and function of nearly all organs. The majority of what we know of cell migration is from studies of single cell migration. However, many cells migrate collectively as a group during organ development in embryos and during cancer. We are performing an RNA interference screen in the fruit fly *Drosophila melanogaster* to identify novel regulators of collective cell migration, The UAS-GAL system is used to drive expression of tissue-specific double stranded RNAs in the process of RNA interference (RNAi) to identify genes responsible for the formation of either the salivary gland or the trachea. We have screened 19 RNAi constructs so far and six show defects in the salivary gland and trachea. We will continue to test the remaining 23 RNAi lines in our collection.

Salinity Tolerance of a Marine Ciliate Co-Isolated with Eggs of the Sea Urchin *Lytechinus variegatus.* Grace Loussakou[1,2], Michael Llano[1,3], Lalitha Jayant[1] and Christine Priano[1], [1]Borough of Manhattan Community College, New York, NY; [2]Rutgers University, Camden, Camden, NJ and [3]The City College of New York, New York, NY.

An unidentified ciliated marine protist was initially co-isolated with eggs of the green sea urchin *Lytechinus variegatus*, an intertidal organism. To identity this protist and elucidate its relationship with the sea urchin, it is essential to establish conditions for its maintenance in the laboratory. The purpose of this study was to determine optimal salinity conditions required to grow this ciliate in culture. Protist growth was examined in varying salinity levels as found in intertidal zones. Salt water was prepared using Instant Ocean sea salt. Six 10 mL protist cultures were inoculated on the same day in the salinity range of 0% to 5.5%. A 3.5% salt culture served as a control for the natural salinity of ocean water. Cultures were given equal amounts of Marine S fish food and agitated at 25 rpm at room temperature. For each culture, protists were counted every 24 hours using a hemocytometer. Results indicated that a minimum concentration of 1.5% sea salt supported protist reproduction and that protists could tolerate salinity up to 5.5%. Most cultures grew exponentially for three to four days before growth slowed. However at concentrations below 3.5%, protists swelled in size and more contaminating organisms were observed. It was concluded that optimal salt conditions for laboratory growth is between 3.5% and 5.5%. These results will help to optimize conditions for growing and maintaining this protist in the laboratory thereby facilitating future work aimed at characterizing this protist species and investigating its possible symbiotic relationship with the green sea urchin. This work was supported by the BMCC CSTEP program and PSC-CUNY Award #TRADA-45-567, jointly funded by The Professional Staff Congress and The City University of NY. Travel for student presenters was paid by an award from the BMCC Office of Academic Affairs. We thank Jenny Paredes for her invaluable laboratory assistance.

Investigating the Role of CPAR-1 in Cell division in the Nematode *C. elegans*. Madeleine Maas, Gabe Makar and Joost Monen, Ramapo College of New Jersey, Mahwah, NJ.

CENP-A is a highly conserved Histone-H3 like protein, critical to centromere specificity and kinetochore assembly in all eukaryotes. Failure to properly produce or localize CENP-A leads to aneuploidy and cell death. In most organisms CENP-A has a single variant; however, in the nematode *C.elegans* CENP-A has two homologs, HCP-3 and CPAR-1. Based on previous studies, HCP-3 is responsible for specifying the centromere and thus critical for chromosome segregation in mitosis. CPAR-1's role however remains to be elucidated, albeit CPAR-1 is known to be essential as CPAR-1 mutants are embryonic lethal. The first step in understanding the role that CPAR-1 plays in embryonic development is to characterize where CPAR-1 localizes endogenously. To this effect, we are utilizing an immunofluorescence assay, which allows us to visualize chromosomes, microtubules, and the CENP-A homologs in the developing embryo to get a sense of where these proteins localize in the dividing cells. To date, we have an HCP-3 specific antibody that localizes to the centromere, and we are in the process of developing a CPAR-1 specific antibody for comparison. To test the functional role of CPAR-1, we are utilizing time-lapse microscopy to visualize microtubules and chromosomes in a dividing embryo and comparing wild-type to CPAR-1 deficient embryos. Here, we will describe our current progress, future molecular strategies and experimental design to assess the role of CPAR-1 in cell division. Through these studies, we will better understand what role CPAR-1 plays in embryonic development, and perhaps gain insight into a divergent role for CENP-A not yet characterized.

Effect of Fertilization on Native and Non-native Wetland Plants. Martha Mahady and Dirk Vanderklein. Montclair State University, Montclair, NJ.

Purple loosestrife (*Lythrum salicaria* L.) an herbaceous perennial native to Europe and Asia, was introduced to North America as early as 1830. It has since spread in wetlands throughout the eastern United States and Canada, becoming a serious threat to the biodiversity of wetlands. In particular, purple loosestrife forms dense stands that crowd out common cattails (*Typha latifolia*), an important member of wetland communities. Purple Loosestrife can be observed growing in wet areas that also receive runoff containing higher levels of nutrients due to inorganic or organic fertilizer. The ability to use these nutrients efficiently may contribute to purple loosestrife's invasive ability. The hypothesis being investigated is that the addition of fertilizer will result in greater growth in purple loosestrife compared to native species. Seeds for purple loosestrife from Sussex County NJ and the United Kingdom, and seeds for winged loosestrife (*Lythrum alatum*), Joe Pye weed (*Eupatorium macalatum*), and common cattails (*T. latifolia*) from Sussex County and Kentucky were grown under greenhouse conditions and four fertilization conditions. Purple loosestrife plants that received fertilizer were taller and had greater mass than those did not. This response did not occur in the three native species, with fertilizer and unfertilized plants growing to similar height and mass. These results show that the ability to respond more efficiently to fertilizer may contribute to the invasiveness of purple loosestrife in North America.

Histamine Mediates the Response to Light in the Sensory Motor Integration of Gill Lateral Cell Cilia in the Bivalve Mollusc, *Crassostrea virginica.* Kimone Marrett[1], Danellie Semple[2], Edward J. Catapane[2] and Margaret A. Carroll[2]. [1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY.

Gill lateral cells of *Crassostrea virginica* are innervated by serotonin and dopamine nerves. Most bivalves have lateral cell cilia that respond to serotonin and dopamine, with serotonin being the neurotransmitter that increases beating rates and dopamine being the neurotransmitter decreasing it. The motor aspects of gill lateral cell innervation have been well studied, but not the sensory side, with limited information about sensory inputs. Our previous work found *C. virginica* can sense and adjust gill lateral cell cilia beating to the presence of food, crab extract and light, as well as various chemical cues including histamine when applied to mantle rim. Shining light on the mantle rim or applying histamine decreased gill lateral cell cilia beating rates, but did not alter cilia beating rates when applied directly to gill. In many invertebrates histamine is a neurotransmitter involved in photoreception. We hypothesize that in *C. virginica,* histamine is the neurotransmitter of mantle rim photoreceptors. To test this we used whole animal preparations in which the innervation of the gill from the cerebral and visceral ganglia is intact and tested the actions of a histamine H2 antagonist, famotidine, on the response to light. Cilia beating was measured by stroboscopic microscopy. An eleven lumen, ¼ inch diameter spotlight source was used to stimulate the mantle rim in the vicinity of the siphons. Stimulating the mantle rim with light decreased cilia beating in the gill. Adding the H2 antagonist famotidine caused a statistically significant, dose-dependent blockage of this action over the range of 10^{-9} - 10^{-3}. The study further demonstrates the sensory-motor integration of beating of lateral cilia involving the sensory mantle rim and visceral/cerebral ganglia, supporting the hypothesis that histamine is the sensory neurotransmitter in mantle photoreceptor 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.

Mathematical Model of Cancer Cell Viability After Different Regimes of Treatment with Doxorubicin. Margaret Massett, Mina Youssef, Jan Osea, Wayne Eby and Natalia Coleman, New Jersey City University, Jersey City, NJ.

Despite the intensive research effort and promising discoveries, cancer still is the leading cause of death in the US. In a treatment of cancer, it is essential to understand the growth dynamics of cancer cells to develop a successful treatment strategy. We propose to combine a theoretical and experimental approach and develop a mathematical model to make quantitative predictions of cancer cell growth as a function of the concentration of doxorubicin and duration of exposure. Our interdisciplinary research may enhance the understanding of cancer biology and in turn increase the foundation of the chemotherapy effectiveness. We would like to thank the LSAMP- NSF grant for funding this research.

Manipulation of Gene Expression in the Chick Embryo Brain Via Electroporation. Margo McGrath, Natalia Plawiak, Martin McGrath and Renée E. Haskew-Layton, Mercy College, Dobbs Ferry, NY.

Neuronal development and the survival and function of neurons in the adult brain and spinal cord relies on the coordinated roles of glial cells. One such glial cell type, the astrocyte, serves diverse roles in the central nervous system including the regulation of cerebral blood flow, facilitation of neuronal communication, and coordination of metabolic and antioxidant support of neurons. The manipulation of astrocytic gene targets *in vivo* provides an ideal tool for determining the role of specific targets in astrocytes that support neuronal function. Electroporation is a technique used to reversibly permeabilize cells, allowing for the introduction of plasmid DNA into cells and subsequent heterologous gene expression. We plan to use *in ovo* electroporation of the chicken embryo to introduce the pro-survival gene Akt in astrocytes. Preliminary data from primary cell culture shows that protein tyrosine phosphatase (PTP) inhibition in astrocytes protects neurons from oxidative stress. We hypothesize that the specific PTP – PTEN (phosphatase and tensin homolog) - induces astrocyte-dependent neuroprotection via the activation of the pro-survival kinase Akt. To induce expression of Akt in astrocytes and a subpopulation of neural precursor cells, we subcloned the Akt gene downstream of a GFAP promoter. Currently, we are optimizing a protocol to electroporate the GFAP-Akt plasmid into the optic tectum of chicken embryos at various embryonic stages. Immediate goals are to determine the appropriate developmental stage to induce astrocyte-specific Akt expression using the GFAP promoter and to screen alternative astrocyte-specific promoters for increased specificity. Future goals include exploring the role of oxidants in astrogenesis in the developing chick brain and modeling oxidative stress in older embryos expressing heterologous astrocytic Akt.

Understanding the Kinetics of Lymphocyte Activating Ligands on Cord Blood Derived B Cells During Early Infection with Lytic Epstein Barr Virus (EBV). Ayana McLeod[1], Gumperz Jenny[2], Nicholas Zumwalde[2] and Akshat Sharma[2], [1]Medgar Evers College, Brooklyn, NY and [2]Univ. of Wisconsin-Michigan, Wisconsin, MI.

Epstein-Barr virus (EBV) is a successful virus in transforming B-lymphocytes *in vitro* and is known to have association with B lymphomas. EBV alters proliferation of B-lymphocytes influencing activating ligands CD1d, MicA MicB and BTN3.A1 role in effectively communicating with

the immune system. The two reporter ligands investigated CD1d and BTN3.A1 are known to be present on the cells surface, which suggest that upon infection with EBV an upregulation of these ligands is likely to occur at an early time point. Whereas the stress induced ligand MicA MicB could experience an upregulation at a later time point given that it is absent from cells until stress is detected. We hypothesize that CD1d, MicA MicB, and BTN3.A1 will become upregulated upon infection with EBV, and then down regulated within a short duration of time. We used flow cytometry to monitor a lab strain of EBV lytic (M81) that express GFP, to monitor infected cells over uninfected cells. We found that upon infection there was an upregulation of CD1d and MicA MicB. However BTN3.A1 remained unchanged. After eleven days we found a down regulation of CD1d, which may have been caused by the use of PBMC (peripheral blood mononuclear cells), which is positive for EBV. Our study strongly suggested that CD1d is down regulated upon EBV infection at an early time point when compared to MiCA MicB. Our study also suggests that BTN3.A1 may not be influenced by the presence of EBV at earl time points. The signaling pathways that regulate BTN3A1 expression, and thereby cell activation, are incompletely understood and is being further studied.

Lipophilic Green Tea Polyphenols Inhibit Biofilm Formation in the Cavity Causing Bacteria *Streptococcus mutans.* Amy Lynn Melok, Christopher Chen and Lee H. Lee. Montclair State University, Montclair, NJ.

A frequently underrated infectious disease, dental caries, or cavities, are one of the most commonly seen diseases in patients of all ages. Although this disease is preventable, dentists treat caries daily. Providing additional precautionary treatments will help decrease the occurrence of this disease. Interventions to disrupt growth of carious bacteria will impact dental communities around the world. *Streptococcus mutans (S. mutans)* is the most dominant of the cavity causing bacteria found in the oral cavity. The gram-positive bacteria are capable of forming well-organized communities called biofilm. Biofilms are held together by extracellular polymeric substances, and have unique characteristics that allow them to survive in fluctuating environments like the oral cavity. Teeth provide the perfect surface for biofilm attachment and are destructive because the bacteria reacts with carbohydrates consumed to form an acid byproduct that destroys tooth enamel. In this study, two modified green tea polyphenols, LTP and EGCG-S, were used to evaluate their effect on biofilm formation in *S. mutans*. Bacteria were grown in Tryptic broth with 1% glucose and exposed to different concentrations of each compound. Samples were incubated for 4 days at 37 ^{o}C to allow biofilm formation to occur. Quantitative analysis of biofilm was carried out using crystal violet assay; distribution of alive and dead cells were carried out by staining the cells with Live/Dead Bacterial fluorescence kit and observed under a microscope. The morphology and cell surface of untreated and treated cells were observed under scanning electron microscope (SEM). The results indicated that all the tea polyphenols used had a % of inhibition ranging from 90 to 100%. The majority of cells in the treated samples were killed. Our results support the role of green tea polyphenols as an encouraging, natural anti-cariogenic therapeutic agent by demonstrating its capability to inhibit *S. mutans* biofilm formation.

Analysis of a Listeria Monocytogenes Infection in Adult Zebrafish Central Nervous System; a Light Microscopic Study. T. Mendez and C.P. Corbo, Wagner College, Staten Island, NY.

Listeria monocytogenes is a gram-positive bacterium that invades host cells causing listeriosis in immunocompromised patients and may cause death. Listeria's ability to avoid the immune system plays an important role to its pathogenicity. This pathogen is motile, traveling from the initial site of infection into the nearest pathway of the peripheral nervous system (PNS). From here listeria travels through the PNS towards its core location of colonization and replication called the central nervous system (CNS), particularly within the brain. This project has set out to characterize the cellular pathology at the ultrastructural level. Infected zebrafish brains and retinas which had previously been infected with *L. monocytogenes* were fixed with glutaraldehyde and osmium tetroxide at specific time points, dehydrated through an increasing ethanol concentration, and dried for scanning electron microscopy or embedded and sectioned for light and transmission electron microscopy. At the light microscopic level, cells of the periventricular grey zone (PVGZ) were seen to be unhealthy in appearance and listeria were recorded inside host cells. Transmission electron microscopy revealed the presence of *Listeria* in the optic tectum of the zebrafish brain. Specifically residing in and among the cells of the PVGZ. This region of the brain is the direct input of the optic nerve and the major visual processing cortex of the zebrafish. *Listeria* cells can be seen between the cell bodies of the PVGZ. The cells of this region were also, in some cases damaged, appearing as if a hole was punched into the side of cells.

The Sand Fiddler Crab (*Uca pugnax*) Does Not Appear to be a Vector for MSX (*Haplosporidium nelsoni*) Infection of Eastern Oysters (*Crassostrea virginica*). Sana Mian, Gary Sarinsky and Craig Hinkley, Kingsborough Community College, Brooklyn, NY.

The Eastern Oyster (*Crassostrea virginica*) has not been observed in Jamaica Bay, NY since the early 1920's. Our laboratory detected the pathogenic protozoan MSX (*Haplosporidum nelsoni*) in two-year old oysters grown from spats in Taylor floats. MSX causes the disruption of the digestive tubule epithelium which leads to emaciation

and ultimately the death of the oyster. Little is known about the reproductive life cycle of MSX. Early infections are found in the oyster's gills. This indicates that the infective stage is water-borne. Additionally, since spores are not found in infected oysters and experiments in the laboratory have failed to transmit the disease suggests that a vector may be involved. It is hypothesized that the sand fiddler crab (*Uca pugnax*), which co-exists amongst the oysters is the host that serves as a vector for MSX. For this study, we extracted DNA samples from five sand fiddler crabs. Two sets of DNA were prepared. Polymerase chain reaction (PCR) was performed on the first set to amplify the mitochondrial cytochrome oxidase 1 gene (CO1) using Folmer's primer. The amplified products were then subjected to 2% agarose gel electrophoresis to determine correct size (702 bp) and were found to be present in all five samples. The CO1 amplified products were sequenced by Elim Biopharmaceuticals and they were subjected to NCBI blast searches which further verified that the DNA was the CO1 gene from *Uca pugnax*.. The second set and a known sample containing MSX was amplified using the MSXA and MSXB small subunit rRNA primer set. Gel electrophoresis was performed to determine the results of the amplified DNA. The samples of sand fiddler crabs were not amplified for MSX but the positive control was. The results of this experiment do not support the hypothesis that fiddler crabs are vectors for MSX.in oysters.

The Genetic Deletion of IL-13 Receptor in Mice Yields Enhanced Neonatal Vaccine Responses. Fabienne Mondelus[1], Habib Zaghouani[2] and Mindy M. Miller[2], [1]Medgar Evers College, Brooklyn, NY and [2]University of Missouri-Columbia, MO.

Neonates have poorly developed immune systems which make them unresponsive to vaccines and susceptible to microbial infections. T helper 1 cells (Th1), a subset of T lymphocytes, are required for pathogen control and vaccine responses but are lacking in neonates' immune systems. It previously has been shown that neonatal Th1 cells express a cytokine receptor for interleukin 13 (IL-13) and that when IL-13 signals through this receptor it causes apoptosis of the Th1 cells, hence the lack of these cells in neonates. We hypothesized that newborn mice in which IL-13 receptor (IL-13R) has been genetically deleted will have restored Th1 responses and will be able to mount protective immunity upon vaccination. One day old IL-13 Receptor deficient (IL-13R-/-) mice were taken, and they were vaccinated for lymphocytic choriomeningitis virus (LCMV) which allows them to be protected against LCMV upon later infection. In addition, wild type IL-13 receptor (IL-13R+/+) mice along with non-vaccinated IL-13R-/- were obtain for a Plaque Assay. Eight weeks after vaccination, they were taken and were injected with LCMV. Four days post infection, the mice were then euthanized for Plaque Assay studies to measure the virus titers within each strain of mice. Herein, we demonstrate that IL-13R-deficient (IL-13R$^{-/}$) neonates that are vaccinated for lymphocytic choriomeningitis virus (LCMV) are better protected against a later infection with the virus than IL-13R$^{+/+}$ neonates. Moreover, non-vaccinated IL-13R-/- shown better response as opposed to vaccinated IL-13R+/+. In conclusion, diminishing the function of IL-13R could improve neonatal vaccination

Cellulolytic and Xylanolytic Bacteria Associated with Bark Beetles in Fallen Logs. Sherwayne Morrison, Patricia Schneider[1], Raji Subramaniam[1] and Olga Calderon[2], [1]Queensborough Community College, Bayside, NY and [2]LaGuardia Community College, Long Island City, NY.

Most bark beetles live in dead wood and play an important role in decomposition and nutrient recycling. Evidence indicates the beetles metabolize cell wall polysaccharides by producing or ingesting enzymes, or using enzymes produced by symbiotic microbes. This study focused on isolating and characterizing cellulose and xylan (hemicellulose) digesting bacteria associated with bark beetles that burrow in dead trees. Beetle larvae along with associated bark and sapwood were collected in an oak-hickory forest of Alley Pond Park, New York City. Macerated gut, frass, bark and wood samples were inoculated into basal salt broth containing filter paper as a substrate. After six days of incubation, cellulolytic bacteria were streaked onto carboxymethylcellulose (CMC) agar. The twelve strains that grew on CMC were subjected to a second screening on CMC using Congo red stain to visualize zones of hydrolysis. Isolates were also screened for xylanase production using Remazol Brilliant Blue (RBB) xylan agar. *Cellumonas uda* and *Saccaromyces cervisiae.var.elliposides* served as reference/control organisms. On the basis of clearing zones, six isolates were identified that produce both cellulose and xylanase. These bacterial strains were selected for further study and identified by 16S rRNA sequence analysis. Understanding the beetle-microbe relationship is crucial in the development of strategies to combat pests such as the wood-boring *Anoplophora gravipennis* (Asian long-horned beetle) and the practical use of beneficial beetles such as *Palame crassimana*, which contributes to the degradation of fallen trees and recycling of materials. Future work may reveal novel cellulases and hemicellulases with agricultural, industrial or biofuel applications. Sherwayne Morrison is a participant in the NIH Bridges to the Baccalaureate Program at Queensborough Community College.

Potential Zinc Stress Response Mechanisms in *Synechococcus* sp. IU 625. Robert Newby, Jr. and Tin-Chun Chu, Seton Hall University, South Orange, NJ.

Cyanobacterial harmful algal blooms are becoming increasing occurrences globally due to rapid eutrophication resulted from climate change, agricultural run-offs, and other industrial contamination sources. Heavy metals such as zinc are among many of the elements that are contributing to the eutrophication events. In this study, we've investigated the potential zinc stress response mechanism using a model unicellular cyanobacterium *Synechococcus* sp. IU 625 (*S.* IU 625). *S.* IU 625 in medium containing $ZnCl_2$ at levels of 0, 10, 25, and 50 mg/L were collected and monitored over 29 days. Viability analysis with SYTOX® shows that *S.* IU 625 is capable of surviving in all concentrations up to 8 days, however after this point 50 mg/L demonstrated a lethal effect. *S.* IU 625 cultured in 25 mg/L shows several divisionary and membrane defects, as detected with scanning electron microscopy; and pigment deficiencies as measured with flow cytometry. Differences in size, chlorophyll a, and allophycocyanin intensity were observed in the cells exposed to 25 mg/L $ZnCl_2$. Increasing fluorescent signal from zinquin also indicated an increasing intracellular zinc concentration in this population. The results suggested that internal binding proteins, efflux mediated channels, and membrane composition changes could be part of the zinc stress response mechanism in freshwater cyanobacteria.

Elucidation of the Role of Rhomboid Proteins in *Streptomyces.* Wilson Nieves, Naydu Carmona, Peter Novick and Monica Trujillo, Queensborough Community College, Bayside NY.

Streptomyces are gram-positive soil bacteria characterized by a complex developmental cycle involving multiple cell-to-cell communication pathways, and by the production of secondary metabolites. These natural products account for more than 50% of the naturally-available antibiotics, differentiation inducers, apoptosis inhibitors, and antitumor compounds. Metabolite production involves complex signaling mechanisms not fully elucidated yet. Rhomboids are intramembrane proteases with their active site located within the cell membrane. These enzymes are found in all branches of life and have a wide range of biological functions. We hypothesize that rhomboid proteins play a role in the signaling cascades of *Streptomyces*. Bioinformatics tools were used to identify five families of putative rhomboid genes in 30 fully sequenced *Streptomyces* strains. Preliminary transcription assays showed that the 4 putative rhomboid genes from *Streptomyces coelicolor* were transcribed when growing in liquid media. The first step to investigate the role of rhomboids in the *Streptomyces* genus was to clone the representatives of the two most conserved rhomboid families, A and D from *S. coelicolor* (the model organism for the study of the *Streptomyces* genus). Codon optimized genes SCO3855 and SCO2139, representing the rhomboid families A and D, were cloned into vectors suitable to complement and potentially rescue the phenotype of a *Providencia stuartii* rhomboid mutant strain (XD37aarA). The *P. stuartii* rhomboid gene, aarA, has been extensively characterized. Assays built in different media showed that rhomboid gene 3855 is capable of binding to the same protein substrate as aarA and thus recover the phenotype of mutant XD37aarA. Rhomboid gene 2139 shows different phenotypic characteristics after complementation. Rhomboid families A and D, from *S. coelicolor* have been demonstrated to have different functions within the *coelicolor* species. Therefore, the complementation of XD37.A with the genes SCO3855 and SCO2139 provided us with an approach for the study of the possible role that rhomboids could play in *Streptomyces*.

Dichotomy in the Epigenetic Mark Lysine Acetylation is Critical for the Proliferation of Prostate Cancer Cells. Zimuzoh Orakuae1, Ambreka Benson1, Marc Philizaire1, Ravi Pathak2 and Shiraz Mujtaba1, Medgar Evers College, CUNY, Brooklyn, NY and 2Baylor College of Medicine, Houston TX.

The dynamics of lysine acetylation serve as a major epigenetic mark, which regulates cellular response to inflammation, DNA damage and hormonal changes. Microarray assays reveal changes in gene expression, but cannot predict regulation of a protein function by epigenetic modifications. The present study employs computational tools to inclusively analyze microarray data to understand the potential role of acetylation during development of androgen-independent PCa. The data revealed that the androgen receptor interacts with 333 proteins, out of which at least 92 proteins were acetylated. Notably, the number of cellular proteins undergoing acetylation in the androgen-dependent PCa was more as compared to the androgen-independent PCa. Specifically, the 32 lysine-acetylated proteins in the cellular models of androgen-dependent PCa were mainly involved in regulating stability as well as pre- and post-processing of mRNA. Collectively, the data demonstrate that protein lysine acetylation plays a crucial role during the transition of androgen-dependent to -independent PCa, which importantly, could also serve as a functional axis to unravel new therapeutic targets.

Population Structure and Parasitism in the Eastern Painted Turtle (*Chrysemis picta*). Antonios Pappantoniou, Mario Castiello, Juliet Chin and Alessandra Pane, Housatonic Community College, Bridgeport CT.

Aspects of the population structure and parasitism of the eastern painted turtle (*Chrysemis picta)* from a Connecticut farm pond were studied. Turtles were collected using hoop traps. Individual turtles were measured, weighed, had their gender determined, checked for leeches, marked with a unique alphabetic identifier and returned back to their place of capture. Results of this study showed that female painted turtles averaged 128.4 mm carapace length and weighed an average of 321.6 grams while males averaged 261.2 grams and had an average carapace length of 123.2 mm. The male:female ratio was 0.95:1. Female turtles showed a higher frequency of leech parasitism 64.4% vs. 60.4% for the males. The distribution of the leeches on the host was also recorded. Leeches attached to the plastron most frequently. The percentage of parasitized individuals remained steady throughout the term of this project. There was a decline in the catch per unit effort (CPUE) during the 2015 collecting season. Results of the population structure and parasite studies agree with similar research on the biology of painted turtles. The decline in the CPUE may reflect the two severe winters between 2013-2015.

Design of a Gene Transfer Vector to Deliver a Stabilized Anti-EGFR RNA Aptamer to the Glioblastoma Microenvironment. Sachin Parikh and Martin J. Hicks, Monmouth University, West Long Branch, NJ.

Glioblastoma multiforme (GBM) is an incurable and aggressive type of brain tumor. It is the most common central nervous system (CNS) malignancy with a median survival of only 14 months. The epidermal growth factor receptor (EGFR) is a type of tyrosine kinase receptor (TKR) often overamplified in GBM tumor cells. EGFR amplification and over-expression leads to angiogenesis and uncontrolled growth and proliferation of GBM. Although a great deal is known about the biology exhibited by EGFR-activated GBM, the application of therapies against the biologic processes is limited by the blood-brain barrier which restricts systemically administered therapies from reaching the brain. We are creating an *in vivo* tissue culture model to develop a novel strategy to bypass these barriers by developing a gene transfer vector to deliver the genetic sequences of a known anti-EGFR RNA therapy aptamer that binds with high affinity against EGFR. In this approach, we will use a gene transfer system to modify GBM and CNS cells to express the therapeutic anti-cancer RNA aptamer molecule, and using an extracellular RNA "exRNA" localization element, the RNA aptamer will be transported and spread throughout the tumor microenvironment where EGFR is abundant. In addition, we have added an RNA structural element (an inactived hammerhead ribozyme) important for the stabilization of the RNA therapeutic molecule.

Post-Transcriptional Control of Gene Expression by microRNAs Following Lipopolysaccharide-Induced Inflammation of Rat Testis. Mitchell I. Parker and Michael A. Palladino, Monmouth University, West Long Branch, NJ.

MicroRNAs (miRNAs) are a group of small RNA molecules that do not encode for proteins. Instead, they regulate gene expression by blocking translation or causing degradation of messenger RNA (mRNA). Reproductive biologists are interested in miRNAs because proper expression of these transcripts has been linked to normal testis development and spermatogenesis, while atypical expression of certain miRNAs has been implicated in testicular cancer formation and male infertility. Research that examines the functional significance of miRNAs in defending the male reproductive organs from infection is yet to be done. We hypothesized that post-transcriptional control of gene expression by miRNAs plays a significant role in antimicrobial protection of rat testis. The overall goal of our investigation was to determine which miRNAs are involved in regulating inflammation of the testis in response to infection. Previous studies in our laboratory on gene expression following lipopolysaccharide (LPS)-induced inflammation of rat testis demonstrated up-regulation of 11 inflammatory genes. A component of Gram-negative bacterial cell walls, LPS is a common antigen that—when introduced into the bloodstream—provokes a strong inflammatory response in the testis and other tissues of the body. The objective of our study was to discover which inflammatory-related miRNAs (miRNAs that target inflammatory genes) are up-regulated and/or down-regulated following LPS-induced inflammation of rat testis. Testes RNA were extracted from rats that were sacrificed 3 or 6 hours after receiving a 5 mg/kg of body weight injection of LPS (n=4) or saline (n=2), and expression of inflammatory-related miRNAs was determined by real-time quantitative polymerase chain reaction (qPCR). Results showed 7 inflammatory-related miRNAs with a greater than 2 fold down-regulation in rats that were sacrificed 3 hours after receiving an LPS injection ($p<0.05$). Further experiments will examine changes in inflammatory-related miRNA expression in rats that were sacrificed 6 hours after receiving an LPS injection.

Genetic Delivery of a miRNA Cluster with Polycistronic siRNAs Reduces mRNA Expression of Epidermal Growth Factor Receptor in Human Glioblastoma Cells. Imari Patel, Martin J. Hicks, Dennis G. Urbaniak and Diane E. Urbaniak, Monmouth University, West Long Branch,, NJ.

Glioblastoma multiforme (GBM), the most common central nervous system malignancy, is clinically documented as a grade IV astrocytoma. Therefore GBM is one of the most rapidly growing and invasive types of glial tumors of the central nervous system. The standard therapy includes surgical removal, radiation and chemotherapy with a survival of about one year. In addition, systemic therapies are limited by the blood-brain barrier. To bypass the barrier, we are constructing a delivery strategy that inhibits the gene expression of tyrosine kinase receptors (TKR), which are commonly upregulated in GBM. One TKR, epidermal growth factor receptor (EGFR), is overexpressed in GBM leading to uncontrolled growth and proliferation. Our approach is to enlist the RNA interference pathway. Although small interfering RNAs (siRNAs) are often utilized to silence gene expression, exogenously expressed siRNAs are not an effective strategy to treat human disease due to both extracellular and intracellular nucleases as well as activation of cellular immunity against foreign nucleic acids. To bypass these degradatory mechanisms, we are using a natural miRNA cluster genetic background to effectively deliver the DNA encoding multiple anti-EGFR siRNAs by cloning them into the structure of the miRNA cluster, miR-17-92. The anti-EGFR polycistronic miRNA cluster (pAAV-miR-IP1) expresses six siRNAs directed against EGFR specifically targeting the extracellular ligand binding domain, transmembrane domain, intracellular tyrosine kinase domain and 3' untranslated region of the EGFR gene. The therapy vector, pAAV-miR-IP1, was transfected into the human GBM cell line, A172. Results show that pAAV-miR-IP1 was expressed at high levels in the A172 cell line with a subsequent reduction in EGFR mRNA expression. Future strategies include using the polycistronic delivery mechanism to target multiple TKRs in addition to EGFR.

Multi-Functional RNA Antisense Gene Transfer Strategy to Alter HGFR Expression in GBM. Priyal Patel and Martin J. Hicks, [1]Monmouth University, West Long Branch,, NJ.

Glioblastoma multiforme (GBM) is the most common central nervous system malignancy. The aggressive tumor spreads rapidly migrating through the white matter of the brain. Current therapy includes surgical removal, radiation and chemotherapy, extending survival to only about 14 months. Furthermore, the blood-brain barrier is a challenge to targeted therapy. Our research is to develop a novel gene transfer vector to deliver the DNA encoding an antisense RNA (ASR) to alter the splicing pattern of the hepatocyte growth factor receptor (HGFR). In this approach, the ASR blocks recognition of splice sites and splicing enhancers. The current strategy targets the splicing of exon 11 to12 of the pre-mRNA transcript. Blockage of this splicing event would lead to retention of intron 11. Because this intron includes 14 intronic alternative polyadenylation (IPA) signals there is great potential to generate a shortened transcript and its subsequent soluble therapeutic HGFR decoy. To optimize therapeutic efficiency, we have designed a 2nd generation gene transfer construct with multiple elements with distinct functions. These include the ASR with an hnRNPA1 splicing inhibitory element and an Sm-Opt U7snRNA (Sm-Opt/U7) localization signal with the novel tertiary 'kiss domain'. The ASR targets the 5' splice site of Exon 11, the Sm-Opt/U7 signal stabilizes and directs the ASR into the spliceosome of the nucleus, the hnRNPA1 tail blocks the splicing machinery and the 'kiss domain' stabilizes tertiary structure of the therapy vector. The new design makes use of the U7 promoter and 3' transcription termination element. Using the 1st generation therapy vector we have developed assays to measure efficiency of therapy vector delivery, as well as levels of pre-mRNA and spliced HGFR transcript. In the future, using a 2nd generation therapy vector, we expect to see a change in the expression of the full length HGFR in the GBM cells.

Flow Cytometric and Microscopic Analysis of Cyanobacteria and Their Toxins in Greenwood Lake. Ruchit Patel, Robert Newby and Tin-Chun Chu, Seton Hall University, South Orange, NJ.

Algal Blooms have become a rising issue due to rapid accumulations and excessive growth of nutrients such as nitrogen and phosphorus. This can lead to accelerated form of Eutrophication, thus affecting the human health and the ecosystem. Many cyanobacteria including Microcystis, Cylindrospermopsis and Anabaena are the common strains that release cyanotoxins. In this study, water samples were collected from Greenwood Lake and filtered through a series of polycarbonate membrane filters with pore sizes: 30, 20, 14, 10, 5, 2.7 and 0.45 μm. Flow cytometric assay were carried out for all filtrates. Phase-contrast and fluorescent microscopy were used to analyze the cyanobacteria as well as their potential toxins. The results showed filtrates under 5 μm contained lower phycoerythrin and allophycocyanin. Both flow cytometry and microscopic analyses indicated that there were abundant cyanobacteria and Microcystis in the water sample.

Antibiotic Resistance Among Isolates of *Staphylococcus aureus* from Ramapo College Students. Sophia Penkrat, Rebecca Bray and Thomas Owen, Ramapo College of New Jersey, Mahwah, NJ.

Staphylococcus aureus has long been recognized as a cause for a number of human diseases, ranging from the minor skin infection to bursitis to pneumonia. Previous studies have shown that resistance of some strains of *S. aureus* to several widely prescribed drugs such as methicillin and (increasingly) vancomycin has become more prevalent. In this study, a group of students from Ramapo College (~165 individuals, 18-25 years old) was examined for presence of *S. aureus* in the nasopharyngeal cavity using self-obtained nasal swabs plated immediately onto mannitol salt agar (MSA) plates. *S. aureus* colonies (MSA growth positive and mannitol fermentation positive) were isolated from the samples of 38 individuals (~23%), consistent with published estimates that 20-25% of the population carries the bacterium in the nose or on the skin. Colonies of the bacterium were then isolated on MSA and grown out on trypticase soy agar (TSA) for antibiotic resistance testing. All samples were verified as *S. aureus* using the coagulase test. The samples were analyzed for sensitivity to eight conventional antibiotics using the Kirby-Bauer disk diffusion test with each bacterial isolate tested with each antibiotic three times. Post-incubation, the zones of inhibition were measured and compared to analysis charts to determine the susceptibility of the bacterial isolate to each drug. Antibiotics used in this study include ampicillin, ciprofloxacin, clindamycin, linezolid, minocycline, oxacillin, sulfamethoxazole/trimethoprim, and vancomycin. In most cases, the *S. aureus* isolates were susceptible to the antibiotics tested and thus these drugs could potentially be used to treat an infection caused by the particular isolate. However, there were some isolates, which appeared to be resistant to particular antibiotics, indicating the presence of drug resistant *S. aureus* in our college population. Additional Kirby-Bauer testing is being performed to confirm these findings.

Atomic Force Microscopy Measurements of Single-Walled Carbon Nanotube Treated MDA-MB 231 Cells. Mathiu Perez, Veronika Yakovishina, Sunil Dehipawala, Tirandai Hemraj-Benny and Regina Sullivan, Queensborough Community College, Bayside, NY.

Biomedical applications of single walled carbon nanotubes (SWCNT) have the potential to expand treatment options for cancer patients. However biosafety studies are currently inconclusive. These studies have been limited by technical issues related to the hydrophobic nature of the nanotubes. The diameter (1.5 nm) of the nanotube should allow passage through cellular gap junctions and ion channels but aggregation of the nanotubes in aqueous solutions decreases cellular uptake in *in vitro* studies. These carbon rich structures could be associating with and adversely affecting cellular components. Coating single walled carbon nanotubes with collagen has been shown to facilitate cellular uptake thus allowing for such intracellular associations to be investigated. In this study, MDA-MB 231 cells were treated with collagen coated SWCNT. Atomic Force Microscopy was used to measure the Young's modulus of the cells. Young's modulus indicates the degree of flexibility which in turn can be correlated with changes in the actin cytoskeleton. Actin cytoskeletal rearrangement is a key event in the metastatic process. The results suggest differences in the measures and therefore collagen coated single walled carbon nanotubes treatment may be affecting the cytoskeleton of these cells. Future studies will expand the investigation to include other types of cancer cells as well noncancerous cells and may reveal potentially novel cancer treatments.

The Biodiversity and Ecology of Brachycera (Insecta: Diptera) in Alley Pond Park, Queens, New York. Gheorghe Proteasa, James A. Timbilla and Scott C. Sherman. Queensborough Community College, CUNY, Bayside, NY.

Most of the natural areas remaining in cities are fragments of highly degraded habitat where human-made changes to the natural flora have altered significantly the fauna. The remaining natural habitats in urban areas function like ecological islands surrounded by human constructions. The biodiversity and ecology of Diptera in Alley Pond Park are currently being studied. Alley Pond Park is located near the western end of Long Island in the northern part of the highly urbanized New York City borough of Queens. It contains a diversity of habitats including woodlands, wild flower meadows, freshwater wetlands, salt marsh, mud flats, Oakland Lake (a freshwater glacial lake), ponds, streams, and a tidal creek. The park has a surprisingly rich biological diversity of plants and invertebrate and vertebrate animals. The zoological order Diptera is one of the world's most diverse groups of animals with more than 50 extinct families and over 150 extant families. Diptera have evolved an amazing variety of different life strategies and have adapted successfully to most types of habitats. The suborder Brachycera is one of the two primary divisions of Diptera and is subdivided into more than 120 extant families worldwide. The suborder includes bee flies, blow flies, bot flies, deer flies, flesh flies, frit flies, fruit flies, horse flies, house flies, leaf-mining flies, louse flies, robber flies, shore flies, snipe flies, tsetse flies, and many more types of flies. Our research in Alley Pond Park shows the presence of a diversity of brachycerous families including Agromyzidae, Anthomyiidae, Calliphoridae, Dolichopodidae, Drosophilidae, Empididae, Micropezidae, Muscidae, Phoridae, Sarcophagidae, Sepsidae, Sphaeroceridae, Syrphidae, Tachinidae, and Tephritidae.

Study the Inhibitory Effects of EGCG, EGCE-S and PEGCG on Sporulation of Spore Forming Bacilli. Richa Rana, Megha Rana, Shivani Rana, Priya Patel and Lee H. Lee, Montclair State University, NJ.

In many of the Bacilli group, they are able to form endospores when the environment is not favored for cell growth. Endospores are the toughest to kill and the longest surviving than the other specialized cell types. They cause many problems in the plant, humans, and other organism also in food industries, hospitals and restaurants. They are one of the major food poisoning bacteria and spoilage in canned food of short duration. The purpose of this study is to evaluate the effect of green tea polyphenols EGCG, EGCG-S and P-EGCG on bacterial sporulation. Inhibitory actions of various green tea poly phenols were tested against some species of the *Bacillus* such as, *B.megaterium, B. cereus, and B. subtilis* under various conditions. Bacterial cultures were treated with 1% of different tea polyphenols for 1, 2, 4, 6, 8, 24 and 48 hours and then perform spore stain for microscopic observations. The viable count study was also carried out to determine the colony-forming unit (CFU). The results indicated that at 24 hours the spores were formed in all the controls but not in any of the polyphenol treated samples. EGCG, EGCG-S and P-EGCG treated *B. cereus,* percent inhibition was 100%, 87% and 89% respectively; in*, B. megaterium* percent inhibition was100%, 100% and 93% respectively; in *B. subtilis* percent inhibition was 100%, 99% and 89% respectively. This suggested that green tea polyphenols have significant inhibitory effect on these bacteria with EGCG the most effective of these three polyphenols; *B. megatium* is the most sensitive to these treatments. Further study will be carried out to specifically determine the effect of different tea polyphenols on sporulation in these Bacilli species.

Rescuing Juvenile Hormone Receptor Mutants with a Green Fluorescent Protein Tagged Version of the Receptor. Stephanie Rene and Rebecca F. Spokony. Baruch College New York, NY.

The signaling molecule Juvenile Hormone (JH) is an important regulator of insect development and adult reproduction. Most importantly, the absence of the hormone at the end of the last larval phase allows metamorphosis to proceed. In *Drosophila melanogaster*, Juvenile Hormone has two receptors: Methoprene-tolerant protein (Met), and Germ cell expressed protein (Gce). Transgenic flies containing a green fluorescently labeled version of Met (Met::GFP) under the regulatory control found in 100 kb of genomic DNA surrounding the endogenous locus were generated. To determine if Met::GFP is functional, two genetic rescue experiments were conducted. In the first experiment, we determined that Met::GFP can restore hormone sensitivity to *Met*$^-$ mutants. We crossed the Met::GFP construct into a *Met*$^-$ mutant line. The offspring *Met*$^-$*;* Met::GFP white prepupae (WPP) were treated with the juvenile hormone mimic, methoprene. Met::GFP restored methoprene sensitivity to female WPP. In the second experiment, we determined that Met::GFP can rescue lethality in flies missing both copies of the receptor, *Met*$^-$*Gce*$^-$ double mutants. We crossed the Met::GFP construct into a lethal *Met*$^-$*Gce*$^-$ mutant line. *Met*$^-$*Gce*$^-$*/Y;* Met::GFP/+ males survived into adulthood, whereas *Met*$^-$*Gce*$^-$*/Y; +/+* males die as third instar larvae. Both experiments led to rescue. Restoration of both methoprene sensitivity and larval lethality indicate that the Met::GFP protein is functional and expressed at the right places and the right times during development. Future experiments will utilize the GFP-tag to examine when and where the protein is expressed during development as well as where the protein binds to DNA, using an anti-GFP antibody. We would like to thank the Louis Stokes Alliance for Minority Participation fellowship (LSAMP) for funding this research. We would also like to thank Jian Wang for supplying us with the *Met*$^-$*Gce*$^-$ mutant line.

Decline and Distribution of Vulnerable Juvenile Atlantic Horseshoe Crabs (*Limulus polyphemus)* on Plumb Beach, Jamaica Bay, New York. Emmanuel Reyes and Christina P. Colon, Kingsborough Community College, Brooklyn, NY.

Researchers have become concerned about horseshoe crab survival due to population declines, and that's why this study was conducted. It was noticed that there is a decrease in juvenile horseshoe crabs on the west side (disturbed) as well as on the east side (undisturbed) of Plumb Beach. The goal of this project was to monitor the population of juveniles in a nursery tidal creek adjacent to the beach, and continue to survey the depleted tidal flats (front beach), to better understand what is happening to the density and distribution of these vulnerable populations. It was hypothesized that there would continue to be more juveniles on the east side of the Beach compared to the west. Timed visual surveys were used to ensure accurate counts of the crabs. Surveyors moved forward slowly, scanning a one meter area in front; each juvenile found was gently placed into a plastic container, measured then returned to the flats. This was repeated for all flats every two weeks from May 20th to August 12th. Results show that there were no juveniles on any of the tidal flats, although there was an increase in juveniles from 2014 to 2015 in the tidal creek, where, 408 (2015) compared to 155 crabs (2014) were observed. Another aspect of the study involved collecting eggs, and my colleague Kelvin noticed that there was an increase in horseshoe crab eggs. However, my results show that juveniles were not observed. Further studies need to

address the population crash observed in 2015. Data should be collected on beach morphology, temperature, and water chemistry to better understand why there is no survival on both sides of the beach. Despite a healthy population of spawning adults and abundant horseshoe crab eggs found on the beach, the lack of survival of juveniles poses a conservation challenge.

Synthesis of Pyrrolidinium Ionic Liquids. Chanele Rodriguez[1], Sharon Lall-Ramnarine[1], Suraj Shiman[2], James F. Wishart[2], Nicole Zmich[2] and Edward W. Castner, Jr.[3], Queensborough Community College, Bayside, NY; [2]Brookhaven National Laboratory, Upton, NY and [3]Rutgers University, Piscataway, NJ.

Ionic liquids (ILs) are low melting salts composed of cations and anions of dissimilar sizes that are selected to obtain desired properties. Their thermal stability, low vapor pressure, and high conductivity allow them to be used as alternative solvents in a variety of applications such as in supercapacitors, batteries, solar energy conversion and for the storage and clean-up of nuclear waste. However, their high viscosities impede their adoption in many large scale processes. Ether side chains have been shown to lower the viscosity of ILs but there is a lack of understanding of the structural organization of the ions that gives rise to this property. In this project, we have synthesized a series of ten pyrrolidinium ionic liquids bearing ether and alkyl side chains of varying lengths (4 to 10 atoms in length). Their physical properties, such as viscosity, conductivity and thermal profile were measured and compared. X-ray diffraction was also used to study the intermolecular interactions between the ions by collaborators at Rutgers University. Results reveal a dramatic decrease in viscosity with the substitution of alkoxy (ether) side chains for alkyl side chains on the cation. However, as the length of the ether chain increases there is negligible change in the viscosity (of about 50 cP). In contrast, a consistent increase in the viscosity was observed as the length of the alkyl side chain increases. All of the ILs synthesized are room temperature liquids and those containing ether chains did not crystallize upon cooling. These results provide significant insight on the choice of starting materials for researchers designing ILs for specific applications. Incorporation of the most readily available ether side chain into the cation will result in a dramatic reduction in the viscosity of the IL. Chanele Rodriguez is a participant in the QCC NIH Bridges to Baccalaureate Program.

A Phosphorus Sediment Storage Assessment of Lake Hopatcong (NJ). Alessandra Rossi, Kevin Olsen and Meiyin S. Wu, Montclair State University, Montclair, NJ.

The New Jersey Department of Environmental Protection (NJDEP) has identified Lake Hopatcong (NJ) as being impaired because of high phosphate concentrations. Examples of potential sources of phosphorus are surface runoff from the watershed and leakage from septic systems. When a nutrient like phosphorus (but also nitrogen) is present in excess, it causes eutrophication, algal blooms, and invasive plant species usually overgrow and lead to the loss of native species. The objective of this study was to assess sediment phosphorus storage at Lake Hopatcong in order to identify areas with high phosphorus storage or phosphorus hot spots. We sampled sediment at 157 pre-selected study sites, throughout the lake basin. The phosphorus in the samples was extracted by acid digestion in autoclave, and analyzed using a Flow Injection Analyzer (FIA). We found 16 sample points (about 11% of the total samples) belonging to the hot spots category (Total phosphorus TP>4 g/kg of dried sediment). The lake-wide average of sedimentary phosphorus concentrations and the assessment of the hot spots, allowed us to identify areas that might be prioritized for future remediation, and areas where remediation measures performed in the past had a positive outcome.

Antibacterial Activity of Tea Tree Oil, Eucalyptus Oil, and Lavender Oil on Planktonic and Biofilm Cultures of *Staphylococcus epidermidis.* Monserratto Ruiz and Kathleen Bobbitt, Wagner College, Staten Island, NY.

A break in the skin due to a minor scratch or deep wound results in the invasion of microorganisms at the site. Commensal skin organisms, such as *Staphylococcus epidermidis,* that are normally considered nonpathogenic are capable of becoming pathogenic upon entering the site. Due to *S. epidermidis'* ability to form biofilms, its increased level of resistance to antibiotics, and its increased association with hospital-associated infections treatment has become difficult. The ideal topical antimicrobial agent to treat a wound would include periodic reduction of bacterial contamination, as well as the removal of soluble debris without altering the cellular activities that are essential for the wound to heal. Essential oils are increasingly being used as topical antimicrobial agents because they avoid systemic toxicity and side effects, as well as decreasing the formation of bacterial resistance. The objective of this study was to test the antibacterial activity of tea tree oil, eucalyptus oil, and lavender oil on planktonic and biofilm cultures of *S. epidermidis*. The broth microdilution assay was used to determine the antibacterial effects of the three essential oils. Biofilm susceptibility was determined by staining the biofilms with crystal violet. Absorbance measurements (A_{490}) were taken at 24 and 48 hours for the planktonic and biofilm cultures of *S. epidermidis*, respectively. Tea

tree oil, eucalyptus oil, and lavender oil all exhibited antibacterial activity against *S. epidermidis* in planktonic cultures. However, they did not demonstrate antibacterial activity against the biofilm cultures of *S. epidermidis*. As a result, further studies are required to determine their efficacy against biofilm cultures of *S. epidermidis*.

Foraging Efficiency of Immature *Blatta laterialis and Blatta germanica* in Simple and Complex Environments. Stefania Ruiz and Scott L. Kight, Montclair State University, Montclair, NJ.

Foraging involves the time and energy an animal expends while searching for resources. Foraging is considered optimal when resource gain maximally exceeds the cost in time and energy of searching for the resource. In this study, I compare foraging behavior of two cockroach species invasive to North America: the Turkestan cockroach, *Blatta lateralis*, and the German cockroach, *Blattela germanica.* The German cockroach is presently invasive in the Eastern USA whereas the Turkestan cockroach is invasive in the southern USA. I studied how each species uses shelter, food and water resources in two 20x20x8 cm square arenas: an open arena with no barricades versus an arena containing a maze formed from interior walls. In each arena, food/water were located in a corner opposite the location of a small harborage shelter. I observed immature cockroaches of both species for 30 minute trials in the following conditions: non-maze isolated, maze isolated, and paired with the opposite species in both arenas. There were significant differences between species in how they allocated time to harborage versus food/water versus exploring the arena. Social state (alone versus paired) and arena complexity were also associated with foraging behavior. These differences in foraging behavior may be important for understanding differences in the ecological invasiveness of different species.

Development of Cathepsin S Inhibitors Using Ugi Reaction. David Salazar[1], Aisha Ashfaq[1], Lilia Zhahalyak[2] and Sanjai Kumar[2], [1]Queensborough Community College, Bayside, NY and [2]Queens College, Flushing, NY.

Cysteine Cathepsin S (CatS) of the Clan C1 cysteine proteases is a lysosomal protease that has been found to be expressed in the cells of the auto-immune system, such as macrophages, B cells, and dendritic cells. Cystein cathepsins degrade biological molecules not only intracellularly but extracellularly as well. Out of the 11 cysteine cathepsins that have been discovered, Cathepsin S (Cat S) is a dominant member which can function in a wider pH range. The aberrant over expression of CatS in the Homo sapiens has been linked to a variety of diseases associated with an elevated immune response. As a result, by making use of targeted inhibition of CatS, much benefit could be gained in treating diseases such as asthma, and emphysema. In this investigation a small library of compounds were synthesized by making use of the Ugi Four-Component Reaction. Ugi-4CR, while having its economic and ecofriendly advantages can prove as a successful synthetic methodology. The synthesized library is currently being screened against recombinant CatS, and it is anticipated that a highly potent and selective CatS inhibitor will emerge from this study. David Salazar and Aisha Ashfaq are participants in the NIH Bridges to the Baccalaureate Program at Queensborough Community College.

The Effects of *Salvadora persica* (Miswak) on Biofilm Formation in Cariogenic Species *Streptococcus mutans.* Monique Salmon and Jill Callahan, Saint Peter's University, Jersey City, NJ.

Antibiotic resistance among microorganisms has rapidly increased in recent years. It is therefore important to find alternative and natural treatments for their control. Throughout history, the chewing stick has evolved into the modern toothbrush. Nevertheless, in some areas of the eastern world the chewing stick is widely regarded as an affordable, readily available, and easily accessible means of dental hygiene. This study examines the effect of chewing sticks on biofilm development in the cariogenic species *Streptococcus mutans*. *S. mutans* readily adheres to the surface of the teeth, and grows within the oral biofilm known as dental plaque. There, *S. mutans* functions by lowering the oral pH, resulting in the erosion of tooth enamel. If left untreated over a period of time, this breakdown may result in dental caries. In this investigation, polystyrene microtiter well plates were used to assess biofilm formation by *S. mutans* grown in a chemically defined sucrose-based media. Developing biofilms were exposed to various concentrations of *Salvadora persica* (miswak). Following incubation, wells were examined for biofilm formation, using a semi-quantitative standard crystal violet assay. Our findings indicate that miswak inhibits the growth of *S. mutans* biofilms in a dose-dependent manor. The data obtained provide evidence miswak contains antimicrobial agents that inhibits the growth of cavity forming plaque. Although miswak is accepted as a mean of oral care by the World Health Organization, it still has not made an impression on the western world. This project aims to examine natural treatments for dental caries and other biofilm infections.

The Effects of Invertebrate Colonization on Water Flow Around Pier Pilings: Implications on Homeland Security. Kaylee Saltos[1], Naysha Angellucci[1], Allison M. Fitzgerald[1], Jon Miller[2] and Andrew Rella[2], [1]New Jersey City University, Jersey City, NJ and [2]Stevens Institute of Technology, Hoboken, NJ.

Fouling also known as the settlement and growth of marine plants and organisms is a common technique used today as a form of observing underwater life. Fouling can occur on many types of surfaces and structures such as ships, piers, oil rigs, rocks, and crevices. Underwater structures are impacted by fouling organisms in the manner that they grow over time. In the same way that pier pilings are naturally impacted, this project's purpose serves as a 3D lateral profile simulation to show how species and abundance change in size, type, and rate and how water flow differentiates between a naturally fouled pier piling and artificially made substrates. Various parameters such as biofouling, density, percent coverage, and drag of pilings and settlement plates were observed and tested in this process of experiment in order to better understand a 3D simulation of what would naturally occur on living shorelines and natural marine structures and pilings. The project will in turn, resolve homeland security's general ideas of how to protect piers from changes in harsh environment conditions that can potentially destroy or alter their natural habitat. Colonization rates of fouling organisms on different substrates and changes in water flow around fouled pier pilings varies depending on the type of substrate. Considering this, it is hypothesized that the rate of settlement and colonizing organisms will differ based on substrate type, species, and time and in turn, fouling creatures can cause impact on any structures placed in water and the water flow around it. The change of water flow around certain pilings can cause more stress on underwater structures and organisms depending on specific types of fully colonized pilings.

Engineered Cartilage Oligomeric Matrix Protein Based Agents for the Treatment of Osteoarthritis. Nicole L. Schnabel[1], Albert S. Agustinus[1], Liming Yin[1], Takeshi Minashima[2], Thorsten Kirsch[2] and Jin K. Montclare[1,3]. [1]NYU Tandon School of Engineering, Brooklyn, NY, [2]NYU Langone Medical Center, New York, NY and [3]SUNY Downstate Medical Center, Brooklyn, NY.

Osteoarthritis (OA), a degenerative joint condition, can be attributed most commonly to traumatic injuries, causing post-traumatic OA (PTOA) and degradation due to age. Symptoms arise in response to the thinning of articular cartilage between bones, caused by the chondrocytes' imbalance between synthesis and degradation of extracellular matrix (ECM) components, resulting in a decrease of the synovial fluid's viscosity and therefore an increased chance of the bones grinding against one another. The degradation of the cartilage ECM can be directly linked to the small molecule, all-*trans* retinoic acid (ATRA), indicated by significantly high levels present in the synovial fluid of OA affected joints. ATRA is capable of increasing the expression of matrix metalloproteinase-13 (MMP-13), in addition to decreasing the expression of collagen type II. The effects of ATRA on the joints can be inhibited by BMS493, a pan-retinoic acid receptor inverse agonist. However, free BMS493 can be easily degraded and hence presumably has rapid clearance in physiological conditions. Moreover, this hydrophobic molecule has low solubility in aqueous buffers. Therefore, a non-collagenous glycoprotein, cartilage oligomeric matrix protein (COMP), is proposed to be used as a drug delivery vehicle herein. The coiled-coil domain of COMP (COMPcc), a self-assembling homopentamer possessing a hydrophobic cavity has been reported to bind to several hydrophobic ligands, such as vitamin A, vitamin D and curcumin. We investigate the impact of BMS493 on COMPcc structure, stability and binding capacity.

Stromal Cell Interactions with Epithelium in a Model of Lung Injury. Jeffrey Sebrow, Namita Sen, Mathew Lubin and Yakov Peter, Yeshiva University, New York, NY.

In the absence of a multipotential stem cell in adult lungs, cooperative stem/progenitor cell development is required for compensatory growth. Characterization of the cells and the signals involved in organ repair would significantly contribute to our understanding of lung regeneration. Utilizing a method previously reported by our laboratory isolating a mixed population of lung progenitor cells with proliferative and differentiation properties, we studied the molecular phenotype, cell cycle, and protein expression of anchorage-dependent cells (ADC) and anchorage-independent cells (AIC) by real-time polymerase chain reaction (RTPCR), flow cytometry, protein microarray, and immunofluorescence. ADCs display a more committed epithelial cell phenotype as observed by increased *Sftpc* (over 400-fold; $P<0.05$), *Cxcl1* (over 50 fold; $P<0.05$), and *Mmp3* (over 30-fold, $P<0.05$) expression. ADCs were also shown to coexpress the SFTPC and SCGB1A1 markers, specific for lung epithelial progenitor cell types. In contrast, mesenchymal/ myofibroblastic progenitor cells reside in suspension. At day 7, both cell subsets demonstrated proliferative activity, with 15-17% displaying an increased DNA content (4N) reflective of the G2/M phase. ADCs produced and secreted the bulk of paracrine factors which included the osteopontin/secreted phosphoprotein 1 cytokine and the insulin growth factor binding protein 3. These findings suggest that compensatory growth involves multiple progenitor cell types and that, together, these cells undergo a complex pattern of maturation and differentiation. Insights into the processes of progenitor cell development and their interactions may lay the foundation to understanding organ regeneration and mechanisms of disease pathogenesis.

Identification and Cloning of Pyrexia Homologs from *Hydra*. Kathereen Palencia Serna and Susan McLaughlin, Queensborough Community College, Bayside, NY.

Hydra is one of the most primitive metazoans with a nervous system. Despite its simplicity, it is capable of responding to many different types of sensory stimuli, including temperature, which regulates hydra sexual differentiation, development and behavior. Transient receptor potential (TRP) channels are a diverse superfamily of channels that function as polymodal cell sensors. Thermosensitive TRP channels include members of the TRPV, TRPM and TRPA subfamilies. TRP channels regulate thermosensation in a wide variety of animals, and it is therefore possible that TRP channels also regulate temperature responses in *Hydra*. The focus of this project was to identify potential thermosensitive TRP channels in *Hydra*. A blastp search was conducted to identify homologs of the *Drosophila* pyrexia channel in the hydra genome. In *Drosophila*, pyrexia is involved in temperature sensing and circadian entrainment to temperature cycles. Three potential pyrexia homologs were chosen for further investigation. RTPCR was used to amplify segments of these genes; PCR products of the correct size were obtained for two genes. The PCR products were gel-purified and ligated into the vector pGEMT-Easy and the ligated PCR products were used to transform competent *E. coli*. Plasmid DNA was isolated and screened for inserts by restriction digest analysis. The identity of the pyrexia homologs was confirmed by sequencing. The presence of putative pyrexia homologs in the hydra genome suggests that thermally sensitive behaviors in hydra could be regulated by pyrexia proteins. Future experiments will involve (1) the identification of additional putative thermosensitive TRPs in the hydra genome and (2) behavioral experiments to test the effect of the TRP-inhibiting chemicals on hydra thermal sensitivity. Kathereen Palencia Serna is a participant in the NIH Bridges to the Baccalaureate Program at Queensborough Community College.

Determining the Genetic Pathways Involved in Cell Death of Copper Treated *Saccharomyces cerevisiae.* Haseeb Shah and Nidhi Gadura, Queensborough Community College, Bayside, NY.

Copper surface alloys can act as antimicrobial sanitizing agents that kill bacteria, fungi, and some viruses. While the antimicrobial properties of copper have been known for centuries, the specific genetic pathways involved in copper induced cell death of microorganisms still remain unknown. Studies from our lab showed that cell death in bacteria and yeast that occurred soon after contact with copper alloys, had a correlation with increased levels of lipid peroxidation. This led us to our hypothesis that if lipid peroxidation can be induced in cells upon contact with copper, then there must be specific genetic pathways involved in microorganism's response that cause them to react this way. A Saccharomyces cerevisiae FLEXgene ORF collection in the BY011 expression vector was obtained from the Harvard Institute of Proteomics (HIP) which contained 5530 clones. The clones differentiated from one another by the overexpression of an ORF. A high throughput genomic library screening strategy was used for screening the library for survivors on lethal doses of copper. Previous studies from this project indicated that the majority of cell death occurred in wild type Saccharomyces cerevisiae strain W303 at 10mM CuSO4 concentration between 40-50 minutes. Screening the library for survivors for the lethal dosage so far has uncovered a transcription factor FKH2, protein kinase C involved in maintenance of cell integrity RLM1and POS5 gene required for the response to oxidative stress. After the screen is complete, it should help reveal the genetic pathways involved in the copper induced cell death. A better understanding of the genes involved in this pathway could help develop new medical advancements in fighting harmful microorganisms. This project receives funding from the United States Department of Education MSEIP grant to Dr. Gadura.

Maternal Behavior in a Serotonin-Deficient Context: Continuing Analysis of the *Pet-1* Knockout Mouse. Sapna Shah and Jeffery T. Erickson, The College of New Jersey, Ewing, NJ.

Effective maternal care in rodents depends in part on ultrasonic vocalizations by the pups that trigger survival-promoting behaviors by the dam. The ability of pups to produce effective calls and the ability of dams to hear and respond appropriately to these calls are crucial since the pups absolutely depend on the dam for survival during the first few postnatal weeks. Defects in either call transmission or call receipt could lead to sub-optimal maternal care and increased pup mortality. Recently, *Pet-1* gene deletion (*Pet-1*$^{-/-}$) has been associated with a 70% loss of central serotonin neurons and completely ineffective maternal behavior. Specifically, all pups born to *Pet-1*$^{-/-}$ dams die within five days of birth and approximately 25% of *Pet-1*$^{-/-}$ pups born to normally behaving *Pet-1* heterozygous (*Pet-1*$^{+/-}$) dams die within the same time frame, although the reasons for this increased neonatal mortality are not known. We hypothesize that abnormal call production and/or call reception may contribute to this mortality. To determine whether *Pet-1*$^{-/-}$ pups produce abnormal calls, we recorded and characterized distinct ultrasonic vocalizations from individual *Pet-1*$^{+/+}$, *Pet-1*$^{+/-}$, and *Pet-1*$^{-/-}$ pups during brief daily periods of isolation in an anechoic chamber, from the day of birth to postnatal day five. Our initial analysis indicates that the distribution of call types was similar between wild type and Pet-*1*$^{-/-}$ pups shortly after birth (postnatal day 1) but the call type distribution diverged significantly by the fifth postnatal day. In addition, knockout pups tended to produce fewer calls compared to wild type littermates during the first 2 minutes of the 10 minute

recording period. We anticipate that the results of these studies will provide important insights and inform future experiments aimed at fully understanding the connection between the brain serotonin system, ultrasonic vocalizations, and maternal behavior. Supported by a TCNJ Support for Scholarly Activity award (JTE).

The Effect of Semi-Precocial Development on the Movement of Juvenile Common Terns (*Sterna hirundo*) from the Nest. Margaret Shaw and Brian Palestis, Wagner College, Staten Island, NY.

The objective of this observational study was to examine how the semi-precocial development of common terns (*Sterna hirundo*) affects distance of chicks from the nest as they age. Semi-precocial development means that chicks can move from the nest soon after hatching and hatch with downy feathers already present, but that extensive parental is still needed until they are able to capture food on their own. Over the course of two months, three sites in Barnegat Bay, off Long Beach Island, New Jersey were observed to examine *S.hirundo* chick movement from the nest. It was hypothesized that as chicks aged, fewer chicks would be found close to the nest. We also predicted that the presence of large bodies of water would have an effect on chick movement, however it was determined that distance to water was not a significant factor. Observations of *S.hirundo* chicks from five different age groups supported the primary hypothesis that chicks move from the nest as they mature. In the first age group of 1 to 3 days, about 79% of the chicks were found in their nest. Before the chicks reached two weeks only 10% of the chicks found were at their nest, and by the time the chicks were about to fledge, no chicks were found at their nest. As the chicks aged, moved from their nest sites and hid, it became more difficult to find them. In addition, many chicks were lost to storm floods. Despite these shortcomings, enough mature chicks were observed to determine that the need to stay near the nest is greatly reduced as *S.hirundo* chicks age, due to their ability to seek cover shortly after hatching. This work was supported by the John Deane Fund for Environmental Sciences and Wagner College.

The Biodiversity and Ecology of Nematocerous Diptera (Insecta) in Alley Pond Park, Queens, New York. Scott C. Sherman, James A. Timbilla, and Gheorghe Proteasa, Queensborough Community College, CUNY, Bayside, NY.

Urbanization has destroyed many natural habitats for wild plants and animals. Some cities, including New York City, have parklands that contain natural or semi-natural areas that provide habitat for native plants and animals. Unfortunately, natural areas in some urban parks are still not protected from development and are being destroyed to make more roads, buildings, parking lots, and recreational facilities. There are many reasons to protect, maintain, and restore natural habitat in cities. Foremost among the reasons is the intrinsic value of the diversity of life itself; other reasons include providing flood and erosion protection, increasing the productivity of nearby fisheries, maintaining populations of essential pollinators, and providing an environment that encourages low impact outdoor activities (e.g., hiking, orienteering, birdwatching, and botanizing) and that helps students and the public acquire greater appreciation and knowledge of life and the natural world. We are studying the biodiversity and ecology of Diptera in Alley Pond Park in Queens, New York. Diptera are of great positive biological and economic importance as pollinators of plants; decomposers and recyclers of organic material; predators, parasites, and parasitoids of noxious invertebrates; components of food chains; and indicators of the health of ecosystems. Diptera are used for medicinal maggot wound therapy, in forensic science investigations, and in many different types of scientific, medical, and technological research. The zoological order Diptera is traditionally divided into two primary groups: the nematocerous Diptera and the brachycerous Diptera. There are over 30 currently recognized extant zoological families of nematocerous Diptera. The nematocerous Diptera include black flies, crane flies, gnats, March flies, midges, mosquitoes, moth flies, sand flies, and other types of flies. Our research shows that Alley Pond Park contains a diversity of nematocerous Diptera including the zoological families Cecidomyiidae, Chironomidae, Culicidae, Mycetophilidae, Sciaridae, Simuliidae, and Tipulidae.

A Bioinformatics Study on the Binding Between the Tea Polyphenol EGCG-S and HSV-2 Glycoproteins. Peter Stamos, Siti Ayuni, Mohamed Yussof, Sandra D. Adams and Lee H. Lee, Montclair State University, Montclair, NJ.

Epigallocatechin gallate-stearate (EGCG-S) is a lipophilic green tea polyphenol modified from EGCG that exhibits potent anti-tumorigenic and broad antiviral properties. It has been suggested that EGCG prevents the attachment of Herpes simplex virus 1 (HSV-1) to host cells by inhibiting the binding of the virus to heparan sulfate during the initiation of viral entry. This finding suggests that EGCG may bind to the envelope of HSV, thus preventing binding and entry into susceptible host cells. In this study, bioinformatics tools were used to predict the binding site of EGCG-S to two different glycoproteins on the surface of HSV-2 (gpB and gpD). Further analysis determined which glycoprotein is more favorable for the binding interaction with EGCG-S. *ClustalOmega* alignment was used to determine the homology between the two glycoproteins. Based on this alignment of their amino acid sequences, they are only 22% homologous. The protein structure of gpD was obtained from PDB (accession number: 3SKU), but there is no available crystal structure for gpB. The *SWISS MODEL* protein structure prediction server was

used to develop an *in silico* model of gpB based on its high degree of amino acid sequence homology with gpB from HSV-1, which has a known structure. Based on the analysis done by Autodock Vina and Pymol, the results suggest that EGCG-S forms 10 hydrogen bonds with the following amino acids: 107 (Gln), 536 (Asn), 540 (Arg), 555 (Arg), 617 (Asn) 644 (Tyr) and 657(Arg) on gpB, resulting in a favorable binding affinity of 8.4 kcal/mol, or -35.1 kJ/mol. Further simulations must be carried out on gpD to determine the favored binding of EGCG-S.

Integrated Taxonomy: Traditional Approach and DNA Barcoding for the Identification of Native Plant Species at Bronx Community College. Irving Steel[1], Stephen Mensah[2], Huyen Nguyen[2], Alex Robert[2], Rujin Tian[2] and Martin Fein[2], [1]City College of New York, NY and [2]Bronx Community College, CUNY, Bronx, NY.

DNA barcoding relies on the use of a standardized DNA region as a tag for simple, rapid and affordable species identification. To get hands-on experience on species identification using molecular tools and to explore the genetic biodiversity of New York City, we participated in the Urban Barcoding Project conducted by the DNA Learning Center of Cold Spring Harbor Lab (CSHL). The gene region that is proposed as the standard barcode for plants by CSHL is a ~600 base pair fragment from the RuBisCo (ribulose bisphosphate carboxylase/oxygenase) large subunit (rbcL) located in the chloroplast. We began our investigation by collecting and selecting a total of 10 native plant specimens located in the campus of the Bronx Community College of New York City with the help of two mobile apps (Google Maps and Garden Compass). Next, we successfully optimized the protocols provided by the CSHL to achieve DNA purification, rbcL amplification and sequencing. Finally, we applied bioinformatic tools (sequence alignment; substitution rate and time computation; 3D structure comparison) for DNA-based species identification, protein structure homology modeling and phylogenetic analysis. Our research experience helped us develop a greater appreciation for the DNA sequence based modern taxonomy in urban environments while gaining an introduction to bioinformatics tools.

Methylation Profile in Ovarian Cancer Implicates a Role for GSK3β in Platinum Resistance. Jamie Stern, Britni Hinderhofer, Tyler Walther, Nicholas Branker, Peter Vath, Bryan Massey, Brandon Michaels and Noelle Cutter. Molloy College, Rockville Centre, NY.

Ovarian cancers are highly heterogeneous and platinum based chemotherapy, which induces DNA crosslinking resulting in apoptosis of the cell, is the preferred treatment. However, many patients are intrinsically resistant or quickly develop resistance. Recent evidence suggests that epigenetic deregulation, such as methylation, may be a key factor in the onset and maintenance of chemoresistance. Previous microarray analysis results in our lab correctly identified a subset of about 300 genes that when methylated altered the chemoresistance of the ovarian epithelium cells in culture. Of the genes identified in the analysis, we further characterized one gene, glycogen synthase kinase 3 beta (GSK3β), a serine/threonine kinase, to determine if we could elucidate the mechanism by which it increased resistance. Using several in-vitro assays, we determined that the loss of GSK3β decreased the level of apoptosis in response to carboplatin. Furthermore, in cells with reduced GSK3β, tumorigenesis was increased. These results implicate an important role for this Wnt/β-catenin enzyme in the regulation of chemoresistance. Moreover, GSK3β expression might represent a therapy response predictor and could be a future therapeutic target for ovarian cancer. In addition, methyl-transferases may present a valid treatment for increasing carboplatin sensitivity in resistant patients.

Examining the Effect of Anti-Phospholipid Antibody on MicroRNA Regulation of Tissue Factor in Breast Cancer Tumor Progression. Irene Sun[1], Elaine Lin[2], Yuanyuan Wu[2] and Andrew Van Nguyen[1], [1]Queensborough Community College CUNY, Bayside, NY and [2]Albert Einstein College of Medicine, Bronx, NY.

Tissue Factor (TF), a transmembrane glycoprotein known originally as the initiator of blood coagulation cascade, was recently shown to be involved in cell signaling and angiogenesis. Dr. Andrew Nguyen along with his collaborators recently demonstrated that anti-phospholipid antibody (aPL) stimulates TF expression in less aggressive tumor cell lines (MDA-MB-468). In our examination of the mechanism by which aPL stimulation leading to TF up regulation, we have discovered that microRNAs (miRs) play a significant role. We are currently evaluating the effect of aPL treatment on miR106b expression in both MDA-MB-468 and MDA-MB-231 cell lines. We hypothesize that aPL antibody treatment can transform MDA-MB-468 dormant cells to become malignant via increased TF expression by down regulating miR106b by using real time PCR.

Effects of Habitat Degradation on Reproductive Tissue and Reproductive Potential of Eastern Oysters, *Crassostrea virginica.* Bill Surena and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

Habitat degradation within the Hudson Raritan Estuary is a preliminary cause of decline of local aquatic species, such as the eastern oysters, *Crassostrea virginica*. This research aims to find out the effects of habitat degradation on reproductive tissue and reproductive potential of oysters located at Soundview Park, Bronx, NY. Oysters were randomly collected monthly from the site and dissected to determine their sex and to measure condition

index on them. Condition index is a proxy for oyster health that can help determine the effects of environmental factors on oyster meat quality. The results were compared with local (NY) oysters purchased from Whole Foods, which were from non-degraded waters. There were no significant differences with respect to sex ratios between the native oysters and the store bought oysters; however, many of the oysters were found to be indeterminate (no sperm or egg observed in gonad tissue). It is possible these oysters had already spawned (low gonad amount observed) or that they were immature. With respect to condition index, the oysters from the store had a higher condition index than the oysters found at the field sites. This data is important to managers who are to restore oyster populations in degraded areas.

Molecular Approaches in Detecting Cyanobacteria and Their Toxins in Greenwood Lake. Sally Tarabey, Ruchit Patel, Robert Newby Jr., Jose L. Perez and Tin-Chun Chu. Seton Hall University, South Orange, NJ.

Cyanobacteria are photosynthetic microorganisms that are very often associated with the development of harmful algal blooms. Microcystis is one genus of cyanobacteria named after the cyanotoxin that it known to have the ability to produce, microcystin. Algal blooms are developing on drinking and recreational water sources, necessitating the identification of the populations present in order to determine possible toxic contaminations in such sources in order to protect public health. In this experiment, water samples from Greenwood Lake were collected in the summer of months of this year. The raw water samples have been filtered through various filter sizes ranging from 30 to 0.45 μm in order to separate and identify populations present. DNA extractions from the different filters were carried out. The polymerase chain reaction (PCR)-based assays were carried out with both general and specific primers including phyto-specific Psf/Ur, cyanobacteria-specific CPC1f/CPC1r, and microcystin synthetase mcyA-specific Msf/Msr primer sets. Gel electrophoresis was then performed on all PCR products and the positive identification results were sequenced. The results showed the presence of phyto-specific microorganisms and cyanobacteria in the water samples. In addition, the result indicated the presence of microcystis in Greenwood Lake, which may pose a threat for this waterbody.

The Importance of Diptera (Insecta) in Urban Biodiversity and Ecological Research. James A. Timbilla, Gheorghe Proteasa and Scott C. Sherman, Queensborough Community College, CUNY, Bayside, NY.

There has been an increasing interest in urban biodiversity and urban ecology among biologists, conservationists, and the public. Nearly all taxonomic, biodiversity, and ecological studies of Diptera have focused on nonurban environments. Recent studies have shown extensive species diversity of the zoological family Phoridae within the cities of London and Los Angeles, and research in Japan has demonstrated an astonishing diversity of zoological families and species of Diptera living near the center of Tokyo. Diptera are excellent organisms for biodiversity and ecological research because they have adapted to live in most types of environments and microhabitats, and have evolved a wide range of successful feeding strategies including coprophagy, detritivory, exudativory, fungivory, gallivory, hematophagy, kleptoparasitism, microbivory, myiasis, nectarivory, parasitism, parasitoidism, phycophagy, phytophagy, pollenophagy, predation, saprophagy, saprophytophagy, secretophagy, xylophagy, and zoosaprophagy. Our research on the urban biodiversity and ecology of Diptera has shown the presence of a diversity of dipteran families, genera, and species.

Preliminary Survey Results on the Abundance, Host Preferences, and Economic Importance of Horse Flies (Insecta: Diptera: Tabanidae) in Ghana, West Africa. James A. Timbilla and Scott C. Sherman. Queensborough Community College, CUNY, Bayside, NY.

Tabanidae (horse flies, deer flies, and clegs) is a diverse, speciose family of Diptera that is distributed widely in all primary biogeographical regions and has adapted to live in a broad range of habitats. Adult females of most known species are hematophagous and seek blood meals from humans, domestic animals, and wildlife. Tabanidae are vectors of diseases including anaplasmosis, anthrax, equine infectious anemia, loiasis, surra, and tularemia. Their host-seeking and blood-feeding behavior and their ability to transmit pathogens make Tabanidae of considerable biological and economic importance. The Afrotropical Region has a very rich biodiversity of Tabanidae and other Diptera. Reconnaissance surveys about horse flies were conducted in Ghana in West Africa in 2014 and 2015 using a questionnaire written by the two authors. The surveys set out to collect data about the perceived importance of three genera (*Atylotus* Osten Sacken, 1876; *Haematopota* Meigen, 1803; and *Tabanus* Linnaeus, 1758) of Tabanidae to humans and to livestock care. Colored photographs on the survey forms were used to help the respondents identify these genera. Information was gathered through the surveys from agricultural and veterinary extension officers on the occurrence, seasonal abundance, livestock host preferences, and the economic importance of these flies. According to the survey results the flies are most abundant during the wet season from June to September and were noted to attack cattle, sheep, horses, goats, donkeys, and humans. Respondents indicated that the blood-feeding behavior of these flies caused harm to livestock and humans. The economic importance of horse flies in sub-Saharan Africa and prospects for their control are discussed.

The Production of Byssal Threads by *Geukensia demissa* Under Food Limitations. Na'Vonna Turner, Naysha Angelucci, Christian Bojorquez, Kaylee Saltos and Allison Fitzgerald, New Jersey City University.

Ribbed mussels, *Geukensia demissa*, are found locally on the shore line of salt marshes where their byssal threads are used to attach to a *Spartina* stalk. These byssal threads, made up of collagen, are produced from the groove of the mussel foot (Babarro, 2008). The strength of the byssal threads, and their attachment to a substrate, are affected by a large number of factors with one being availability of their food source. In this experiment, the effects of food limitation on the production of byssal threads by the ribbed mussel was investigated. Ribbed mussels were collected from a marsh in Fresh Kills, Staten Island, and brought back to the lab. Three experimental tanks were cleaned, filled with artificial seawater, made to ambient salinity and room temperature, and fed according to the following treatments: high (3ml/24hr), medium (1ml/24hr) and low (1ml/48hr). The number of byssal threads were counted, and the force of attachment of the threads to a substrate, glass plate, were measured using the Dual force sensor weekly for one month. When under stress the trend of towards byssal thread production and food stress is observed. Byssal threads were also preserved to examine protein structure under an SEM microscope.

The Use of Environmental Bacteriophages from Waste Water in the Control of *Salmonella typhimurium* on *Gallus gallus domesticsus* and *Lactuca sativa.* Michael L. Ufnowski and Kathleen Bobbitt, Wagner College, Staten Island NY.

Salmonella is a common food borne pathogen most notably causing gastrointestinal distress. In recent decades the prevalence of this pathogen has increased because of centralization of the food packing industries. The increase in cases indicates more actions to be taken for reducing the Salmonella content of food. One way of reducing the numbers is by the use of bacteriophages, these are viruses responsible for killing bacteria. Some commercial makes have isolated phages able to reduce the *Salmonella* content of food. The present study looks at doing this by using phages isolated from a waste treatment plant to reduce the numbers of *Salmonella typhimurium* on ground breast meat from *Gallus gallus domesticsus*, commonly referred to as chicken and the inner leaves of *Lactuca sativa*, or lettuce. Phages were isolated from the joint meeting of Essex and Union counties waste treatment plant by using *S. typhimurium* ATCC 14028 in LB broth. The sample were then centrifuged for 30 minutes at 3000g and filtered through a 0.22 µm corning filter. The samples were diluted 1:10 to a final concentration of 10^{-7}. An agar overlay was done to titer the phages. The final concentrations of the phages achieved were $3.5*10^{8}$ PFU /mL. Three distinct phages were found. Then 100µl of each phage was added to 5 ml of water and 1 g of either *Gallus gallus domesticsus* or *Lactuca sativa* and incubated at 37º C for 24 to 48 hours. The samples were blended in 99ml of water and diluted 1:100 to a final concentration of 10^{-6}. The samples were pour plated using HE agar. The results showed a decrease at the 24 hour time point and no difference at the 48 hour time point. This research shows environmental phages can be used for the temporary reduction of *Salmonella* on food.

Evaluation of Synergistic Antibacterial Activity of Natural Compounds and Antibiotics. Jonathan Valsechi-Diaz, Garrett Almeida and Tin-Chun Chu, Seton Hall University, South Orange, NJ.

Every year, over two million people are infected with antibiotic-resistant bacteria in just the United States alone. It costs more than eight billion dollars annually for US healthcare system to combating methicillin-resistant *Staphylococcus aureus* (MRSA). Natural compounds, such as black tea polyphenol theaflavins, green tea extract and Chinese knotweed, are known to possess many medical and health benefits. In this study, the synergistic antibacterial effects of eleven antibiotics and three natural compounds were evaluated. Three Gram negative bacteria, *Enterobacter aerogenes, Escherichia coli*, *Proteus vulgaris*; two Gram positive bacteria, *Bacillus* cereus and *Staphylococcus epidermidis,* were included in this study. Eleven antibiotics including Ampicillin (AM10), Chloramphenicol (C30), Erythromycin (E15), Gentamycin (GM10), Kanamycin (K30), Neomycin (N30), Penicillin (P10), Streptomycin (S10), Triple Sulfa (SSS250), Tetracycline (TE30) and Vancomycin (VA30) were selected for Kirby-Bauer disc diffusion assays. The results indicated that theaflavins were able to increase the antibacterial activity from ~10% to ~200% when combined with 10 out of the 11 antibiotics tested. Green tea extracts showed synergistic antibacterial activity with all 11 antibiotics ranging from ~10% to ~200%. Chinese knotweed also displayed ~10% to over 200% synergism when combined with 9 out of 11 antibiotics. The results provide evidence that each of the three natural compounds/antibiotics combination could be novel natural antimicrobial agents and serve as antibiotic alternatives.

The PKD2 Activator Triptolide Stimulates Cnidocyte Discharge in *Hydra.* Maria Villa and Susan McLaughlin, Queensborough Community College, Bayside, NY.

Hydra is a primitive metazoan belonging to Phylum Cnidaria, and like other cnidarians is characterized by the possession of cnidocytes (stinging cells). Most cnidocytes are located on the hydra tentacles, where they are organized along with sensory cells and ganglion cells into battery complexes. The function of the battery complexes is to integrate mechanical, chemical and photo stimuli for the regulation of cnidocyte disharge. The molecular mechanisms regulating the discharge of cnidocytes are not yet fully understood, but it is known that discharge

depends on extracellular Ca^{2+}. TRP channels are a diverse superfamily of nonselective cation channels. The most abundant hydra TRP subfamily is the polycystin (PKD2) subfamily and has been shown to be involved in the transduction of both mechanical and chemical stimuli. *In situ* hybridization experiments have shown that a PKD2 gene is expressed in the ectoderm of hydra tentacles. The presence of PKD2 in the tentacles, its ability to be mechanically gated and its activity as a Ca^{2+} channel suggests it could play a role in cnidocyte discharge. The focus of this project was to implement a cnidocyte capture assay to examine the effect of PKD2 inhibitors and activators on the discharge of cnidocytes. A gelatin-coated probe was used to mechanically stimulate the hydra tentacles; discharged cynidocytes were captured in the gelatin and subsequently counted. The PKD2 activator triptolide increased the number of cnidocytes discharged upon mechanical stimulation. Treatment of the hydra with the non-specific PKD2 inhibitor neomycin dramatically inhibited the number of discharged cnidocytes, but the addition of triptolide with the neomycin removed this inhibition. The results of these experiments support the possibility that a PKD2 protein is involved in the mechanical and/or chemical stimulation of cnidocyte discharge.

Comparison of Cytosine Methylation Between Eastern and Pacific Oysters. Brittney Vincent, Elizabeth Mulligan and Ivan Shun Ho, Kingsborough Community College, Brooklyn, NY.

In our project we conducted experiments on two organisms, the Pacific oyster *Crassostrea gigas* (*C. gigas*) and the Eastern oyster *Crassostrea virginica* (*C. virginica*). The gene we are observing in these oysters is macrophage expressed protein 1-like protein (MPEG1LP). This is thought to be similar to a protein, MPEG1, which evolved into perforin in humans. In oyster, this protein's function has not been determined, however it has been postulated to have cytolytic functions and immunity. Its functions in immune responses intrigued us because of the difference in immunity to DERMO between *C. gigas* and *C. virginica*. Previous studies have examined the methylation of MPEG1LP in *C. gigas*. We wanted to compare the methylation of this gene between the two species. Our hypothesis is that the methylation of the MPEG1LP gene between the two oyster species is different due to their difference in immunity to DERMO. To determine the methylation pattern of MPEG1LP in both oyster species, we used Methylation Sensitive PCR (MSP) on both species' genomic DNA. DNA methylation enables the proper control of gene expression and silencing. Observing the methylation pattern of this stress-related gene may give insight on why *C. virginica* are susceptible to environmental stresses. Our results indicated that methylation of MPEG1LP is similar in both *C. gigas* and *C. virginica*, which does not support our hypothesis. This work was supported by grant 2R25GM062003-13 of the Bridge Program of the NIGMS and grant 0537-15-1091 of the CSTEP program of the NYSED.

Effects of Dietary Supplements on Blood Cell Tumors in Drosophila. Jermaine Wilson, Ligny Lugo and Chiyedza Small, Medgar Evers College, Brooklyn, NY.

Many signal transduction pathways have been implicated in the development of human diseases such as cancer. One of these disease-related pathways is Janus kinase (JAK)/signal transducer and activator of transcription (STAT). Having only one JAK (Hopscotch), drosophila is used to study the functional requirements of the JAK-STAT pathway across species. Drosophila Hopscotch tumorous-lethal (hop^{TUM-L}) mutation acts as an activated oncogene causing hematopoietic neoplasms called melanotic tumors to form due to over proliferation of cells. Dietary supplements such as Selenium and Folic Acid play important roles in keeping the body healthy and are used by millions of Americans every day. Selenium is an essential mineral antioxidant with anti-carcinogenic properties. Folic Acid helps the body break down, use, and create new proteins. Studies suggests that people who consume lower amounts of selenium could have an increased risk of developing cancers of the colon and rectum, prostate, lung, skin, esophagus, and stomach. Whether selenium supplements reduce cancer risk is not clear. The role that Folic acid plays in cancer prevention is also unclear. More research is needed to understand the effects of selenium and other dietary supplements on cancer risk. Our studies investigate the effect of Selenium and Folic Acid in food on the development of melanotic tumors in Drosophila JAK-STAT mutants. Understanding the role of these supplements in this mutant pathway-specific context may shed light on their functions in cell proliferation, differentiation and growth. Results from these ongoing studies will be presented.

Green Tea Polyphenols as Synergistic Agents to Enhance Antibiotic Erythromycin Activity on Bacteria. Siti Ayuni Mohmaemed Yussof, Chris Chen, Amy Melok and Lee H Lee, **Montclair State University, NJ.**

Green tea is formulated from unfermented leaves of *Camellia sinensis* and commonly found in major Asian countries such as China and Japan. The polyphenols extracted from the leaves of the green tea plant have shown to have anti-inflammation, anti-cancerous, antioxidant, antibacterial and anti-viral effect. The increase of antibiotic resistance infection has led the science community to search for a novel alternative therapy to combat such infection. Three different bacteria: *Pseudomonas aeruginosa, Gram-negative; Bacillus megaterium,* Gram *positive and Mycobacterium smegmatis, acid-fast bacteria* were used in this study. Green Tea Polyphenols (GTP), Lipophilic Tea Polyphenols (LTP), Epigallocatechin-3-gallate (EGCG) and Epigallocatechin-3-gallate-Sterate (EGCG-S) were used along with Erythromycin (E) at different concentrations individually or in combination to determine if the tea polyphenols can produce synergistic effect on Erythromycin against these bacteria. Disk diffusion test was first used to determine bacteria susceptibility to Erythromycin, tea polyphenols individually or in

combination. Colony forming unit test (CFU) was used to determine the viability and percentage of inhibition of the bacterial growth. The results indicated that the best synergistic result for both *P. aeruginosa* and *B. megatarium* is the combination of E15 ug/ml and EGCG-S 25 ug/ml, with inhibition of 95% and 96% respectively. For *M. smegmantis,* the best combination is E15 ug/ml and EGCG-S 50 ug/ml, with inhibition of 92%. The result shows a potential for the polyphenols to be used alongside antibiotic to overcome antibiotic resistant infection. Further study need to be done to determine the application of the combination study in the inhibition of biofilm formation and also to determine the mechanism of these tea polyphenols on killing these bacteria.

Understanding mRNA Trafficking and its Role in Localized Translation in the Nervous System. Oscar J. Zagalo[1] and Kevin Czaplinski[2], [1]Queensborough Community College, Bayside NY and [2]Stony Brook University, Stony Brook NY.

Localized protein synthesis plays an important role in vertebrate nervous system development and function. For instance, neurons actively traffic mRNA in order to reinforce useful connections between synapses. However, the molecular details as to how a particular mRNA traffics in mammalian cells are limited. To understand mRNA trafficking at the molecular level, we study the β-actin (Actb) mRNA as a model for an mRNA that is actively trafficked in the cytoplasm. For this project we will characterize β-actin mRNA movement in real time within live cultured neurons. To do so we used the bacteriophage MS2 Coat Protein (MCP), which binds specifically to a stem loop in the MS2 RNA genome, called the MCP-binding site (MBS). When the MCP is fused to a yellow fluorescent protein (MCP-YFP) this can be used to image an mRNA engineered to contain MBS stem loops. A mouse with a β-actin allele that is tagged with MBS has been created and our aim was to image this mRNA in primary neurons isolated from these mice. Since primary neuron cell cultures also contain glial cells, our experiment was to create a MCP-YFP protein that would express only in neurons. We created a plasmid that expresses MCP-YFP protein from the promoter of a gene that is only expressed in neurons and not glial cells. We cloned the promoters from the Nov and Htr2c genes into plasmid vectors that could be used to create recombinant lentivirus-like particles (VLPs). These plasmids were transfected into HEK293T-17 cells in order to create recombinant VLPs that will be used to infect primary neuron cultures to express MCP-YFP only in neurons. This work was supported by the NIH Grant GM050070.

Bacterial Communities in Luna Moth (*Actias luna*) Caterpillar Fecal Samples. Stephanie Zapata, Elyssa Barron, Isabella Canal Delgado, Satenik Melkoyan, Gissel Cruz, Theresa Aponte, Sara Lamcaj, John Smalley, Elena Tartaglia and Luis Jimenez, Bergen Community College, Paramus, NJ.

16S rDNA sequencing of bacterial isolates and next generation sequencing (Next-Gen) were used to describe the bacterial community present in **l**una moth (*Actias luna*) caterpillar fecal samples. Microbial DNA was extracted from fecal material. Eubacterial 16S rDNA genes were amplified from fecal material using PCR and the resulting 465 base pair amplicons were sequenced using an Illumina protocol. Sequencing of a 1.5 kilobase fragment of the 16S rDNA of culturable bacterial species showed that most bacteria belonged to the phyla Firmicutes (50%), Proteobacteria (10%), and Actinobacteria (40%). Bacterial densities were 1.6 x 10^9 Colony Forming Units/gram of fecal material. The Next-Gen results showed that the bacterial community of the fecal material was comprised of Firmicutes (26%), Proteobacteria (20%), and Actinobacteria (54%). The predominant culturable bacterial genus was found to be *Bacillus,* while the most abundant bacterial genus detected using Nex-Gen was *Arthrobacter*.

Determining if the Hard Clam (*Mercenaria mercerneria)* is a Vector for MSX (*Haplosporidium nelsoni*) Infection of Eastern Oysters (*Crassostrea virginica*) in Jamaica Bay. Genesis Zea, Gary Sarinsky and Craig Hinkley, Kingsborough Community College, Brooklyn, NY.

The Eastern Oyster (*Crassostrea virginica*) is an economic and ecologically important species. No oysters were known to exist in Jamaica Bay,New York since the 1920's. Previous research conducted by our laboratory, introduced oyster spats into the bay to observe if they could survive in the present-day environment. Two years later some of the oysters were found and verified to have been infected with MSX *(Haplosporidium nelsoni*). Little is known about the life cycle of MSX. There is literature that suggests a vector might be involved. MSX reduces the feeding rates of infected oysters which lead to a reduction of stored carbohydrates. This decrease inhibits normal reproduction. Due to the close proximity of the Eastern Oyster to the Hard Clam (*Mercenaria mecerneri*a), we hypothesize that it serves as a vector for MSX to the Eastern Oyster. Gill and mantel tissues were excised from six clams. The DNA was then extracted from the tissues using a DNeasy Blood and Tissue Kit. The twelve samples were amplified by polymerase chain reaction (PCR) in order to isolate the mitochondrial CO1 gene using the Folmer Primer set. Gel electrophoresis of the amplified material was performed to confirm the correct base pair size of mitochondria CO1 gene (702bp). Twelve additional *Mercenaria mecerneria* samples plus a known for MSX were amplified using the MSXA and MSXB small subunit rRNA primer set. They were subjected to gel electrophoresis to verify correct base pair size for MSX (550bp). The twelve samples were negative for MSX while the control was positive. The amplified materials were sequenced by Elim Biopharmaceutical. The mitochondrial CO1 samples were subjected to a NCBI Blast search that confirmed that the mitochondrial CO1 gene was from *Mercenaria mecerneria*. The results of the series of experiments did not support our hypothesis.

The Growth of an Assessment Culture in Bronx Community College's Biology Department. Seher Atamturktur, Shazia Khan and Richard LaManna, Bronx Community College of CUNY, Bronx, NY.

This paper describes the development and implementation of a course assessment method that allows faculty to utilize common questions, collect meaningful data, and implement the findings to improve student learning. This assessment method is governed by four principles: that it be *automatic, systemic, sustainable and meaningful.* Over the years of honing the process, we have naturally expanded our department's teaching philosophy to include outcomes assessment, and no longer regard it as a mandatory task imposed on faculty. Because the department chair and faculty have come to share the belief and experience that successful student learning requires continual assessment, we have been successful in sustaining rigorous assessment. Consequently, assessment results of the Biology courses are continuously examined and discussed in the department and individual course meetings. The Biology department has made a significant effort to ensure that the learning process—from choosing assessment questions to discussing results—is a collective activity for all faculty involved and that their feedback is valued in making adjustments and providing remedies. Overall, we believe that the Biology department has established an "assessment habit." Our efforts continue to refine our current course level assessment and expand it to program level assessment.

Conquering Test Taking Anxiety: Exploring Positive Outcomes of Group Testing. M. Baralt and A. Lassiter. Berkeley College, Woodland Park, NJ.

Test anxiety has been recognized as a culprit in the performance of students during exams. There is an effect on individuals that is collaterally affecting the physical, emotional and cognitive capacity. Students seemingly do inferior on exams because of the biological response to stress or their failure to properly study and retain information. This strategy intends to dissipate feelings of anxiety and insecurity by directing focus on learning and active engagement. Addiction and Obsession, an upper level liberal arts course, is challenging and the amount of information covered can be tedious. This strategy based group testing style has been very successful in my class and this has been shared by other colleagues. The pedagogical basis for this methodology is supported by the fact that students who tend to do poorly academically lack fundamental meta-cognition skills (Brown et al 2013). Rather than a traditional approach which tends to be unilateral, this system tends to promote a variety of necessary skills. The skills students develop and enhance through this strategy are critical thinking, communication, collaboration and creativity. All students are required to prepare a one page hand-written reference sheet, known as the "Cheat Sheet". Students' meta-cognition skills increase because students use their prior knowledge and connect new information acquired to form a conclusion. "Cheat Sheets" consist of word associations, illustrations, symbols, printed words, and colors. Students learn how to create their "Cheat Sheets" and/or reference sheets after participating in a Learning Styles workshop presented by the Academic Support Center. Creating this "Cheat Sheet" enables students the dual task of writing and memorizing which has been seen advantageous and successful. This strategy enhances cooperative learning and successful work dynamic.

A Preliminary Assessment of the Red Mangrove Population Genetics in a UNESCO Biosphere Reserve. James J. Campanella, Paul A.X. Bologna, Dena Restaino, Matthew Lourenco and Melanie Lawrie, Montclair State University, Montclair, NJ.

We have begun a genetic study of the *Rhizophora mangle* (red mangrove) populations of the UNESCO Biosphere Reserve on St. Johns in the U.S. Virgin Island archipelago. Some of these populations (e.g. Hurricane Hole Bay) have remained protected for generations from excessive weather conditions, such as hurricanes, while others have been severely perturbed by both anthropogenic and atmospheric disturbances (e.g. Coral Bay and Great Lameshur Bay). Because these populations are in an internationally protected zone, we are particularly concerned in how well their genetic diversity has persisted amid these disruptions. So far after employing only three of the seven genetic markers that we intend to use, we have found evidence that change in the microsatellite loci of these mangrove may follow the Stepwise Mutation model of Cavalli-Sforza. Also, the Tampa Bay ecotype is strongly supported to be an outgroup from which the St. Johns populations have genetically drifted. All the populations appear to be inbreeding depressed and genetic diversity is minimal. At the upcoming conference we will have further data on effective population size and bottlenecks in the stressed populations.

Is A Picture Worth a Thousand Lectured Words? Drawing to Learn in the College Biology Classroom. A. Dell[1] and I. Ellison[2], [1]St. Francis College, Brooklyn, NY and [2]Mercy College, Dobbs Ferry, NY.

A high nationwide drop-out/failure rate from first year biology courses suggests that educators must do better to reach students of diverse backgrounds and learning styles. However, given the breakneck pace of many introductory courses, instructors may feel at a loss as to how to escape the lecture format and incorporate other forms of learning into their curriculum. We hypothesized that incorporating a short drawing exercise into lecture would improve student understanding of biological concepts both on short- and long-term assessments. In this activity students used drawings to synthesize the information presented in lecture by becoming peer teachers. We chose a challenging concept – generation of the resting membrane potential, and carried out the study in the freshman majors biology course. After a short introductory lecture, students (n=24) were paired and allowed to self-select as "drawers" or "listeners." Drawers were given 10 minutes to explain the concepts they had just learned to their partners, and made a drawing as they explained their work. Students' comprehension of concepts was assessed on a quiz given immediately after the exercise (short term), and on the final exam (long term). Drawers outperformed Listeners on both assessments. In the short-term assessment, improvements were most marked for Blooms Level 1 knowledge/comprehension questions, while on the final exam the students who made the drawing performed better across question types. These preliminary results suggest that "draw-pair-share" might be a valuable addition to lecture for students. For the instructor, the drawing activity also serves as a tool to quickly detect and correct student misconceptions.

The Multicultural Lab: An Interactive Workshop on Ancestral origins, Race and Mitochondrial DNA. S. Danzi Engoron and L. Honey. Queensborough Community College, Bayside, NY.

Uniting 126 nations and 99 languages, Queensborough Community College is a model of multiculturalism and diversity. Yet, it quickly becomes apparent that misperceptions and assumptions about race and ethnicity persist. This workshop was designed to address these misperceptions about race and genetics while drawing on the strengths and opportunities of Queensborough's multicultural experience. The integration of knowledge and methodologies from biology and cultural anthropology are key elements of the workshop. In Dr. Honey's Anthropology class, students learn about evolution, natural selection, the construction of the concept of 'Race,' and the social consequences of racist policies that persist despite the fact that there is no genetic basis for race. To support this concept which is difficult for students to grasp, Dr. Honey's anthropology students come to the laboratory with Dr. Danzi Engoron to extract their own mitochondrial DNA (mtDNA) from cheek cells in saliva for sequencing and analysis to determine each individual's ancestral origins. Students learn that we are all almost identical in our DNA sequences and while we can determine certain ancestral origins from these sequences, it can be difficult to identify which individuals we will be most closely related to (genetically) based on physical characteristics. The workshop culminates in a classroom activity, which includes a personal report for each student, analysis of the relationships between all students in the classroom and comparisons to DNA sequences and haplogroups from all over the world. Students have embraced this activity and their new understanding of the superficiality of physical characteristics. To date, over four semesters, we have included over 100 students and 10 faculty members with overwhelming response. This opportunity brings non-STEM students (and faculty!) into the world of molecular biology as they learn to use the tools of the scientist in this hour-long exercise.

Queensborough MSEIP – Using Traditional Research Internships to Engage, Retain and Graduate Students. Nidhi Gadura, Queensborough Community College, CUNY, Bayside, NY.

Queensborough Community College has successfully engaged community college students in high-caliber undergraduate research for a long time. Our experience, institutional commitment, faculty and upgraded laboratories have positioned us for unprecedented success. With the help of the US Department of Education Queensborough MSEIP (Minority Science and Engineering Improvement Program) grant, our main goal is to use undergraduate research as a tool to engage, retain and graduate Queensborough students. We have substantially expanded the depth and breadth of research opportunities for students, particularly underrepresented females. Students are engaged in a multi-tiered research programs, allowing them to begin research projects early in their academic careers and supporting them through increasingly rigorous research that culminates in placements at partner four-year colleges. The program uses a multiple-prong approach – starting QCC STEM freshmen with seminars and workshops, then pairing them with research mentors for long-term research projects followed by internships at senior colleges they intend to transfer to upon graduation. Students present their research findings in professional conferences that might eventually lead to publications. This multi-tiered model will be presented with the intent to expand it to other CUNY institutions.

Aquarius MISSION DEEP MICROBE. Nasreen S. Haque[1,2,] and Bernie Chowdhury[2], [1]New York Medical College, Valhalla, NY and [2]Genomic Observatory Inc., Staten Island, NY.

Aquarius reef base is the only underwater research laboratory in the world. It is deployed 60 feet beneath the surface in the Florida Keys National Marine Sanctuary. This is also a training site for NASA /NOAA Missions. Aquarius MISSION DEEP MICROBE is the first study undertaken to understand the microbial dynamics of human created spaces underwater; in humans and around humans. A pilot study was conducted to establish the logistics for a planned 10 day Saturation Mission in this habitat. Such studies on microbial behavior have never been attempted and has the potential to inform us of the functioning of the "rare biosphere" that occur in this unique environment providing insights which has applications in human health and disease. This mission is based upon are previous findings on microbial diversity and unique antibiotic resistance genes that occur at two sites surrounding the metropolitan area; namely the polluted waters of Gowanus canal in New York City and the flooded Tilly Foster Mine, Brewster, NY. Resistant bacteria pose challenges to governments, healthcare systems, and drug development. Many factors are involved in the interplay between the microbes and the diverse ecological niches they occupy, however, most of these interactions that occur underwater remain unknown. Targeting these niches for the identification of novel metabolites may offer the next generation of therapeutics. In addition, this mission will be broadcast across the globe to foster learning and enthusiasm for science.

Synergistic Effect of Epigallocatechin Gallate and CystiCran^{R}-40 on Animal and Bacterial Virus Infectivity. S.M. Lipson[1], F. S. Ozen[2], G. Karalis[1], E. Wolfe[1], S. Ponnala[1], W. Samarrai[3] and L. Karthikeyan[3]. [1]St. Francis Col., Brooklyn Heights, NY; [2]Celsuk Univ., Konya, Turkey, and [3]NYC Col. Technol.- CUNY, Brooklyn, NY.

Epigallocatechin gallate (EGCG) of green tea (*Camellia sinensis*) and the semisynthetic CystiCran^{R}-40 (C-40) containing 40% type A proanthocyanidin extract of the cranberry (V*accinium microcardium*), have been associated with numerous health-promoting activities including but not limited to antiviral, antibacterial, and/or anticancer activities. Synergistic activity affecting the loss of viral activity/infectivity by EGCG and C-40 has not been addressed. The purpose of this study is to determine the effect of EGCG in combination with C-40 on the activity and infectivity of coliphage T4II (phage T4) of *E. coli* B and the rotavirus strain SA-11 [RTV; grown in adenocarcinoma cells of the colon (HT-29)]. Phage infectivity testing was performed by plaque assay. Loss of RTV activity in suspension and infectivity testing in the HT-29 cells was performed by antigen (Ag) capture ELISA and Ag detection-cell culture amplification, respectively. Identification of individual and combined EGCG and C-40 in solution was performed by nuclear magnetic resonance (NMR). EGCG and C-40 alone showed anti-phage T4 activity ranging from concentrations of 10 to 80 μg/ml. Synergistic activity was recognized at low dose EGCG and C-40 concentrations. Combined EGCG and C-40 at 30 and 25 μg/ml respectively, reduced RTV antigen activity [loss of viral capsid protein 6 (VP6)]) in suspension, and RTV infectivity in HT-29 cells in monolayer culture. Cytotoxicity testing of EGCG and C-40 by the ToxiLight^{TM} cytotoxicity bioassay at concentrations used in the current work showed no detrimental effect upon HT-29 cellular integrity. NMR testing of EGCG and C-40 in combination showed significant structural differences compared to each phenolic analyte tested individually. Our findings suggest the enhanced loss of phage T4 and RTV activity/infectivity may be associated in part, with a synergistic effect between each flavonoid through an alteration of flavonoid chemical structure.

Learning to Experiment: Providing feedback on higher-order thinking through new cyberlearning tools. E. Meir, D. Pope, J. Conversano , K.J. Kim, S. Maruca and J. Palacio, SimBiotic Software, Inc and J. Clarke-Midura, Utah State University.

Most students require practice in understanding and applying difficult biological concepts before they reach a deep understanding. Efficient practice requires feedback, but it is hard to give good targeted feedback for confusions involving higher-order thinking, especially in large classes where multiple-choice type questions are the only feasible testing tool. On our current research project, we've looked for ways of constraining very open-ended tools such as simulation-based experimental playgrounds to facilitate automated feedback on complex concepts and skills. I'll discuss a case study built on top of SimBio's Darwinian Snails lab, addressing both natural selection and the experimental process. In this talk I'll focus on a tool that asks students to design their own experiment, and discuss data from in person interviews as well from a wide variety of classes showing that the feedback enabled by this tool promotes increased learning. If you have SimBio's Preview app on your laptop, bring it to the talk to actively participate (not required).

Promoting Sustainability Across Disciplines. Kristie Reilly and Laura Mackey Lorentzen, College of Natural, Applied & Health Sciences, Kean University Union.

Scientists have long predicted global climate change. Biologists, who have committed their professional lives to the study of living organisms, know better than most the symbiotic relationship between life on Earth and the planet itself. While traditional science faculty have played a significant role in teaching and promoting sustainability efforts, all educators hold a unique position to expand such efforts across disciplines. This interactive workshop will focus on educational strategies that embed sustainability across disciplines in order to harness the collective power of our universities, educators and most importantly students. Speakers will discuss how they heighten climate change awareness in their courses of expertise such as biology, business and administration, arts and humanities. Mechanisms to approach climate change in the classroom and how to use critical thinking to inspire the practice of sustainability across academics will be explored, with the goal of promoting action to make positive change in various fields of study and careers.

The Juvenile Hormone Sensitivity of an Enhancer Region on the Foraging Gene. Marium Sarder and Rebecca F. Spokony, Baruch College, CUNY, New York NY.

The juvenile hormone is an essential developmental hormone found in *Drosophila melanogaster*. It works to delay early metamorphosis and regulates the insect's physiological development. Juvenile hormone receptors are necessary for hormone function, as it allows juvenile hormone to have an effect on gene expression. In the presence of juvenile hormone there is increased juvenile hormone receptor binding near the foraging gene's promoter site, which suggests the foraging gene is a juvenile hormone target in *Drosophila melanogaster.* The purpose of this experiment is to test if the putative enhancer bound by the receptor controls RNA expression in juvenile hormone sensitive manner. In order to test for juvenile hormone sensitivity in the putative enhancer region an enhancer-reporter gene construct was introduced to the flies. LacZ functions as the reporter gene in this experiment; it was attached to the putative enhancer region and put back into the flies. White prepupae containing the reporter gene construct were either treated with a juvenile hormone mimic: methoprene diluted in acetone, or acetone alone. Following a four-hour post treatment period, RNA was extracted from the groups of whole prepupae. cDNA synthesized from the RNA was then used for qPCR to identify possible changes in gene expression. Preliminary analysis found a mild decrease in LacZ expression among males and a mild increase of LacZ expression in females. We also measured foraging RNA levels in these samples and found no change. We plan to stain white prepupae with the β-galactosidase produced by the LacZ to determine where the enhancer is turning on expression. We will then repeat the qPCR experiments with RNA collected from single tissues, rather than whole animals.

Using Technology Both Inside and Outside the Classroom: How RNAseq, Metagenomics and Bioinformatics can be Combined as Both Teaching and Research Tools with Undergraduate Students. Jeremy Seto[1] and Davida Smyth[2], [1]New York City College of Technology, Brooklyn, NY and [2]Mercy College, Dobbs Ferry, NY.

In an era when technology is at the forefront of every new venture from phones to energy production and beyond, we at NYCCT are committed to the integration of technology into the undergraduate curriculum. We recognize that technology can be utilized to increase the critical thinking and scientific reasoning skills of our students in a real-world context. We also recognize that not all students can partake in research opportunities owing to their working commitments and busy schedules, a practice that has been demonstrated to increase interest and retention in STEM fields. Our mutual collaborations with Brooklyn College and Dolan DNA Leaning Center at Cold Spring Harbor Laboratories as well as our own respective research interests have allowed us to generate and integrate next generation sequencing and bioinformatics modules into both molecular and cell biology and microbiology classes at City Tech. We've also established two collaborative research programs at the college, which run alongside the classroom activities allowing students interested in these projects to get involved in high impact research. These projects have enabled students to gain academic credit, to get research experience and to present at international, out of state conferences. The combined approach of both in class and out of class activities enables all students to gain experience in research, an activity demonstrated to increase retention in STEM. Our activities both inside and outside of the classroom have been well received by students and have resulted in several well-received presentations by our research students at conferences and meetings. Our future work will involve expanding our program to include other interested faculty at NYCCT, training faculty in the modules via workshops and increasing our pool of research students at the college. We hope that our strategy may be adopted by other faculty at institutions similar to City Tech.

A Preliminary Study of the Vascular Flora of Caledon State Park, Virginia. R. Stalter, C. Anozie, K. Arjune, T. Arruda, R. Kerns, R. Kerns, E. Mieses, M. Singh, St. Johns University, Jamaica, NY.

The objective of this preliminary study was to collect, identify and voucher the vascular flora at Caledon State Park, Virginia, a 1044 hectare park (38 21' 09 N, 77 07' 58 W) bordering the Potomac River. Vouchers of vascular plant species collected at this site will be housed at the A.C. Moore herbarium at the University of South Carolina. The study was initiated in May 2015 and will be terminated around October 2017. A preliminary list of the flora includes 302 species in 197 genera within 87 families. The largest families in the flora are the Poaceae, Asteraceae and Cyperaceae. *Carex* is the most common taxon represented by 13 species. Although native taxa compose over two thirds of the flora, the invasive *Microstegium vimineum* is the most abundant species and is the most frequently encountered herbaceous taxon within the wooded portions of the park. This aggressive grass may out compete native herbaceous woodland taxa and thus reduce the parks vascular plant diversity. Yellow poplar, *Liriodendron tulipifera* and sweet gum, *Liquidambar styraciflua* are the dominant trees at the park.

Dendritic Spine Alterations in Hippocampal CA1 Pyramidal Neurons of Alexander Disease. Rujin Tian[1] and Guomei Tang[2], Bronx Community College, CUNY, Bronx, NY and Columbia University, NY.

To better understand the role of GLT-1 on excitatory spine synapses of Alexander disease (R239C mutation of GFAP in astrocytes), we analyzed dendritic spines of CA1 pyramidal neurons in the hippocampus of male mutant mice by either confocal microscopy after microinjection of Lucifer Yellow or multicolor DiOlistic labeling using a hand-held gene gun. Both techniques showed thinner, longer and irregular dendritic spines in AxD mice, suggesting that abnormal dendritic spines, the postsynaptic sites of excitatory glutamatergic synapses in the brain, might precede neuronal loss in the hippocampus of AxD patients

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