MACUB

IN VIVO

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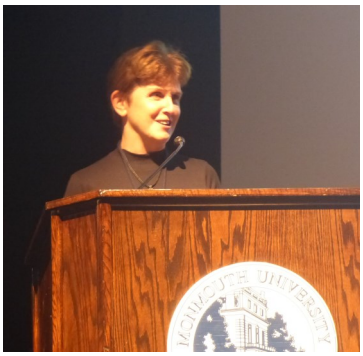
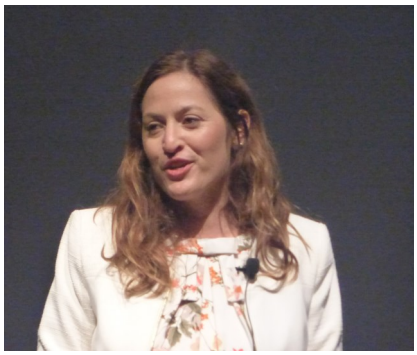
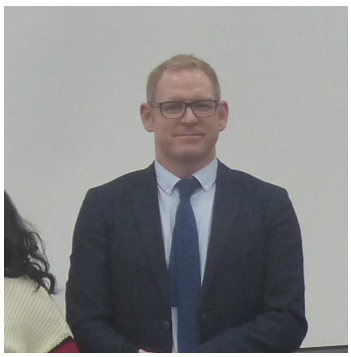
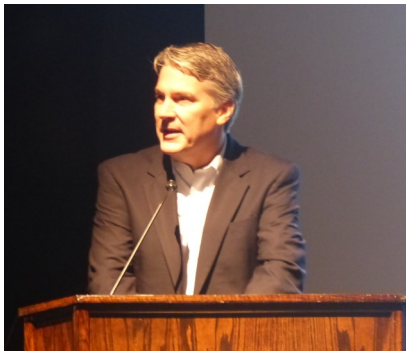
Saturday, October 26, 2019

Monmouth University

West Long Branch, NJ


Instructions for Authors

IN VIVO is a peer-reviewed journal that 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.

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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In This Issue:

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MACUB 2019 Conference

Poster Presentation Award Winners

COMMUNITY COLLEGE

Biochemistry, Biophysics and Biotechnology

First Place

Examining the Prevalence of Salmonella Bacteria in Standing Water
Using Loop-mediated Isothermal Amplification Method,
An Alternative to Polymerase Chain Reaction
Kaylynn Pubill and Andrew Nguyen
Queensborough Community College, Bayside, NY

Developmental Biology and Genetics

First Place

The Influence of Catecholamines in Broken Heart Syndrome
Hannah Rose Toussaint and Rochelle Nelson
Queensborough Community College

Second Place

THZ1 Synergizes With ABT263 To Induce Apoptosis in Cultured Glioblastoma Cells
Azariel Perry and Enyuan Shang
Bronx Community College, Bronx NY

Third Place

Juveniles and their Carapaces:
What Can They Tell Us About the Population of
American Horseshoe Crabs (*Limulus polyphemus*) on Plumb Beach.
Kera Mansfield and Christina Colon
Kingsborough Community College, Brooklyn NY

Environmental Biology and Ecology

First Place

Comparison of Bacterial Communities in New Jersey Soils Using Next Generation Sequencing
Tae M. Kim, Stephanie Zapata and Luis Jimenez
Bergen Community College, Paramus, NJ

Second Place

Mapping the Spread of the Invasive Pest Insect, *Lycorma delicatula* (Spotted Lanternfly) Using Data Generated in the Crowd-Sourced Data Application, iNaturalist
Niko Panagiotopoulos, Elena Tartaglia and John Smalley
Bergen Community College, Paramus, NJ

Third Place

Water Testing From Institutional Water Sources and Freshwater Ponds
Monique Bisasor, Raymeilys Guzman, Genesis Martinez, Gina Ama Frimpong, Cindy Liu, Bianca Chan, Kassim Hakim, Yasmin Edwards, Dickens St. Hilaire, Raffaella Diotti and Jeremy Seto
Bronx Community College, Bronx, NY
New York City College of Technology, and
Brooklyn Technical High School, Brooklyn, NY

Microbiology and Immunology

First Place

Examining the Presence of *Enterococcus spp.* in Water Around NYC Using Loop Mediated Isothermal Amplification (LAMP), an Alternative Method to PCR
Malcolm Fox and Andrew Nguyen
Queensborough Community College, Bayside, NY

Second Place

***Haplosporidium nelsoni* DNA was not Detected in Atlantic Oyster Drills from Delaware Bay**
Jason Cheng, Lilja Nielsen, and Craig Hinkley
Kingsborough Community College, Brooklyn NY

Third Place

"Adropin"- Setting Fire to Fat
Umit Muradi and Sarbani Ghoshal
Queensborough Community College, Bayside, NY

Physiology, Neuroscience and Clinical

First Place

Study of G Protein-Coupled Inwardly-Rectifying Potassium Channel (GIRK) and the Control of Lateral Cell Membrane Potential and Ciliary Response in Gill of *Crassostrea virginica*

Shatema Small[1], Alecia Johnson[2], Mohamed Eid[2], Margaret A. Carroll[2] and Edward J. Catapane[2]
[1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY

Second Place

Carnosine Reduces the Toxic Effect of Manganese on Mitochondrial Membrane Potential

Rosanne Wallach[1], Tenise Bowman[2], Edward J. Catapane[2] and Margaret A. Carroll[2]
[1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY

Third Place

Carnosine Reduces the Neurotoxic Effect of Manganese on the Physiological Response of a Cilio-Inhibitory Dopaminergic System

Christopher Ramirez[1], Janette Quintuna[2], Edna Georges[1], Margaret A. Carroll[2] and Edward J. Catapane[2]
[1]Kingsborugh Community College and [2]Medgar Evers College, Brooklyn, NY

MACUB 2019 Conference

Poster Presentation Award Winners

SENIOR COLLEGE

Biochemistry, Biophysics and Biotechnology

First Place

Simple and Affordable Kinetic Assay of Nucleic Acids by Gel Staining
Danielle Guillen, Mika Schievelbein, Kushkumar Patel, Davis Jose and Jonathan Ouellet
Monmouth University, West Long Branch, NJ

Second Place

Spectroscopic Evaluation of the B To A Conformational Transition In Duplex DNA Using Fluorescent Base Analogues
Michal Kalisz, Brianna Miller, Kirsten Lawson and Davis Jose
Monmouth University, West Long Branch, NJ

Third Place

Synthesis of an RNA-Therapy to Alter Overly-Expressed Tyrosine Kinase Receptors in Glioblastoma Multiforme.
Reina Montero and Martin J. Hicks
Monmouth University, West Long Branch, NJ

Developmental Biology and Genetics

First Place

Silence of the Genome: The Effects of DNA Methylation on Medulloblastoma Cell Survivability and Development
Anika Chowdhury, Benjamin Honigsfeld, Barbara Pepe, Christina Rubino and Noelle Cutter
Molloy College, Rockville Centre, NY

Second Place

Analyzing the Expression Level of $GABA_A$ Receptor Genes in *Gallus gallus* Chick Tissues Through Embryonic Development
Taylor Nason and Cathryn Kubera
Monmouth University, West Long Branch NJ

Third Place

Designing and Testing RNA Therapeutics to Block VEGFR2 and EGFR Activation in Human Glioblastoma.
Flobater Gawargi and Martin J Hicks
Monmouth University, West Long Branch, NJ

Environmental Biology and Ecology

First Place

Differences in PC:CHL Ratio Across a Reservoir Series in Southern New Jersey During the Summer
Aysenne Bartlebaugh, Leandra Bello, Michael Pierce, Samantha Boich, Michael Grove, Courtney Richmond and Nathan Ruhl
Rowan University, Glassboro NJ

Second Place

An Evaluation of Fecal Indicator Bacteria Along the Coast of Monmouth County, NJ Post Rainfall Events
Kelly Hanna, Lohnes, Victoria, Erin Conlon, Skyler Post, Maria Riley, Ariel Zavala, Jeffrey H. Weisburg and Jason E. Adolf
Monmouth University, NJ

Third Place

Variation in Reproductive Traits Among Mice Adapted to Different Regions of the Americas
Tiffany Longo, Jesse Bragger, David Grossi and Megan Phifer-Rixey
Monmouth University, West Long Branch, NJ

Microbiology and Immunology

First Place

Sequencing the Smoke: The Unseen Microbial Hazards of Vaping
Simon Chen, Kristoff Misquitta, Davida Smyth
The New School, New York, NY

Second Place

Analysis of Microbial Populations Associated with Electric Hand-Dryers Using 16s rRNA Gene Sequencing
Sabrina Catanese, Pam Monaco, Jodi Evans and Veronica Feeg
Molloy College, Rockville Centre, NY

Third Place

Accessing Bioluminescence: Exploring Sustainable Environments for Bioluminescent Microorganisms and the possibility of using bioluminescence for disaster relief
Leah Hughes, Davida Smyth and Eugene Lang, The New School, New York, NY

MACUB 2019 Conference

Poster Presentation Award Winners

Physiology, Neuroscience and Clinical

First Place

The Effects of Developmental Pb-Exposure on Pilocarpine and Kainic Acid Induced Seizures

Jewel N. Joseph[1], Michelle A. Vasquez[1], Ericka Cabanas[1], George Cruz[1], Evan Clarke[1], Eric Khairi[1], Jean-Martin J. Chrisphonte[1], Isra Ahmed[1], Kirsten P. Lynch[1], Jalen R. Bonitto[1], Lorenz S. Neuwirth[1] and Youngjoo Kim[1,2]
SUNY Old Westbury, Old Westbury, NY and [2]iCARE, Old Westbury NY

Second Place

Behavioral Outcomes of Co-use of Alcohol and Amphetamine in a Rat Model for ADHD

Jessica N. Baals, Grace L. Haemmerle, Nicholas R. Pillarella and Dennis E. Rhoads
Monmouth University, West Long Branch, NJ

Third Place

Examining Microglia Morphology through Extrinsic Manipulation

Sara Mroziuk, Alicia C. Barrientos, Arya Lahijani and Joshua C. Brumberg
Queens College, CUNY, NY and [2]The Graduate Center, CUNY, New York, NY

MACUB 2019 Conference

Poster Presentation Award Winners

Graduate Masters Level

Developmental Biology and Genetics

First Place

Anaylsis of the Mps1-PP1 Interaction I*n Vivo*
Gina Moretti, Steven Almazan, Janet K. Jang, Kim S. McKim and Elizabeth A. Manheim
Rutgers University and Kean University, NJ

Second Place

TFIIIB Isoform Expression in Zebrafish
Jason Ramdeo, Carlo Belifore and Laura Schramm
St. John's University, Queens NY

Environmental Biology and Ecology

First Place

Sexual Dimorphism in Asian Shore Crabs and Its Influence in Predation on Whelks
Prachi Saxena and Aaren Freeman
Adelphi University, Garden City, NY

Second Place

Sample Preparation for Metabarcoding: How to Reduce False-Positive Results?
Julia Annuzzi, Yassel Hernandez and Maria Shumskaya
Kean University, Union City, NJ

Third Place

Bacterial Diversity and Community Composition of Cyanobacteria and Cyanophages in Barnegat Bay, New Jersey
Roksana Rahman and Tinchun Chu
Seton Hall University, South Orange, NJ

Microbiology and Immunology

First Place

Evaluation of Sporicidal Effects of Natural Formulations Containing Lipophilic Green Tea Polyphenol
Sabrina Lopez and Tinchun Chu
Seton Hall University, South Orange, NJ

Graduate Doctoral Level

Microbiology and Immunology

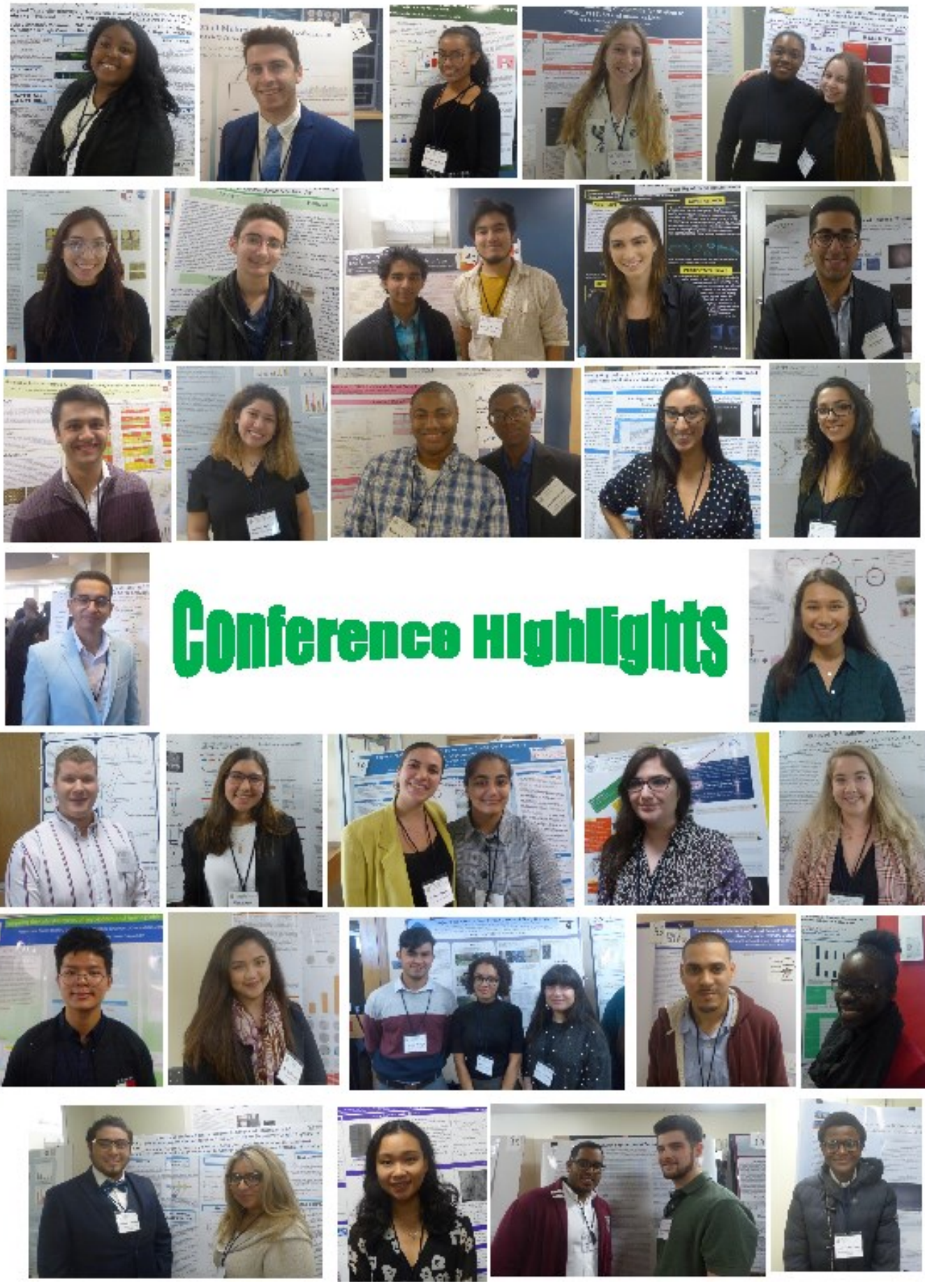
First Place

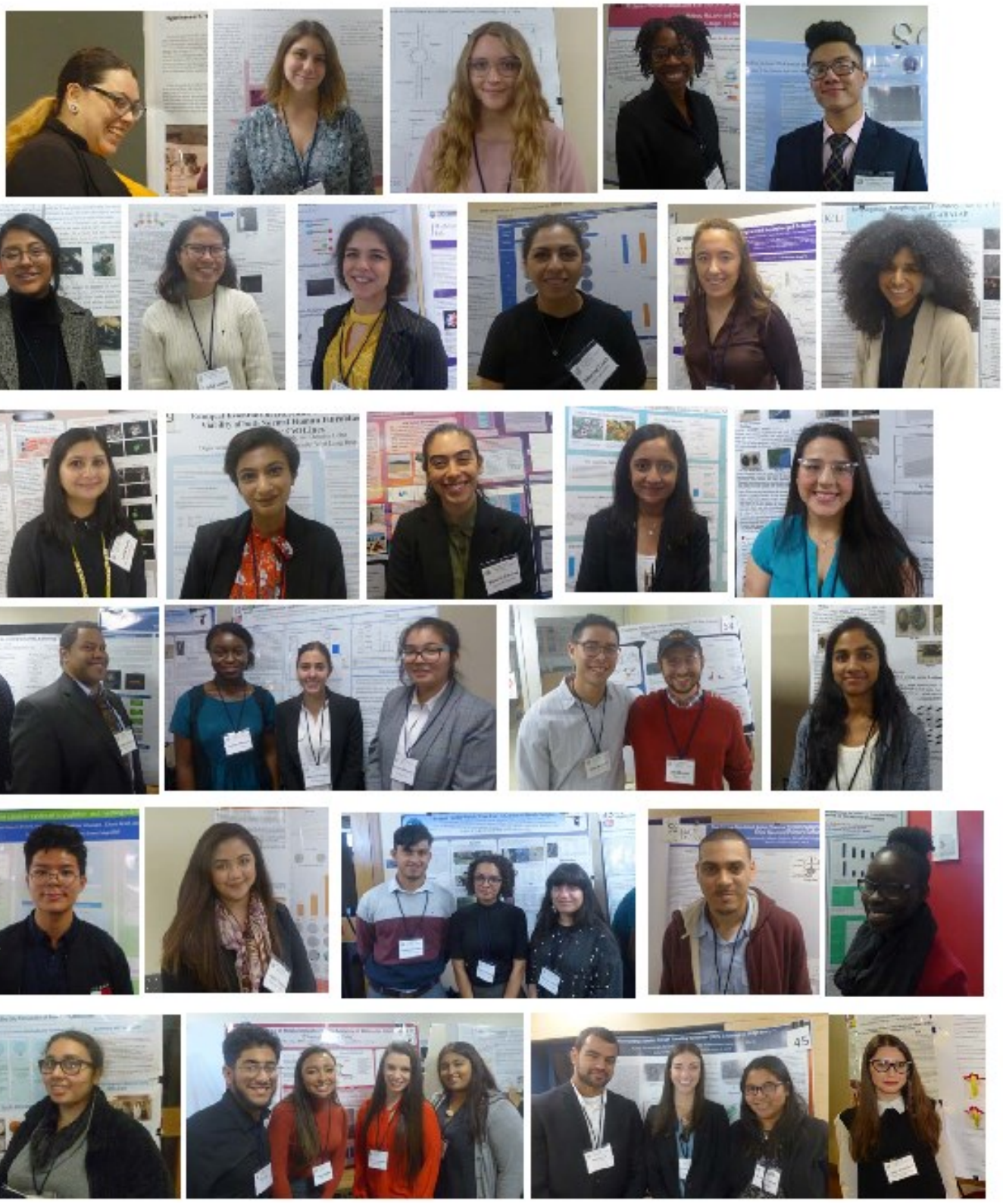
Anti-Spore Activity and Potential Application of Theaflavin
Ayuni Yussof and Tinchun Chu
Seton Hall University, South Orange, NJ

Environmental Biology and Ecology

First Place

Molecular and Physiological Characterization of *Microcystis aeruginosa* Under Zinc Stress
Jose L. Perez and Tinchun Chu
Seton Hall University, South Orange, NJ


Conference Highlights



Determination of an Optimal Solvent System for the Extraction of Hydroxycinnamic Acids (HCA) From Plant Material: A Study of Antioxidative Properties of Basil Extract. Na'lmah Alston, Andrea A. Archer, Alberto Badillo, Jeffery P. Bethea, Marie L. Colon, Nicole Dobrijevic, Mikhail T. Hamilton, Indira Hernandez, Jonathan I. Hernandez, Marina Kostenikova, Sherise N. Martin, Fardausi (Annie) K. Mukti, Jaffanie Rojas, Darius A. Tomlinson and Ilirian Dhimitruka, Mercy College, Dobbs Ferry NY.

Hydroxycinnamic acids (HCA), specifically caffeic acid, ferulic acid and sinapic acid, offer beneficial medicinal properties, due to their antioxidative capacity in vivo. HCA exhibit anti-collagenase, anti-inflammatory, antimicrobial, and anti-tyrosinase activities, as well as ultraviolet (UV) protective properties. There is great interest in the development of optimized methods to extract HCA in high yield from plant material. The interest stems from the potential of using HCA as safe, nontoxic active ingredient in a variety of medicinal and nutritional supplements. In this work, dry basil was used as model plant. The extraction efficiency of two different solvent systems was evaluated. The antioxidative capacity, the capacity to neutralize harmful free radicals, of basil extract was measured via UV spectroscopy using the DPPH assay. HCA were extracted efficiently from dry basil, which is used as model plant, using a mixture of ethanol/water. The increased polarity due to the addition of 30 % water to ethanol lead to 15 fold increase in extraction efficiency of HCA, and dramatic increase in the purity of HCA extract as determined by UV spectroscopy and DPPA assay. Principles of green chemistry were applied in this project, such as use of environmentally friendly solvents, and minimal use of toxic materials. This research was part of a project based learning sequence incorporated into the curriculum of organic chemistry I laboratory.

A Survey for the Presence of *Enterococcus* indicator Species *Salmonella* and Shiga toxin-producing *E. coli* (STEC 0157) in Fresh Produce Obtained From Farmers Market in Brooklyn, New York. Hunter-Ann Alves, Abdessamad Ramzaoui and Anupam Pradhan, Kingsborough Community College, Brooklyn, NY.

Farmers' markets are attractive for local shoppers for fresh, less-processed, locally grown produce. However, reports suggest statistical correlation with such markets and outbreaks of fecal coliforms like *Salmonella sp.* and *Escherichia coli*; reinforces the need for investigation of our local produce. The objective of this course embedded authentic research is to investigate the presence of fecal contaminant indicator sp. on selected foods from farmers' market of Brooklyn. Students collected and analyzed selected produce (salads, vegetables and poultry) from their farmers' market of choice for the presence of *Salmonella sp.* and *E. coli* by utilizing microbiology lab techniques and created a report on their research findings. Findings from 5 class sections (16 students each) enrolled in an undergraduate microbiology course (Fall 2017-Spring 2019) of Kingsborough Community College, Brooklyn, NY. Briefly, many analyzed samples showed consistent indication of *Salmonella* and *E. coli* species grown in a specialized media Xylose Lysine Deoxycholate Agar (XLD Agar). Serological analysis of the positive colonies using Microgen latex agglutination beads confirmed presence of *Salmonella* and *E.coli* (0157:H7) in few samples. Detection of *Salmonella* and *E.coli* (0157:H7) in produce samples violates New York State Department of Health (NYSDOH) guidelines. We recommend frequent surveys of farmers market by state officials and education of public on the need to proper handling and hygiene.

Evidence of Anti-Tumor Activities of Piperlongumine in Retinoblastoma. Baffour Amponsah-Antwi[1], Stephen Redenti[1] and Rajendra Gharbaran[2], [1]Lehman College/CUNY and [2]Bronx Community College/CUNY, Bronx, NY.

Retinoblastoma is a cancer that affect the retina of newborns, born with mutations in the retinoblastoma (Rb) gene. In this study, we tested the effects of piperlongumine, a compound found in long pepper on Y79, a cellular model of retinoblastoma. Piperlongumine treatment caused as dose-dependent decrease in cell growth after 48 hours, as assessed by water-soluble tetrazolium (WST-1) cell proliferation assay. This result was also supported by automated hemocytometry. Cell death assay using a solution consisting of acridine orange and ethidium bromide showed dose-dependent increase in cell death: live cells are green due to updated of acridine orange and dead cells red due to staining of their nucleic acid with ethidium bromide. Staining of the treated cells with a caspase-specific dye showed increased caspase activities, indicating cell death by apoptosis. These preliminary results suggest that piperlongumine may have anti-tumor activities in retinoblastoma.

BacM Isoforms are Generated Through Alternative Start Site Selection. Christopher Annabi and David Zuckerman, Iona College, New Rochelle, NY.

Bacteria are prevalent in the environment and can have an effect on human health, as they contribute to disease. Over time, there has been high antibiotic overuse, which contributes to antibiotic resistance. In order to attack bacteria that may now be resistant to antibiotics, new targets need to be considered. One potential new target includes the bacterial cytoskeleton; one system unique to bacteria are the bactofilins. BacM is one of the four paralogs of bactofilins encoded in *Myxococcus xanthus*, a bacteria used as a model organism for studying social interactions, biofilm formation, and motility. BacM contributes to the proper rod-shaped morphology of *M. xanthus*. BacM has been observed as a large form (BacM-L) and a small form (BacM-S). They differ at the N-termini, where BacM-S lacks ~27 amino acids. Two hypotheses regarding the generation of these isoforms of BacM were considered. The first hypothesis suggested BacM-L is synthesized as a precursor protein that is cleaved by a protease at the sites of cytoskeleton elongation. The second hypothesis suggested that BacM-L and BacM-S are generated through alternative start site selection by the ribosome. These hypotheses were tested by engineering a plasmid containing *bacM* with its 5′ untranslated sequence; point mutations were introduced using PCR-directed mutagenesis. Mutants were made to abolish the start codon (M1L), introduce a frameshift after the start codon (K8 frameshift), abolish the putative second start codon (V24L), and abolish a putative internal ribosome binding sequence using silent mutations (ΔRBS2). When observed by immunoblot, mutants M1L and K8 frameshift expressed only BacM-S, whereas mutants V24L and ΔRBS2 expressed only BacM-L. Additional mutants were made, one which changed the valine start codon to a methionine (V24M), another which mutated the valine start codon to a normal valine (V24V), and a third intended to prevent the ribosome from stalling during polymerization (KK7). When observed by immunoblot, mutant V24M expressed both the large and small isoforms, mutant V24V expressed only the large isoform, and mutant KK7 expressed more of the small isoform than the large. These results are consistent with the second hypothesis, that BacM-L and BacM-S are generated through alternative start site selection.

Sample Preparation for Metabarcoding: How to Reduce False-Positive Results? Julia Annuzzi, Yassel Hernandez and Maria Shumskaya, Kean University, Union City, NJ

The focus of our research is to evaluate the potential of Next Generation Sequencing (NGS) method in identification of dead wood fungal species from a specific location, such as an urban park. In North America the research on biodiversity of dead wood fungi is still developing and there is no complete database so far. For our project, 37 fruiting bodies of various dead wood fungi were collected from Ocean County Park and 35 fruiting bodies were collected from Belleplain Forest during Fall 2017. The species were identified morphologically where possible, with the conformation by DNA-barcoding. For the barcoding, DNA was isolated from each individual fungal body using DNeasy PowerSoil kit, then amplified by PCR using ITS specific primers to obtain a fragment of ITS gene, which serves as a barcode in fungal identification. This fragment was sequenced, the resulting sequence was compared to the database of fungal ITS sequences in NCBI portal using BLAST and species identified. As a result, a local database of the species found in Ocean County Park and Belleplain Forest was created. NGS sequencing was used as a method allowing metabarcoding of a mixed DNA sample. This method allows to identify species all at once, without individual sequencing. The efficiency and reliability of this method in comparison to the individual species identification is discussed.

Strong Antimicrobial Activity Displayed by Newly Synthesized Hydroxamic Acids and Their Derivatives. Daniel Antunes, Stephanie Ramirez, Rameen Shah, Robert Aslanian and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

Antibiotic resistant pathogenic bacteria are a growing worldwide health concern according to the Centers for Disease Control and Prevention. These bacteria are responsible for most of the infectious diseases and healthcare-associated infections in hospitals (HAIs). The need for new therapeutic approaches using novel antimicrobial compounds is becoming vital as the number of infections caused by antibiotic resistant strains of bacteria such as Staphylococcus aureus and Staphylococcus epidermis has drastically increased. The focus of our study is to test newly designed and synthesized therapeutic agents for antimicrobial properties. Several hydroxamic acids and their analogs were newly synthesized by the chemistry department and tested in our laboratory for antibacterial activity against five different ATCC strains of pathogenic bacteria. The antimicrobial activity of each compound was evaluated using the disk-diffusion assay and the liquid broth assay. All compounds displayed a various spectrum of antibacterial activity that will enable us to narrow down the potential active site or functional group in the molecules responsible for the activity. Future work will focus on designing and testing new derivatives with a broader spectrum of activity that will be further tested for cytotoxicity against plant and human cell lines.

Strong Antimicrobial Activity Displayed by Newly Synthesized Hydroxamic Acids and Their Derivatives. Daniel Antunes, Stephanie Ramirez, Omar Aqani, Hershal Desai, Robert Aslanian and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

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The Effects of HIV on the Blood Brain Barrier Protein Purification of HIV TAT 86 & 101. Chelsea Anyaegbu, Andres Cabezas and Yufeng Wei, New Jersey City University, Jersey City, NJ.

The human immunodeficiency virus (HIV) is one of the most detrimental diseases present around the globe. It has various negative impacts on health. Patients suffering from HIV tend to develop neurocognitive degeneracy, which advances into AIDS dementia complex (ADC), causing high mortality. It is hypothesized that HIV TAT protein is the cause of ADC. Human brains are protected from pathogens and infection due to a structure known as the blood brain barrier (BBB), a highly selective semipermeable border, that restricts the entry of large molecules and pathogens while allowing the diffusion of hydrophobic molecules (O_2, CO_2, hormones) to enter the brain. We suspect that the HIV TAT protein disrupts BBB, and allows harmful molecules to enter the brain. Thereby, causing AIDS related dementia and other catastrophic and irreversible damages to the brain and the nervous system. Our research focuses on isolating the HIV TAT protein so that further analysis can be done on its role in BBB disruption. In order to accomplish this goal, *Escherichia coli* cells were transformed, and allowed to express HIV TAT. Cell lysis and protein purification was carried out to isolate the protein. Gel electrophoresis and western blots were used to determine the presence of this protein. Lastly, utilizing human brain microvascular endothelial cells (HBMEC) to observe morphological changes and simulate the events that possibly occur in the BBB.

Invasional Meltdown? *Corydalis incisa*, a New Non-Native Plant Is Facilitated by a Non-Native Ant Along the Bronx River. Alexis Ayrey and Christina M. Andruk, Iona College, New Rochelle NY.

Corydalis incisa (incised fumewort) is a myremecochorous invasive plant located along the Bronx River and other watersheds in Westchester County and the Bronx. This region also has a high diversity of native myrmecochorus plants such as *Asarum canadense* (wild ginger) that may be negatively impacted by this invasion. We tested the following hypotheses between June and August 2019: A) Ants disperse seeds of *C. incisa*. B) The most likely ant disperser of the *C. incisa* seeds is *Aphaenogaster rudis*, a keystone species native to North American forests. C) Ants prefer the seeds of the native *A. canadense* over the seeds of *C. incisa*. D) Myrmecochory occurs both in native forests and in areas invaded by *Fallopia japonica* (Japanese knotweed), however *A. canadense* is likely to be more attractive in the native forest and *C. incisa* is more attractive in the knotweed area. Two 10-meter transects were set out, one each in the native forest area and the knotweed area. Three depots were set out per transect: *C. incisa* seeds alone, *A. canadense* seeds alone, and competition. Four plates were placed at each depot: control which was inaccessible to all, open which was accessible to all, ant-accessible only, and vertebrate-accessible only. The experiment was replicated four times. Ants were collected via pitfall trap on each sampling date. Experiments were observed for 30 min after set-up and ants were collected from seeds during observation. The effect of species, location, choice, and their interaction on the number of seeds removed was analyzed with a logistic regression with date as a random effect. Ants were found to disperse the seeds of *C. incisa* and *A. canadense* in both native and knotweed invaded areas. The most commonly found ant in pitfall traps and *C. incisa* seeds was the *Nylanderia flavipes*, not *A. rudis* as expected. No seeds were removed from the control or vertebrate only plates. Ants spent more total time interacting with *A. canadense* than *C. incisa*, but most of these interactions were unsuccessful as they spent more time dispersing *C. incisa* than *A. canadense*. Ants spent more time successfully dispersing the native *A. canadense* in the native area and more time successfully dispersing *C. incisa* in the knotweed invaded area. Both species were removed more often alone than in competition, but the impact was greater for *A. canadense*, indicating a stronger preference for *C. incisa* when given the choice. *C. incisa* is being successfully dispersed more than the native *A. canadense* in knotweed-dominated areas, which are particularly common along the Bronx River. In addition, the non-native ant, *N. flavipes* is playing a critical role in its dispersal. These observations demonstrate the importance of studying urban ecosystems to examine these increasingly common novel interactions. We argue that our data are a possible example of an invasional meltdown whereby a non-native ant facilitates the spread of a new non-native herbaceous plant more often in sites that are dominated by the invasive Japanese knotweed.

Examining Interactions of CaMKIIα and GRIP as a Possible Mechanism of Regulating Inhibitory Synapses. Azka Asim, Kendall Carter, Chelsea Anyaegbu and Reed Carroll, New Jersey City University, Jersey City, NJ.

Calmodulin-dependent protein kinase (CaMKIIα) plays a role in the regulation of synaptic plasticity at both excitatory and inhibitory synapses. Inhibitory synaptic plasticity is modulated by CaMKIIα through the enhancement of the GABAA receptor insertion and phosphorylation. However, it is unclear what enables CaMKIIα to localize at inhibitory synapses in the brain to induce such changes. In this research project, a possible interaction between CaMKII and GRIP (Glutamate Receptor Interacting Protein) as a mechanism for localizing the kinase at inhibitory synapses was tested. Co-expression conditions were optimized, and co-localization was assayed. GRIP was co-transfected with several CaMKIIα constructs in HEK cells. Co-expression and co-localization was examined for GRIP with wild type and CaMKIIα mutants (T286D and T305D) by immunocytochemistry and fluorescence microscopy. Ongoing, co-immunoprecipitation experiments are examining the possible interaction of activated kinase mutants with the GRIP protein.

Behavioral Outcomes of Co-use of Alcohol and Amphetamine in a Rat Model for ADHD. Jessica N. Baals, Grace L. Haemmerle, Nicholas R. Pillarella and Dennis E. Rhoads, Monmouth University, West Long Branch, NJ.

Non-medical use of amphetamine and other stimulants prescribed for treatment of attention deficit hyperactivity disorder (ADHD) peaks in adolescence and is of growing concern when combined with binge consumption of alcohol. Previous studies in our lab modeled chronic ethanol-amphetamine co-use in adolescent Long-Evans rats and provided evidence that amphetamine attenuates alcohol withdrawal symptoms in a manner that may lessen an individual's awareness of impending alcohol dependence. The current project was designed as a pilot study to test repeated ethanol-amphetamine co-use in adolescent Spontaneously Hypertensive Rats (SHR), an experimental model for study of ADHD. The interest is in determining if this brain will respond differently to the co-use of alcohol and amphetamine, considering amphetamine is therapeutic for an ADHD brain. SHR adolescents were randomly assigned at P33 to liquid diets corresponding to one of four treatment groups: control (no drug), ethanol, amphetamine, or ethanol combined with amphetamine. Rats were withdrawn from treatment groups at four different time points: 5 days, 12 days, 19 days, and 26 days and tested for alcohol withdrawal symptoms after 6-8 hours. Computer controlled activity chambers equipped with a dark box insert were used to assess general locomotor activity and anxiety-like behavior. Overall alcohol withdrawal severity was also evaluated. After 5 days consuming alcohol, SHR adolescents showed hypo-activity typical of alcohol withdrawal. However, hypo-activity declined with additional periods of ethanol administration. The SHR adolescents appeared resistant to progressive signs of alcohol withdrawal used to gauge alcohol dependency in rodents. Overall withdrawal severity after consuming alcohol for 26 days was much lower than 'control' Wistar Kyoto or Long-Evans rats. Amphetamine administration had to be modified for SHR adolescents to lower the dose and avoid anorexic effects not seen with Long-Evans rats. Also in sharp contrast to control rats, amphetamine co-administration with alcohol in SHR adolescents appeared to prolong alcohol withdrawal hypo-activity and increase anxiety-like behavior. Thus, as a model for ADHD, adolescent SHR showed altered responses to alcohol, to amphetamine, and to the combined administration of both drugs. The results speak to the importance of better understanding alcohol-stimulant interactions in an ADHD population as educational and preventive strategies are developed.

Differences in PC:CHL Ratio Across a Reservoir Series in Southern New Jersey.During the Summer. Aysenne Bartlebaugh, Leandra Bello, Samantha Boich, Michael Grove, Courtney Richmond and Nathan Ruhl, Rowan University, Glassboro NJ.

Many studies predict cyanobacterial bloom (cHAB) dynamics in a given lake, but cHABs are poorly understood across lake-systems. In the study presented here, we took a cyanobacterial dominance approach (PC:CHL ratio) to monitoring cHAB development during the summer of 2018. A cHAB did not occur at any of the reservoirs we were monitoring in 2018, but cyanobacteria were present and 35.6% of the variation in cyanobacterial dominance was explained by water temperature and pH across all sites combined. Between-site differences in phycodom were explored via ANOVA and canonical ordination. These results demonstrate proof-of-concept for the use of PC:CHL ratio to construct predictive models of spatiotemporal variation in planktonic autotroph communities and provide us with a baseline to compare to future years when a cHAB may occur.

Effects of Manganese on the Cilio-Inhibitory Actions of Dopamine D2 Agonists in Gill Lateral Cells of *Crassostrea virginica*. Kameca Baxter[1], Tia Foster[2], Krystle Ernest[2], Edward J. Catapane[2] and Margaret A. Carroll[2], [1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY.

Cilia of gill lateral cells of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervations from their ganglia. Dopamine is the neurotransmitter causing cilio-inhibition, while serotonin causes cilio-excitation. Manganese (Mn) is a neurotoxin causing manganism, a Parkinson's-like disease in people characterized by aberrant dopaminergic neurotransmission. The mechanism by which Mn produces this dysfunction is not fully resolved and lack of effective treatment for manganism has been a major obstacle in its clinical management. Previous work in our lab showed Mn

selectively disrupts the cilio-inhibitory actions of dopamine in *C. virginica* and that the post-synaptic dopamine receptors present on gill lateral cells are D2-like. Dopamine D2 receptors (D2R) are G protein-coupled metabotropic receptors. Since Mn interferes with the D2R signal transduction pathway preventing a normal cilio-inhibitory response, we hypothesized that Mn also would interfere with the D2R pathway when dopamine D2 agonists were utilized to activate the receptor. We tested a dose response (10^{-6} - 10^{-4}M) of three different dopamine D2 agonists (piribedil, N-propyl piperidine and ergocryptine) to determine their efficacy on reducing lateral cilia beating rates on excised gill, in the presence or absence of Mn. The results for each agonist also were compared to gill treated with or without Mn using the natural ligand dopamine. Cilia beating rates were measured using stroboscopic microscopy. In the absence of Mn, each of the 3 agonists was cilio-inhibitory, with N-propyl piperidine being the most effective reducing beating rates similar to that of dopamine. Repeating the experiments in the presence of Mn (10^{-5}M) caused a slight to moderate reduction in the cilio-inhibitory effectiveness of ergocryptine and piribedil, but did not generate any significant reduction in the ability of N-propyl piperidine to reduce cilia beating rates. The results of this study supports our hypothesis that Mn would interfere with the cilio-inhibitory actions of D2R agonists, however not all three agonists were equally affected. Since the cilio-inhibitory actions of two of the three agonists were impaired by Mn the results suggest that Mn toxicity may not be targeting the dopamine molecule itself, but rather interfering with one or more steps of the D2R signal transduction pathway. In addition the three agonists had different cilio-inhibitory effectiveness and therefore likely to have different D2R binding capacities on the gill lateral cells. This may explain their varied response to Mn, especially if Mn is directly interfering with ligand binding or subsequent activation of D2R. This study is helpful in furthering the understanding of the neurotoxic mechanism of action of Mn and may be of value to investigators searching for therapeutic treatments in patients with manganism. Supported by NIGMS grant 2R25GM06003, NIH grant K12GM093854-07A1, PSC-CUNY grant and 62344-00-50 0537-19-1091 of the CSTEP Program of NYSED.

Water Testing From Institutional Water Sources and Freshwater Ponds. Monique Bisasor, Raymeilys Guzman, Genesis Martinez, Gina Ama Frimpong, Cindy Liu, Bianca Chan, Kassim Hakim, Yasmin Edwards, Dickens St. Hilaire, Raffaella Diotti and Jeremy Seto. Bronx Community College, Bronx, NY; New York City College of Technology and Brooklyn Technical High School, Brooklyn, NY.

The quality of public water sources is an issue of paramount interest because of their potential effects on the ecosystems that they support and for the humans that depend on them. Within institutions water quality may be determined by the age of the building with administrations working to ensure that sources for human consumptions are safe. Similar efforts have been made to restore natural water sources in the New York area parks. Our project focused on testing the quality of the water collected from institutional water sources and freshwater ponds within the New York City park system using hydra and planaria, two organisms that have traditionally been used to test water toxicity. Water was collected from drinking water fountains at Brooklyn Tech HS, Bronx Community College and New York City College of Technology as well as from other sites in the institution. Samples from the New York City parks. Samples were sterilized and used as the basis for hydra and planaria media. After exposure the organism morphology, range of motion and survival were monitored for acute or chronic effects. pH testing and solute analysis were performed on the water samples. Unexpected results from known park sample as well as hypertoxicity from drinking water sources were observed, at times within an hour of exposure. The study highlights how further testing is necessary, in particular for drinking water in institutions, to protect the welfare of the organisms depending on the water sources.

Increased Experience with Class Presentations Does Not Decrease Self-Reported Public Speaking Anxiety and the Physiologic Stress Response in Undergraduates. Courtney Boisette, Jodi Evans and Melissa Gebbia, Molloy College, Rockville Centre, NY.

Undergraduate students experience stress brought on by many factors during their academic career. One very notable stress-inducer is public speaking. Social-evaluative stimuli like public speaking tend to trigger physiological responses, such as increases in one's cortisol levels. This research study focused on the stress response produced in undergraduate students that occurs due to giving an in-class presentation. Using undergraduates as participants allows for the observation of a broad range of experience levels in a natural setting. This study tested the hypothesis that more experienced undergraduate students would have lower anxiety and physiological stress than inexperienced undergraduate students after an in-class presentation. It also tested the hypothesis that chewing gum before presenting will help with the presenter's physiological stress recovery. Previous studies have reported that chewing gum increases both concentration and alertness. When a person is faced with a stressor, chewing gum has the potential to reduce both cortisol levels and mental stress. Seventeen participants were recruited for this study from two groups of students: one with relatively little experience in public speaking at the collegiate level (freshmen) and the second with substantially more experience (juniors and seniors). They varied in age and gender and were randomly assigned to either the control group or the experimental group. The experimental group was asked to chew sugar-free, aspartame-free gum for 15 minutes before presenting. Students filled out self-report

questionnaires addressing both students' demographics and their attitudes toward public speaking based on the Public Speaking Anxiety Scale (PSAS). All participants were asked to provide a saliva sample a week before their presentation, right before their presentation, and right after their presentation. The saliva samples were then used to determine students' cortisol level, which provides a physiological measure of their stress. Although the number of presentations and therefore experience in public speaking increased with age, the anxiety experienced, as assessed by the PSAS score, does not decrease as we found no negative correlation with experience level. While cortisol was significantly elevated from baseline, no significant relationship was found between participants' self -evaluation of public speaking anxiety and cortisol levels before or after a public speaking task. No significant relationship was found between age/gender/experience and cortisol levels after a public speaking task. Elevations in cortisol did not significantly differ based on one's level of experience giving collegiate presentations, and chewing gum did not have a significant effect on participants' cortisol levels after a public speaking task. Given that this was a pilot study, the number of participants recruited limited the study analysis especially when considering the impact of gum chewing. Overall, our results demonstrate that increased experience with in-class presentations does not lower self-reported public speaking anxiety and the physiological stress response. Future studies, with greater numbers of participants, are needed to confirm these data and to examine further the potential for gum-chewing as an intervention. This work was supported by NSF grant # 1626093 and the Molloy College Biology Chemistry and Environmental Studies Department.

Inhibition of Pathogenic Bacterial Growth and Biofilm Formation using Pure, Organic, Chemical and Hexane-Free Jojoba Oil and Cell-Free Extracts of Two Bacteria Isolated from the Environment. Youklendy Calderon, Mariana Metry and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

Antibiotic-resistant, biofilm-forming microbes are major causes of global systemic and nosocomial human infections. The virulence of bacterial biofilms enables attachment to catheters, pacemakers, and eye contacts; and resistance to the immune system. In an attempt to address this problem, cell-free extracts from two unidentified bacteria, Y2 and Y4, that were isolated from Lincoln Park in Jersey City, NJ, in addition to jojoba oil were tested for their ability to kill or inhibit the growth or attachment of more than a dozen pathogenic bacterial strains and *Candida albicans*. Disk-diffusion, broth, and biofilm assays were used to test the compounds, which demonstrated various degrees of antibacterial and antibiofilm inhibition. However, the compounds' antifungal activity was minimal as *C. albicans* was only susceptible to the cell-free Y2 and Y4 extracts in the broth assay. Most bacterial strains had increased susceptibility to the extracts in the broth assay, suggesting the extracts are more effective when suspended in fluid or with increased microbial contact. Future testing involves the identification of the active ingredients in the cell-free extracts and jojoba oil, the minimum inhibitory and fungicidal concentrations of the extracts, and the identity of Y2 and Y4. This project received support from US Education Department Title III Part F HSI-STEM grant # P031C160155.

Investigating the Role of Centromere Protein CENP-C in Meiosis. Naomi Campos[1], Jessica E. Fellmeth[2] and Kim S. McKim[2], [1]Medgar Evers College, Brooklyn, NY and [2]Waksman Institute of Microbiology, Rutgers University Piscataway, NJ.

In meiosis, a type of cellular division, chromosome numbers are reduced by half, producing four reproductive haploid cells. Improper chromosome segregation is known as aneuploidy and is a leading cause of infertility in women as well as developmental disorders and some cancers. Components of the centromere and kinetochore are critical to ensuring accurate chromosome segregation during meiosis, and while many of these components are expressed in mitosis as well, they are not well studied in female meiosis. The reason for this is the difficulty in getting sufficient quantities of oocytes with which to perform experiments. Drosophila are an ideal model for studying oocyte meiosis due to their fast generation time, cheap husbandry, expansive genetic toolkit, and the large amount of oocytes produced per female. In this study we are using Drosophila to assess CENP-C, a key protein at the centromere-kinetochore interface. On the chromosome, localized in the inner kinetochore plates alongside the centromere is CENP-C, a required chromosome protein that maintains proper kinetochore size and a well-timed transition to anaphase. Evidence supports that the inactivation of CENP-C causes mitotic delay during prometaphase, chromosome missegregation, aneuploidy, and apoptosis. We hypothesized that CENP-C has a dosage effect on fertility and nondisjunction. By using loss of function mutants and transgenic expression of wildtype CENP-C, we investigated whether dosage of CENP-C is important for fidelity of chromosome segregation by quantifying fertility and ploidy by following visible phenotypes markers on the Y-chromosome. Our data suggests a critical balance of CENP-C expression for optimal function as both mutants (less than 25% of control fertility) and overexpression (less than 50% of control fertility) leads to subfertility. Surprisingly, there was not a significant increase in aneuploidy in the mutant or overexpression group. At this juncture, it is unclear the cause of these phenotypes. For example, aneuploid oocytes may fail to fertilize resulting in subfertility but also no aneuploidy in the surviving offspring. This is an early exploration into the functions of CENP-C in meiosis and future studies will investigate the mechanisms of the observed phenotypes. Supported by the RiSE at Rutgers program and NIH grant K12GM093854-07A1.

Analysis of Microbial Populations Associated with Electric Hand-Dryers Using 16s rRNA Gene Sequencing. Sabrina Catanese, Pam Monaco, Jodi Evans and Veronica Feeg, Molloy College, Rockville Centre, NY.

The use of electric hand-dryers in public restrooms has increased in response to environmental concerns of overuse and waste of paper products. However, because hand drying is essential to prevent the spreading of infection, controversy has arisen regarding the efficacy and sanitation of electric hand-dryers. In this pilot study we focused on the microbial populations associated with electric hand-dryers in public bathrooms. The aim was to determine the types of microbes left in the recess or base of the dryer, a location likely to allow spreading, and compare them to the types located in a control area of the dryer not likely to be spread. Sterile swabs were used to collect microbial populations from the base (Experimental) and top surface (Control) of electric hand-dryers located within both public New York City bathrooms and campus bathrooms of a Nassau County college. The swabs were then used to inoculate nutrient agar petri and blood agar petri dishes. The petri dishes were incubated for 48 hr and subsequently examined for growth. The colony count was recorded and described. Growth on nutrient agar was extracted for DNA, quantified and sent to LC Sciences for 16s rRNA gene sequencing. Growth on the blood agar was used for gram staining analyses. Based on the sequencing data there were significant differences in microbial populations in the experimental and control regions of the hand-dryers at all taxonomic levels. At the species level microbial populations associated with shedding of human skin are represented to greater extent amongst the control samples while those associated with soil and the human gut are represented to a greater extent amongst the experimental samples. Gram staining results support these findings. Overall these initial data from this pilot study warrant additional studies designed to determine whether electric hand-dryers prevent or promote the spread of microbe-associated disease. These studies were supported by the Department of Nursing and the Department of Biology, Chemistry and Environmental Studies at Molloy College.

Analysis of the Genome of TDanisky. Biling Chen and Urszula Golebiewska, Queensborough Community College, Bayside, NY.

We annotated and analyzed the genome of Mycobacterium phage TDanisky. TDanisky was discovered in 2015 at James Madison University in Virginia. The phage is a member of cluster F and subcluster F1. TDanisky has morphology of *Siphoviridea* with a long and non-contractile tail. It has a genome length of 56,275 bps with 112 predicted genes. We used DNA master, BLAST, HHpred, GeneMark, Phamerator, and other programs to analyze the genes and identify homologies. The closest relatives of TDanisky are Mycobacterium phages Sparkdehily, Saal, and SwaggPiglett. We observed that TDanisky has mainly forward genes with exception of genes 10, 26, 39-45 and 47-49 which are reversed. In addition, we further compare TDanisky with other members of F1 subcluster, the gene content similarity varies from 39.7% to 78.91%. Here we report the functional annotations of TDanisky and additional analysis of specific genes. We were interested in the genes with homologies to WhiB, which is a transciptional regulator. Phages from the F1 subclaster have from one to five WhiB genes. WhiB of TDanisky shares over 40% homology with the WhiB of Mycobacterium smegmatis, its host.

Sequencing the Smoke: The Unseen Microbial Hazards of Vaping. Simon Chen, Kristoff Misquitta, Davida Smyth, The New School, New York, NY.

An e-cigarette epidemic is infecting America's youth: 1 in 5 high school students now "vape," inhaling carcinogens like heavy metals, formaldehyde, and nicotine with each puff. While the dangers of the aerosols produced are well-established, the risks posed by the e-cigarette cartridges themselves–shared among peers, stored uncapped in desks and lockers, and infrequently cleaned–remain unexplored. The objective of this study was to analyze the diversity and potential pathogenicity of bacteria isolated from e-cigarette cartridges, users' noses, and a control group of non-users' noses. Bacteria present on cartridges and nasal swabs were isolated using selective and differential agar plates. The microbiome of each sample was also determined by 16S rRNA sequencing. While few colonies were isolated from the cartridges, several colonies were observed on agar plates from user and non-user noses. Bioinformatic analyses revealed that the nasal bacteria of users were more pathogenic than the nasal bacteria of non-users and different from the bacteria found on the cartridges. These results imply that while e-cigarette surfaces may not contribute to bacterial transmission, the aerosols they produce may still adversely affect the nasal microbiome.

***Haplosporidium nelsoni* DNA was not Detected in Atlantic Oyster Drills from Delaware Bay. Jason Cheng, Lilja Nielsen and Craig Hinkley. Kingsborough Community College, Brooklyn NY.**

Haplosporidium nelsoni is a protozoan parasite that causes the disease MSX (Multinucleated Sphere Unknown) in oysters. The parasite infects the oyster through the gills, spreading to all tissues through the blood vessels, and can eventually lead to death. This parasite has proven to be very problematic, not just to the economy of the seafood market, but to the environment as well. Oysters are considered a keystone species because they provide habitats and shelters for many other aquatic organisms. Therefore, this parasite may result not only in the deaths of oysters, but also many other species of plants and animals that rely on the oysters. The mode of MSX transmission is unknown, and attempts to spread the disease from oyster to oyster have not been successful. In addition, transmission of the disease to uninfected oysters is not dependent on the density or infection level of surrounding oysters. This suggests there could be an intermediate host for transmission of MSX. The main goal for this research is to identify possible intermediate hosts for MSX. A possible candidate as an

intermediate host is the Atlantic oyster drill (*Urosalpinx cinerea*), as it feeds directly on oyster tissue through holes it makes by drilling through the oyster's shell. If oyster drills are an intermediate host, then we should be able to isolate *H. nelsoni* DNA from oyster drill tissue. My hypothesis is that *H. nelsoni* DNA will be present in oyster drills from Delaware Bay. The reason Delaware Bay was chosen is that MSX was first discovered there and the bay still has periodic outbreaks of MSX in its oyster populations. To test this hypothesis, DNA was extracted from the tissues of 12 oyster drills collected at the Strawberry 5 site within Delaware Bay. The extracted DNA was used to PCR-amplify a region of the *H. nelsoni* small ribosomal RNA gene and amplified DNA was separated on a 2% agarose gel. There was no *H. nelsoni* DNA detected in any of the oyster drills that were tested. To show that there was amplifiable DNA present, we PCR -amplified a portion of the oyster drill cytochrome C oxidase I (COX-I) gene. A COX-I gene PCR product was detected for seven of the twelve oyster drills that were tested. Since it is likely that DNA was not extracted from the five oyster drills that tested negative for both the MSX gene and the COX-I gene, we cannot say whether MSX DNA was present. However, the results for the seven oyster drills that tested negative for the MSX gene and positive for the COX-I gene indicate that MSX was not present and we therefore reject our hypothesis. In the future, I would like to test more oyster drills from the Strawberry 5 site and other sites within Delaware Bay. I would also like to test other species that prey on oysters such as boring sponges or whelks. This work was supported by grant? 0537-19-1091 of the CSTEP Program of NYSED.

Natural Variations in Blood Composition of Drosophila. Areeba Choudhry, Jessica Sparacio and Rebecca Spokony, Baruch College, New York, NY.

There are three types of hemocytes present in *Drosophila melanogaster*; plasmatocytes, lamellocytes, and crystal cells. Our project focuses on crystal cells to study the natural variation in the blood composition across ten different genotypes treated with methoprene and ethanol respectively. We treated larvae with 25 microliters of the methoprene-ethanol solution, (1 microgram methoprene / 1 mL ethanol). We treated the control larvae with 25 microliters of ethanol. We hypothesized that there would be variation in crystal cell numbers across the lines and methoprene treatment would lead to an increase in the number of crystal cells. For each genotype and treatment, 10 third-instar males and females were collected, and we used whole-body imaging to compare the different numbers of cells among the larvae. The third instar larvae are heated at 70□ for 10 minutes in a DNA Thermal Cycler. The number of crystal cells present on the dorsal, ventral, and lateral sides is manually counted using clickers. Our results also revealed the variation in crystal cell numbers across the genotype lines. For example for methoprene treatment, genotype line 28247 had the greatest number of crystal cells with the average being 729 crystal cells. The genotype line 28145 had the least number of crystal cells with the average being 111 crystal cells. Our results confirmed our initial hypothesis that for the majority of the genotype lines, the number of crystal cells was greater for the methoprene treatment in contrast to the ethanol treatment. There was also a difference in the response between genotypes to each treatment. For example, genotype line 28233 produced more lamellocytes when treated with methoprene versus ethanol. However, in contrast, genotype line 28179 produced fewer lamellocytes when treated with methoprene versus ethanol. The next steps of this experiment include doing a genome-wide association study (GWAS) to determine if specific genes influence the number of crystal cells in different *D.melanogaster* genotype lines. The work was supported by the National Sciences Foundation and the PSC-CUNY.

Silence of the Genome: The Effects of DNA Methylation on Medulloblastoma Cell Survivability and Development. Anika Chowdhury, Benjamin Honigsfeld, Barbara Pepe, Christina Rubino and Noelle Cutter, Molloy College, Rockville Centre, NY.

Medulloblastoma (MB) is the most common malignant brain tumor of childhood, and it accounts for about 20 percent of all pediatric brain tumors. Survival rates in children vary depending on the patient's age and tumor malignancy. Treatment options for medulloblastoma tumors consist of neurosurgery, craniospinal radiation, and chemotherapy. Unfortunately, many patients become resistant or are intrinsically resistant to treatment. Therefore, a better understanding of the molecular biology of tumor function and survivability is essential. There are four subtypes that have been identified in children with medulloblastoma:WNT-activated, SHH-activated, Group 3 (non-WNT / non-SHH), and Group 4 (non-WNT / non-SHH). These heterogeneous subgroups of MB frequently have rare individual genetic alterations, but have been shown to have altered epigenetic regulation, such as distinct methylation profiles. Another concern in the progression of tumors is angiogenesis; New blood vessels supplying the tumor with blood, oxygen, and nutrients allows for tumor growth, development, and metastasis.We hypothesize that tumor cells take advantage of alterations in methylation to become resistant to treatment. Our results indicate that Group 3 and Group 4 MB cell lines treated with chemotherapy reagents have altered methylation profiles, avert apoptosis, and demonstrate angiogenic potential. Furthermore, our in-vitro analysis identified that when cells from the SHH MB cell line DAOY are treated with cisplatin, they exhibit an altered methylation pattern which we suggest is linked to a change in gene expression. This in turn suggests responsibility for increased chemoresistance. Molecularly treatment options are limited, and targeted therapies are still in preclinical development. Therefore, using multiple approaches, such as epigenetic modification to attack these aggressive tumors are needed to improve survival rates.

The Curious Case of Medulloblastoma: An Analysis of Molecular Alterations in Chemoresistant Cells. Paul Cuellar, Debora Vargas, Cara Lucarelli, Melissa Husein and Noelle Cutter, Molloy College, Rockville Centre, NY.

Medulloblastoma (MB) is one of the most common and aggressive CNS tumors in children. Tumors are formed as a result of the aggregation of abnormal cells; studies have identified a subset population of tumor cells which elicit stem cell like properties. The Cancer Stem Cell (CSC) hypothesis states that tumors arise from normal cells, this relates to the hypothesis as CSCs express self-renewal capabilities similar to that of developmental cells. Stem cells serve as the foundation for somatic cells, having the ability to develop into different cells. Being that stem cells are not differentiated, they do not elicit properties that a developed cell presents. This relates to CSCs as they can regenerate tumors in vivo and do not present distinct tumor cell qualities. These CSCs represent a significant clinical challenge as they are resistant to conventional cancer therapies and play essential roles in metastasis and tumor relapse. The aim of this study was to investigate the significance of CSC gene expression in MB cell lines. Our data indicates that several key developmental markers such as FZD1, FZD9, TWIST1, Ecat1 and OCT4 play a central role in the development and differentiation of multiple cell lineages. Along with genotypic effects, phenotypic analysis of MB cell lines were studied in relation to chemoresistance. Our observations showed a distinct enlargement of cell circumference which resembles early cellular development. We hypothesize that the presence of these cells in tumors contributes to a patient's likelihood of recurrence post-treatment, and may be the cause of resistance in tumors that do not respond to traditional chemotherapy regimes. Taken together, our results indicate that changes in cellular phenotype involving gene expression results in the elaboration of a cell's particular morphology and function. This morphology is key in the development of resistance to therapy. Therefore, therapeutic approaches targeting CSCs in MB may have great significance on the cancer treatment, but there are still several issues requiring extensive future investigations.

Demographic Parameters, Control Efforts and Impacts of the Invasive *Corydalis incisa* Along Riparian Habitat in Westchester County. Matthew DiJoseph and Christina M. Andruk, Iona College, New Rochelle, NY.

Corydalis incisa is an annual, biennial herb that's native to Asia. Its distributed across several states of the US, discovered in NY in 2005 and in Westchester County in 2014. We have detected populations along the Bronx River and in parks in different watersheds and have been monitoring its presence since 2017. Data show that *C. incisa* is shade tolerant and is commonly found in riparian areas with flood deposition. Ninety, 1 m2 plots were established along the Bronx River Parkway Reservation in spring 2017 and surveyed in 2018 and 2019. We found that populations of *C. incisa* have an average of 29 adult plants per m2. We found a significant negative correlation between *C. incisa* cover and another spring dominant non-native, *Ficaria verna*, indicating competitive effects. However, we found an overall positive relationship between *C. incisa* cover and total non-native cover, indicating that it thrives in disturbed areas. We did not find a significant relationship between *C. incisa* cover and total native cover, indicating that it may not impact native diversity as much as previously hypothesized. We are using the plots to study the effects of control efforts including pulling, clipping, and seeding with native species. Preliminary analysis has found that clipping is not effective, and that seeding has limited efficacy. We sampled 50 individuals in two populations of *C. incisa* from two different watersheds to obtain demographic parameters. On average, adult plants have 24 fruit and flowers, so each square meter populated with *C. incisa* will have 696 reproductive organs. The average seed pod contains 7 seeds, resulting in an average of 4416 seeds/ m2. We measured seed viability with tetrazolium staining and found average viability of 86% over 3 years. We have begun a long-term analysis of seed viability in the soil seedbank. Seeds were placed in plastic teabags and buried at 3 different sites. Samples will be collected every 3 months and the viability change over a 3-year period will be determined. Analysis of plot data and our personal observations have demonstrated the difficulty in studying an ephemeral plant species in a dynamic riparian system. *C. incisa* was often absent from our permanent plots the following year, even though it was still present in the vicinity. We discuss alternative monitoring and assessment techniques.

Assessment of Enterococcus Levels in NY Harbor During the 2019 Recreational Boating Season. Marinha Domingues, Marjona Mardonova, Joshlyn Mensah, Robert Buchanan, Kathy Nolan and Victoria E. Ruiz, St. Francis College, Brooklyn, NY and NYC Water Trail Association, New York, NY.

New York Harbor is a widely used resource for aquatic recreational activities including kayaking and canoeing. Human use and illegal spilling of industrial and human waste may have harmful effects on aquatic organisms and impact human health. Enterococci detection is frequently used as an indicator of fecal contamination. In collaboration with the Citizens Water Quality Testing Program, we assess levels of the bacterial genus Enterococci over an 18 week period, from the East River at Brooklyn Bridge Park and Coney Island Creek, at Calvert Vaux Park. We hypothesize that increased human and animal activity is associated with increased Enterococci levels. To test this hypothesis, water samples were collected from the East River (Pier 2, Pier 4, and DUMBO Pier) and Coney Island Creek (Calvert Vaux

Park). Enterococci levels were measured using the Enteroalert IDEXX kit. Samples were placed in IDEXX quanti-trays for subsequent enumeration and incubated at 41□ for 24 hours. Calvert Vaux Park exhibited higher levels of Enterococcus compared to the sites located at Brooklyn Bridge Park, which had moderate to high levels of Enterococcus. The average Enterococci levels at Calvert Vaux Park were 8201 MPN per 100mls of water, this was 10 times greater than last year. Pier 4 also displayed high levels of Enterococcus however significantly less than Coney Island creek. Increased anthropogenic activity is not correlated with Enterococci levels suggesting other factors associated with increased Enterococcus levels. The sustained high levels of Enterococci may have potential public health implications and may be correlated with combined sewage overflow and rainfail.

Testing the Expression of Multiple Bactofilin Isoforms in *Myxococcus xanthus.* Jack Dunican and David Zuckerman, Iona College, New Rochelle, NY.

The bactofilin BacM, a polymer-forming cytoskeletal protein, of *Myxococcus xanthus* has been observed as two isoforms with different molecular weights. Though it was originally hypothesized that the protein matured by proteolysis, our lab has new evidence that there are two different start codons within the bactofilin mRNA, allowing for translation to be initiated at both the first (generating the larger isoform) or second (generating the smaller isoform) start codon. Three additionalbactofilins are encoded by the *M. xanthus* genome (*bacN*-*P*) and whether any of these other bactofilinsare expressed as separate isoforms is unknown. Vectors encoding each of the four bactofilins in *M*. *xanthus* were engineered with an epitope tag (FLAG) attached to the 3' end of the gene. Genes were amplified by PCR, and the primers included the FLAG sequence. PCR products and a vector were digested by restriction enzymes and joined in a ligation reaction. The resulting plasmids will be transformed into *M*. *xanthus* and expressed as a fusion with the FLAG epitope. The expression of these constructs will be analyzed by immunoblotting with an anti-FLAG antibody, allowing us to determine if additional bactofilins are expressed in multiple isoforms.

Secondary Structure Analysis by Shape-Map of the EGFR Pre-MRNA Transcript: Uncovering Novel Regions for RNA Anti-Sense Targeted Therapy. Ryan Fink and Martin Hicks, Monmouth University, West Long Branch, NJ.

Glioblastoma Multiforme is the most common primary brain malignancy with a median survival time of thirteen months. A common aberration in Glioblastoma Multiforme is the overexpression and constitutive activation of tyrosine kinase receptors (RTK). One RTK, epidermal growth factor receptor (EGFR), is dysregulated in 57% of all GBM. Standard care of GBM includes temozolomide, radiation and resection which increases survival time to 14-15 months. Many therapeutic strategies in the pipeline are unable to cross the blood brain barrier. Therefore, our lab developed a novel therapeutic approach which delivers a gene directly to the CNS using an adeno-associated virus gene transfer vector to encode either RNA or protein therapeutics. Our current approach is to deliver an RNA molecule with complementarity to critical splicing elements surrounding Intron 10 of the EGFR pre-mRNA transcript. Cryptic splice sites embedded within intron 10 allow for transcription to produce a shortened EGFR transcript. Alternative splicing is regulated by secondary structure of the pre-mRNA nascent transcript. To improve our therapeutic strategy, we have begun experiments to analyze the EGFR secondary structure using selective 2' hydroxyl acylation and primer extension followed by mutational profiling (SHAPE-MaP). The SHAPE reagent 1-methyl-7-nitroisatoic anyhydride (1M7) or 5-nitroisatoic anhydride (5-NIA) reacts with the 2' hydroxyl of RNA molecules when the RNA molecule is in a conformationally flexible position creating a 2' O-adduct. The modified RNA is reverse transcribed, incorporating mismatches at the acylated positions; a comparison of unmodified to modified RNA will allow us to determine RNA nucleotides that are involved in secondary structure, part of RNA-binding-protein complexes, or single stranded. Single stranded RNAs and RNAs with minimal structure are a preferential target of our therapy. We hypothesize that the secondary structure of the RNA of Intron 10 will determine the most effective way to approach synthetically altering the splicing of the EGFR pre -mRNA. Also, the secondary structure of the pre-mRNA will give further insight into understanding the mechanism of alternative transcripts induced by nature. SKMG-3 cells were grown in DMEM with 10% FBS and passaged 4 times. DNA was extracted from a confluent T-175 with Qiagen DNeasy Kit and used as the template in subsequent PCR. The DNA sequence of Exon 10, Intron 10, Exon 11 was PCR amplified and ligated with tA cloning into the pMINIT2.0 plasmid. The plasmid was sequence was verified with Sanger sequencing. The plasmid was amplified in PCR with a T7 promoter-tail forward primer and reverse primer corresponding to exon 11, this generated the template for T7 RNA transcription. RNA was purified by RNA gel electrophoresis. 0.5-10 pmol of RNA was used in acylation reactions. RNA was acylated, reverse transcribed under SHAPE conditions with Superscript II and converted to dsDNA. The dsDNA was sequenced on Oxford Nanopore Minion. Currently, millions of reads are being processed through the ShapeMapper2 pipeline. ShapeMapper2 output will determine a per-nucleotide structure that will help us determine targets of our current gene therapy.

Examining the Presence of *Enterococcus spp.* in Water Around NYC Using Loop Mediated Isothermal Amplification (LAMP), an Alternative Method to PCR. Malcolm Fox and Andrew Nguyen, Queensborough Community College, Bayside, NY.

Contaminated food and water are a major public health concern. Monitoring waterborne microorganisms resulting from poor sanitation or sewage run off is essential to prevent future outbreaks. One microorganism commonly examined in the water is Enterococcus spp. In New York City, there are several wastewater treatment centers, which process the sewage and water runoff before flushing the treated water into the East River. High levels of microorganisms in the water would increase the risk of developing gastrointestinal tract infection in those who are exposed to it. We hypothesize that the runoff from heavy rain in New York City will increase the level of Enterococcus spp. in the water of the East River. The Standard Fecal Indicator Bacteria (SFIB) is a common test used to detect microorganisms in water. This test relies on Polymerase Chain Reaction (PCR) to amplify several genes found in Enterococcus spp. This method requires a thermocycler and 3 to 4 hours for completion. We used a quicker method which does not require a thermocycler. The loop mediated isothermal amplification (LAMP) was used to test the hypothesis. Enterococcus spp. was monitored in water samples collected from the East River in New York City over a three-month period and tested for the presence of the 23S gene of Enterococcus spp. using LAMP method. The sensitivity and specificity of LAMP was compared to the EPA approved IDEXX test. Amplification products of the 23S gene for the Enterococcus spp. using LAMP method can be detected by ethidium bromide staining, Sybergreen intercalating to amplified DNA and molecular beacon. Evidence from this work supports the hypothesis that after heavy rain, there was a spike in Enterococcus spp. in the water from the East River of New York City. Malcolm Fox is a participant in the NIH Bridges to the Baccalaureate Program at Queensborouh Community College R25GM065096.

The Deciphered Voynich Manuscript As a Key To the Preserved Biology Knowledge During The Early Renaissance Period. Yekaterina Gabova and Sergey Gabov, University of Bridgeport, Bridgeport, CT.

The Voynich the manuscript is an ancient illustrated codex, carbon-dated to approximately the 15th century C. E., hand-written in an unknown writing system, and considered to be one of the most prominent unsolved cryptography cases. Some pages of the manuscript display the drawn images of different herbs, their leaves, and roots. We suggest that decoding the manuscript promises to expand the modern biological and ecological concepts. Similar to the Great Pyramid of Giza, which had been sealed until a certain time, the manuscript contains the preserved and ancient understanding of plants. The hypothesis became a foundation for this work, which, after 5-years of extensive research, yielded significant results. We show that the author used a digital code to write the manuscript, using the dots on a number line to encode the letters within the characters. Based on the statistical analysis, we locate the coordinate system on the codex and provide the digital code for consonants, vowels, and abbreviations. Using the method stated above, we were able to detect the code and the original language of the enciphered codex. The names of three different plants and their descriptions in the manuscript were compared to the already existing knowledge of evidently the same or similar plants in herbal medicine. The results show that the recipes from the manuscript not only correspond to the already studied properties of the plants but also contain information that needs to be further researched and that has the potential to expand the horizons of the biological and medical understanding of the plants. The manuscript can help analyze the different techniques used for the treatment of various diseases during the Early Renaissance and it can help study the ancient understanding of the properties of the plants. This paper proposes the hypothesis that the Voynich manuscript is a collection of recipes that provides more insight into the properties.

Designing and Testing RNA Therapeutics to Block VEGFR2 and EGFR Activation in Human Glioblastoma. Flobater Gawargi and Martin J Hicks, Monmouth University, West Long Branch, NJ.

Glioblastoma multiforme (GBM), is the most common and aggressive malignant primary brain tumor with a median survival of 14 months. Current therapies are limited by the blood brain barrier. Tumor blood vessel formation depends on vascular endothelial growth factor receptor 2 (VEGFR2), while tumor cell proliferation is stimulated by epidermal growth factor receptor (EGFR). Both are important for tumor cell survival. In our lab, we are developing an innovative therapy that can bypass the blood brain barrier by developing RNA therapies to alter the splicing mechanism of the VEGFR2 and EGFR genes to reduce or block their activation, thus stop tumor cell angiogenesis and growth. Can we generate therapy vectors that encode antisense RNA therapeutics that either block or activate splicing motifs and alter the expression of functional VEGFR2 and EGFR in GBM? Forty-five antisense sequences were designed to target the EGFR gene and nine antisense sequences for VEGFR2, to potentially block their activation. The antisense sequences were cloned into pAAV-U7-smOPT. In addition, multiple strategies were used to clone the exonic splicing silencer 4G-quadruplex and five distinct exonic splicing enhancer motifs into the RNA anti-sense therapy vector. Moreover, another aspect of this research is to isolate the mRNA of multiple tyrosine kinase receptors from GBM cancer cells, clone the cDNA into a T7 expression vector to transcribe control RNA to use in our high throughput sequencing

experiments. Multiple cell lines including U87 and SKMG3 cell line are being cultured and transfected with our novel therapies. Total mRNA was collected, analyzed, and compared to the same cell lines without treatment. The collected data allow analysis of efficacy of current anti-VEGFR2 and anti-EGFR therapeutic strategies to move into a mouse model using adeno-associated virus (AAV) vector.

Development of a Plant Cytotoxicity Assay For Testing Newly Synthesized Antimicrobial Compounds Against Plant Pathogens. Sommer Gomez, Daniel Antunes, Youklendy Calderon and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

Antibiotic resistant pathogenic bacteria are a growing concern for economically important crops. *Erwinia amylovora* and *Pectobacterium carotovorum* are Gram-negative bacteria of the *Enterobacteriaceae* family. These bacteria have been found to affect many plant host species such as potatoes, squash, apples, and pears causing contagious plant disease such as fireblight. Finding new therapeutic approaches using novel antimicrobial compounds is vital as the number of antibiotic resistance infections including Streptomycin resistance are increasing. Several hydroxamic acids and their analogs were synthesized by the chemistry department and tested in our laboratory for antibacterial activity against different ATCC strains of pathogenic bacteria. Our focus was to develop a plant infection cytotoxicity assay using different fruits and vegetables. This plant model will allow us to test the cytotoxicity of the agents that have shown significant antimicrobialactivity against bacteria of the *Enterobacteriaceae* family. Future work will focus on testing all chemical compounds for antibacterial property and cytotoxicity using the plant assay.

Project FeederWatch, Year Five: A Garden of Birdly Delights. Sara Gonzalez, Alaa Barbour, Catherine Argueta, Julia Diaz, Claudio Amaya, Bianca Cantillano, Gabriela Mosqueda, Valeria Hernandez, Busayo Adewale, Disleiny Perez, Pamela Fernandez, Escarleth Quinonez, Alexis O'Callahan, Brittanie Fils, Vy Giang, Sherane Raymond, Jill Callahan, Brandy Garrett Kluthe and Katherine S. Wydner, Saint Peter's University, Jersey City, NJ.

Project FeederWatch (PFW) is an annual winter survey of birds that provides information about changes in bird distribution and abundance across North America. From November to April, birds at and around feeders are counted according to an established protocol and reported to a database managed by the Cornell Lab of Ornithology and Bird Studies Canada. Data on bird species and the highest number of each species are recorded. On our urban campus in Jersey City, NJ, PFW has been conducted for five seasons. Over the first four seasons (2014-2017), a total of eighteen species were identified although only five species were present every season: house sparrows, mourning doves, European starlings, American robins, and northern mockingbirds. In the summer of 2018, a grant enabled us to begin to renovate the PFW count area by removing foreign invasive plants, restoring natural habitat through planting native flora such as wildflowers, and adding a water bath and a second feeder with sunflower seeds. As a result, the season just completed (2018-2019) has demonstrated a significant increase in species diversity on a weekly basis with visits from many native songbirds, some observed for the first time.

Simple and Affordable Kinetic Assay of Nucleic Acids by Gel Staining. Danielle Guillen, Mika Schievelbein, Kushkumar Patel, Davis Jose and Jonathan Ouellet, Monmouth University, West Long Branch, NJ.

In an effort to circumvent the pitfalls of using radioactive labeling to measure kinetics in undergraduate labs, a gel staining kinetics assay was developed. The IR-3 enzyme and substrate, a single stranded DNA that cleaves another single stranded DNA only in the presence of Zn++, was used as a simple and inexpensive DNA model. The rate of the IR-3, or D-Zyme , was successfully determined by staining PAGE-Urea gels with SYBR Gold and then viewing them at 302 nm with epi-illumination. The open source software ImageJ (version 1.52K) was utilized to quantify the relative band intensities, the ratio of cleaved product to the addition of product and substrate gave percent cleavage. When percent cleavage was plotted against time in Minitab (version 18.1, Minitab, Inc.), the rate of the reaction could then be determined by nonlinear regression curve-fitting to the single exponential. To certify this technique, it was also tested on two other models, one being a modified version of the D-Zyme, while the other was a known Hammer Head Ribozyme, trans RzB. It was demonstrated that the use of SYBR Gold post-migration staining can be used to quantify RNA and DNA bands for cleavage kinetic analysis, without substrate labeling. Although this method is comparatively less sensitive than radioactive and fluorescence.

An Evaluation of Fecal Indicator Bacteria Along the Coast of Monmouth County, NJ Post Rainfall Events. Kelly Hanna, Lohnes, Victoria, Erin Conlon, Skyler Post, Maria Riley, Ariel Zavala, Jeffrey H. Weisburg and Jason E. Adolf, Monmouth University, West Long Branch, NJ.

Monmouth County beaches accommodate an abundance of recreational activity. Many locations, however, are near stormwater or coastal lake outfall pipes. The New Jersey Department of Environmental Protection (NJDEP) performs weekly testing of fecal indicator bacteria (FIB) known as Enterococcus. These bacteria are found in mammalian intestinal tracts and are indicative of fecal matter containing other harmful bacteria, protozoa, and viruses present in the water. Fish and birds provide a portion of what is found from testing, but higher amounts have suggested runoff from pipes after high rainfall events. The current limit of the FIB is 104 CFU per 100 mL of water. Evidence of increased Enterococcus levels after high rainfall events is acknowledged, but in-depth research providing numerical data for these correlations has yet to be published. Forecast models used to predict this data are also absent. This study has provided quantifiable data on the relationship between environmental

conditions and Enterococcus levels, including time between rainfall events at five sites between Long Branch and Asbury Park, New Jersey. The project will continue to assess trends as it progresses through Fall and Winter in the hope of creating a forecast model to give surfers and beachgoers the ability to determine how safe the water is before travel to the beach. As FIB in coastal waters is a global issue, these models may provide application to future research and broader regions.

Frequency of Antibiotic Resistance Genes and Sensitivity to Antibiotics and Natural Oils in Bacteria Isolated from Human and Environmental Samples. Erica M. Hernandez, Sara Hernandez, Lindsey Njanja, Valeria Correa, Mina Echreshzadeh, Riya Chaudhary and Luis E. Jimenez, Bergen Community College, Paramus, NJ.

Antibiotics are used to treat common bacterial infections such as skin infections, gonorrhea, syphilis, pneumonia, and tuberculosis. Misuse of antibiotics causes many of these bacteria to evolve resistance so when people get sick treatment becomes ineffective. Bacteria isolated from different parts of the human body and environmental samples were analyzed to determine their antibiotic profile and the presence of antibiotic resistant genes. All bacterial colonies were identified using PCR analysis and sequencing of 16S rRNA genes. Body samples showed that some people were colonized by *Staphylococcus aureus* while environmental samples showed the presence of *S. epidermidis, S. haemolyticus, S. cohni, S. sciuri*, and *Bacillus endophyticus*. Different levels of sensitivity to antibiotics and natural oils were detected. Of all antibiotics tested, novobiocin showed the greatest zones of inhibition while tea tree and lavender oil were the best antibacterial oils. Some bacteria showed the presence of antibiotic resistance genes. Of all 5 genes tested, mecA was the most abundant gene detected in bacteria.

Accessing Bioluminescence: Exploring Sustainable Environments for Bioluminescent Microorganisms, and the Possibility of Using Bioluminescence for Disaster Relief. Leah Hughes, Davida Smyth and Eugene Lang, The New School, New York, NY.

The goal of this project is to create bioluminescent portable lights that are particularly directed towards disaster relief. With continuously growing reliance on electricity, as well as increasing destruction caused by natural disasters with rising intensity due to climate change, it is important to consider new technologies for providing assistance to communities that are in crisis. Bioluminescence could provide a short term emergency light source for communities that are in transition or have been damaged, until a more reliable source of light can be implemented. Throughout this project, simplified alternatives to recommended requirements of bioluminescent organisms are being studied in order to make bioluminescence accessible as a resource to the public. The bacterial strain *Vibrio fischeri* expresses bioluminescence through quorum sensing. In high density they have been found to provide light consistently in the dark. *V. fischeri* however are highly sensitive to the nutrients provided to them. While research is being conducted to create nutrient sources for these bacteria, the dinoflagellate *Pyrocystis lunula* is also being researched, as it is less sensitive to its living conditions and may therefore be more accessible as a producer of light to communities in states of emergency. It has been determined that sources of nutrients for dinoflagellates can be created using fertilizer and minerals found in vitamins. Research is being conducted to determine an affordable and sustainable recipe for dinoflagellate nutrients. Dinoflagellates provide a challenge in that they must be irritated constantly in order to provide sufficient lighting, therefore vortex variations have been constructed and experimented with in order to maintain bioluminescence. This vortex must also operate without electricity, so research is being conducted to determine alternative methods of producing power through a coil powered and mudd-watt battery. Research will culminate in the design and construction of a sustainable, scalable environment for bioluminescent microorganisms to grow and be self sustaining in a solution with the least amount of maintenance necessary from the user. While research primarily is directed towards the production of short term lighting alternatives for areas affected by natural disasters, research will naturally produce a template for artists and designers to further their work with bioluminescence. It will allow them to scale their projects for marketability and will decrease the amount of resources spent on research, experimentation and maintenance. This research will discuss the time it takes the bacteria to reproduce, the living conditions they require to thrive, nutrient alternatives, the types of solutions they can exist in and whether that affects the light they produce, and ways of maintaining population size.

The Effect of Landscape Fragmentation on the Mycobiome of Seedlings Through the Lense of the Janzen-Connell Hypothesis. Salem Hunter[1], Alison Thorson[1], Madeline Rauch[1], Michelle Hersh[1] and Cathy Collins[2], [1]Sarah Lawrence College and [2]Bard College, Bronxville, NY.

Landscape fragmentation has become an increasing concern in many ecosystems as humans are expanding and intensifying our environmental impact. Fragmentation can disturb ecological processes that are vital to maintaining biodiversity. The Janzen-Connell hypothesis is a mechanism for biodiversity maintenance. It states that host-specific pathogens of a parent plant make the nearby soil unfavorable for that species' seedlings, thus as distance from a parent plant increases, likelihood of seedling survival also increases. Understanding this process can help us understand how biodiversity is maintained. With this research we aim to examine the relationship between fragmentation and fungal pathogen biodiversity by looking at the mycobiome of seeds of

seven plant species within small fragments and large fragments. We hypothesized that both fragmentation and host identity would alter the fungal mycobiome within these seeds. Our field study site was an experimentally fragmented landscape in Lawrence, Kansas at the University of Kansas field station. Our lab group cultured approximately 1500 fungi from seven plant species whose seeds were buried in the fragments and unearthed one year later. Fungal DNA was amplified using PCR and was then sequenced. We identified the fungi using DNA barcoding using the BLAST database. Our sequences revealed 95 OTUs with more than one representative sequence, as well as 86 singleton OTUs, for a total of 188 OTUs so far from 863 sequences. This study is important for understanding how biodiversity will continue to be affected by fragmentation through the lense of the soil mycobiome. This could also provide more insight into how seed-specific pathogens affect the survival of different plant species.

Examining the Role of Fascin in Primary Brain Cancers. Mehdi Husaini and Cathryn Kubera, Monmouth University, West Long Branch, NJ.

As one of the main actin-bundling proteins found in the body, fascin plays an important role in maintaining many regulatory behaviors, such as proper cell-cell adhesion through cytoskeletal structures as well as a cell's motile and invasive properties, making it important to study in cancer cells due to established fascin overexpression. Upregulation of fascin in colorectal and breast cancer cells leads to increased metastatic and invasive properties, and the protein has been implicated in gallbladder, pancreatic, and prostate cancer as well. Primary brain cancers, which can be very aggressive, also seem to have elevated fascin levels that correlate with tumor grade but have not been studied to the degree of other cell lines, disrupting the traditional ideology behind the investigation. We previously characterized fascin gene expression in brain cancer cell lines using RT-qPCR and immunocytochemistry to determine relative protein abundance, where preliminary results show robust fascin mRNA and protein presence in Neuro2a neuroblastoma and A-172 glioblastoma cells when compared to controls such as Human Embryonic Kidney cells (HEK293), which have reportedly low fascin expression levels. Current findings have allowed us to move into manipulating fascin expression to assess its effects on cell motility using a 2D invasion assay. Using a Biotek Cytation 5 multi-mode plate reader, we have accumulated extended time-lapse imaging of cancer cell invasion across varying fascin expression conditions. These video montages have allowed us to conduct computerized evaluation of whether fascin overexpression increases cell motility related to metastasis and invasion, while using the designed invasion assay to observe cell movement into unoccupied space in real time. This project provides a visualization of the effect of varying fascin expression on the motile properties of primary brain cancer cell lines in hopes of identifying a therapeutic target.

Mitochondria Transfer Through Tunneling Nanotubes (TNT): A Method For Image Analysis. Ariana Incantalupo, Brandon Leon, Kimberly Fuentes and Jodi Evans, Molloy College, Rockville Centre, NY.

The phenomenon of intercellular transfer of mitochondria was first discovered in 2006, and since then many researchers have continued to investigate its role in cell-cell mediated rescue of cellular respiration and restoration of cellular function. The primary mechanism(s) of mitochondria transfer are still under investigation and include transfer through tunneling nanotubes (TNT), gap junctions, exosomes, and cell fusion. Mesenchymal stem cells (MSC) are multipotent stromal precursor cells that can differentiate into a variety of connective tissues, such as osteoblasts, adipocytes, neurons, and epithelial cells. MSC have been shown to be capable of forming TNT when in culture with macrophage cells. These TNT, which are cytoplasmic bridges between the cells, facilitate the transfer of mitochondria. Our method for analyzing the mitochondrial transfer between cells through TNT's, began with the labeling of the mitochondria in MSCs using MitoTracker™. This dye selectively accumulates in the mitochondrial matrix where it covalently binds to mitochondrial proteins by reacting with free thiol groups of cysteine residues. The Mitotracker is partially selective in labeling towards some mitochondrial proteins. This selectivity stems from the high MitoTracker™ concentration in the mitochondrial matrix that favors alkylation of the available thiol groups in this subcellular compartment. MSCs were plated in 8 - well chambered cover glass at 5.0 $\times 10^4$ cells/mL and after 24 hr of culture they were labeled for 45 min with 200 nM MitoTracker™. While the MSC mitochondria were being labeled, the macrophage cells were labeled with PKH67 Fluorescent Cell Linker in preparation for co-culture. The cell linker consists of intensely fluorescent dye moieties attached to long, lipophilic tails. The lipophilic tails diffuse into the cell membrane, leaving the fluorogenic moiety exposed near the outer surface of the cell. After labeling, they were plated with the MitoTracker labeled MSC at 5.0 $\times 10^4$ cells/ mL. Images of the co-cultured, labeled cells were taken at time points of 1, 3, 5, 7, 8, and 24 hours using the appropriate filter sets to detect the fluorescent dyes. It was imperative to label the membrane and mitochondria of the cells separately to ensure the transfer seen in the images was genuine. Many methods of observing these TNT's fail to account for the possibility of MitoTracker™ leaking out of cells distorting the image, as well as using an overextended time frame to observe the connections. We observed that any time frame that exceeded about 5 hours resulted in the loss of image quality and an increase in MitoTracker™ leakage. Using ImageJ software, we were able to quantify the length and numbers of TNT formed by the MSC when in co-culture with macrophage. This method can be applied to future studies investigating the mechanisms of MSC modulation of repair activity and immune cell function in normal and disease states.

Are Native Crab Species in the Bronx River Being Affected Via Direct Competition by the Invasive Crab Species *Hemigrapsus sanguineus*? Emily Jaramillo and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

After non-native invasive species colonize a habitat they can have devastating effects on the native flora and fauna. Such species are known to endanger the populations of native species and wreak havoc by interfering with established food webs. More specifically, the benthic region of Soundview Park in the Bronx has been invaded by the Asian shore crab (*Hemigrapsus sanguineus*) and its population size since then has exponentially increased. Such a sharp increase in abundance of the species may be due to increased competition between crab species due to a niche overlap. Using the ribbed mussel, *Geukensia demissa*, both a field experiment and lab trials were conducted to collect data related to the invasive behavior and effects of *H. sanguineus* in Soundview Park. We proposed that *H. sanguineous* will outcompete native crab species when smaller bivalves are present; native crabs will preferentially consume larger bivalves in order to avoid competing with *H. sanguineus*. Results for both the field and lab experiment indicate that *H. sanguineous* shows no preference for any size *G. demissa*, which maybe attributed to the relative abundance of *G. demissa* in Soundview Park as well as the presence of other largely preferred food sources such as worms, clams, and oysters.

The Effects of Developmental Pb-Exposure on Pilocarpine and Kainic Acid Induced Seizures. Jewel N. Joseph[1], Michelle A. Vasquez[1], Ericka Cabanas[1], George Cruz[1], Evan Clarke[1], Eric Khairi[1], Jean-Martin J. Chrisphonte[1], Isra Ahmed[1], Kirsten P. Lynch[1], Jalen R. Bonitto[1], Lorenz S. Neuwirth[1] and Youngjoo Kim[1,2], SUNY Old Westbury, Old Westbury, NY and [2]iCARE, Old Westbury NY.

Lead (Pb) is a neurotoxin that causes lifelong cognitive dysfunction by altering the levels of brain excitability. Here we examined whether or not the effects of an environmentally relevant Pb exposure (1,000 ppm) in Long Evans Hooded rats would increase the seizure susceptibility in response to the cholinergic muscarinic receptor agonist Pilocarpine and the glutamatergic agonist kainic acid. Cholinergic neurons project from the medial septal nuclei to the entorhinal cortex (the main entry pathway of the hippocampus), which are most susceptible for evoking seizures. The projection fibers from the medial septal nuclei to the entorhinal cortex are comprised of ~45% cholinergic and ~30% GABAergic neurons, respectively. Further, Pb treatment showed less frequent and a reduced degree of seizure severity when compared to Control rats dependent upon sex. In contrast, the seizure phenotype was different in Pb-exposed rats when challenge by kainic acid when compared to pilocarpine. Pb -exposed rats showed more brain excitability and sensitivity to kainic acid induced seizures over pilocarpine induced seizures. Taken together, the present study suggests that Pb-exposure may selectively destroy cholinergic neurons via excitotoxicity (i.e., cholinotoxicity) thereby reducing the ability to evoke medial septal cholinergic seizures in the entorhinal cortex as a plausible explanation of altered brain excitability through this neurochemical pathway. In contrast, given the nature of Pb/Ca competition via glutamatergic NMDARs, Pb-exposure is more sensitive to this pathway. These results suggest that a behavioral pharmacological dissection of the brain excitability patterns are required to better understand how Pb-exposure may not only alter seizure threshold and activity, reduce cortical inhibition, and more importantly dysregulate brain activity patterns that may be responsible for cognitive and intellectual abilities in response to this environmental neurotoxin (SUNY-OW Faculty Development Grant).

Spectroscopic Evaluation of the B To A Conformational Transition In Duplex DNA Using Fluorescent Base Analogues. Michal Kalisz, Brianna Miller, Kirsten Lawson and Davis Jose, Monmouth University, West Long Branch, NJ.

The transition of the standard B-form DNA helix to A-form DNA was first seen by X-ray imaging of DNA fibers in 1953. Over time, the structures of B and A DNA have been further characterized with many higher resolution crystal structures. The transition of B-DNA double helix to A-form is essential for biological functions as recognized by the presence of A-form DNA in many protein-DNA complexes. Recently it was proposed that the shorter length of the A-form DNA compared to the B-form DNA might play an important role in duplex DNA packaging in bacteriophages and that this conformational change might itself serve as the source of the large forces generated by the DNA packing motors. Even though it is known that the B to A conformational transition occurs, the specifics like where in the DNA it originates, how it propagates, and the detailed step-by-step mechanism involved is still unknown. By using site specifically positioned fluorescent oligonucleotides, we explored the local and global conformational changes in this highly biologically relevant transition. Our results showed that by using 2-Aminopurine (2-AP), a fluorescent analogue of Adenine, we could monitor the local and global conformational change simultaneously.

Evaluation of Physical and Chemical Characteristics of NYC Harbor During 2019 Recreational Boating. Karishma Kalloo, Mariah Allen, Robert Buchanan and Victoria E. Ruiz, St. Francis College, Brooklyn, NY.

The bodies of water of New York Harbor are hubs for summertime recreational activities. Although water quality levels in these locations are recorded to be the cleanest within the last century, the increased anthropogenic activity can still impact water quality and thereby affect both aquatic life and potentially human health. Enterococci is used as an indicator for levels of fecal contamination

and water quality. In collaboration with the Citizens Water Quality Testing Program, levels of bacterial Enterococci were assessed over an 18 week period from Brooklyn Bridge Park (East River) and Calvert Vaux Park (Coney Island Creek), Valentino Park, and Bush Terminal Park (Inner and Outer Pools). Previous work has demonstrated high Enterococci levels in Coney Island Creek compared to East River sites (DUMBO, Pier 2, Pier 4). We hypothesize that physical and chemical characteristics are directly correlated with Enterococcus levels. Nine physical and chemical characteristics of the water were measured in conjunction to Enterococci levels for each location. Water samples were collected from each location from Brooklyn Bridge Park (Pier 2, Pier 4, DUMBO Pier) and Calvert Vaux Park. Three probes were used on site each week; for Dissolved Oxygen, Conductivity, and Temperature. Six probes / ion selective electrodes were used in the lab; for Turbidity, Salinity, pH, Calcium, Chloride, and Ammonium ions. Salinity and Chloride levels decreased over time across all across all sites. Conductivity, temperature and pH increased during the 18 week period. There were very little changes in the levels of Ammonium, Calcium, Turbidity, and Dissolved Oxygen during the study period and between sites. Correlation between enterococcus levels and chemical characteristics were not significant. We continue to gather further data on these levels to use to relate the biological and chemical aspects NYC harbor sites.

Self-Assembling Protein Biomaterials For Ocular Drug Delivery. Jay Kang[1], Kamia Punia[1],Katharina Hüll[1], Yifei Wang[1], P. Douglas Renfrew[1], M. Lane Gilchrist[2], Richard Bonneau[1], Dirk Trauner[1] and Jin Kim Montclare[1,2], [1]New York University and The City College of the CUNY, New York, NY.

Photochromic ligands, such as diethylamine-azobenzene-quaternary-ammonium (DENAQ) bearing an azobenzene moiety, have been shown to treat degenerative blinding diseases caused by the progressive loss of rod and cone photoreceptors DENAQ photoisomerizes from *trans* to *cis* in picosecond upon exposure to visible light and impacts the biological activity of transmembrane channels of the retinal ganglion cells. DENAQ can restore light sensitivity on voltage gated ion channels in retinas, but needs to be re-administered consistently to reach the target tissue. To enable this drug to persist longer in retinas, we introduce a protein-engineered biomaterial, Q, in which its design is based on the coiled-coil domain of cartilage oligomeric matrix protein (COMPcc). Using DNA recombinant technology, we have designed Q so that the homopentamer has an optimal surface charge distribution that contributes to its ability to self-assemble into nanofibers at pH 4 and further assemble into microfibers upon binding to small hydrophobic molecules. We have demonstrated that Q successfully binds DENAQ into the hydrophobic pore to produce microfibers of 19.23 ± 7.01 μm size, protecting DENAQ. The impact of DENAQ on the protein conformation is assessed via circular dichroism spectroscopy to verify the increased helicity of the protein. Sustained drug release from DENAQ bound Q fibers is evaluated. These results show that our novel protein Q does have functional properties as an efficient ocular drug delivery tool that can consistently re-administer the drug to the ocular tissue.

RNA Therapeutic Strategies To Block VEGEFR2 Expression and Angiogenesis in Glioblastoma Multiform. Kinneret Hannah Kanik and Martin J. Hicks, Monmouth University, West Long Branch, NJ.

Glioblastoma Multiform (GBM) is an aggressive malignant brain tumor originating in the blood vessels of the brain. Patients with GBM tend to have an over-expression of Tyrosine Kinase Receptor (KDR) Protein, Vascular Endothelial Growth Factor Receptor Type 2 (VEGFR2), which is responsible for the growth of blood vessels. When over expressed, it promotes the development of tumors. Antisense RNA therapy is used to induce an alternative isoform. To reduce VEGF over-expression, we are using this strategy to develop a gene, encoding an antisense RNA that will create a soluble decoy to block VEGFR activation. This will alter the splicing site of the exons of VEGFR2 pre-mRNA transcript, effectively prohibiting the receptor from binding in the cell. We hypothesize that the secondary structure of VEGF Exon 13_Intron13_Exon14 will determine the most effective way to approach synthetically altering the splicing of the VEGFR pre-mRNA. Through Polymerase Chain Reaction (PCR) quantification, we have successfully treated Glioblastoma cells with anti-VEGFR2 coding sequences directed against 5' splice site of intron 13, which significantly reduced VEGFR2 mRNA and protein expression. In Hicks Lab, I have learned and carried out basic molecular biology protocols specific to our lab. In order to characterize VEGFR2 and EGFR transcripts, I grew and maintained GBM cell lines, isolated their cytoplasmic and nuclear RNA using trizol, and reverse transcribed the RNA to complementary DNA. To isolate the EGFR isoform, I designed quantitative PCR (qPCR) primers. PCR helps us characterize pre-mRNA structures. qPCR enabled us to monitor VEGFR2 expression in GBM cell lines, HEK293 and SKMG3. To verify the products of qPCR and PCR, I ran an agarose gel electrophoresis. Through these experiments, I have contributed to each of the Hicks Lab projects as well as gained expertise to initiate experiments onto my own individual product directed against KDR Protein, VEGFR2.

Comparison of Bacterial Communities in New Jersey Soils Using Next Generation Sequencing. Tae M. Kim, Stephanie Zapata and Luis Jimenez, Bergen Community College, Paramus, NJ.

Soil is vital for human life. Soil microorganisms are highly diverse. Microbes play an important role in the decomposition of plant and animal matter to support plant growth, soil structure, and fertility. However, most bacteria in soils are not culturable so culture-independent molecular analysis provides a higher detection and resolution to understand the structure and diversity of bacteria in soils. 16S rRNA clone libraries were constructed using DNA extracted from 5 different soils sites at Bergen Community College in Paramus and 1 site in Fair Lawn, New Jersey. When all 6 soils were analyzed the average number of bacterial phyla was 15 with soil P2 showing the highest numbers, 20, and F1 the lowest, 12. The Actinobacteria and Proteobacteria were the predominant bacterial phyla in all 6 soils. Sixty five percent of bacteria present in soils belonged to either phyla. Soil P4 showed the highest percentage of Actinobacteria with 45%. Soil P5 showed the highest percentage of Proteobacteria with 44%. The dominant bacterial groups in soils at all taxonomic levels belonged to the Actinobacteria with 32% followed by Proteobacteria (22%), Chloroflexi (6%), and Acidobacteria (6%). The genus *Bradyrhizobium* from the phylum Proteobacteria which is related to nitrogen fixation was the most widely distributed bacteria in soils. However, the family Nocardiodiaceae from the phylum Actinobacteria was the number one bacteria found in two soils, P1 and P4.

Design and Engineering of Plasmids for Deletion of *mxan_rs13160* and *mxan_rs33480.* Kelli M. Kinlen and David M Zuckerman, Iona College, New Rochelle, NY.

Myxococcus xanthus is a gram-negative, rod-shaped bacterium that is commonly found in soil. The *M. xanthus* genome contains two genes (*mxan_rs13160* and *mxan_rs33480*)that resemble phage genes associated with host cell lysis. In the phage infection cycle, the Holin protein cuts holes in the host cell's cytoplasm, causing the contents of the cell, including the progeny phase, to disperse from the cell. Under starvation conditions, *M. xanthus*undergoes a process in which cells aggregate to form a fruiting body, a process that generates starvation-tolerant spores, but results in the death of a majority of the cells. It is unclear whether the cell deaths are altruistic or fratricidal. In order to test the potential contribution of the holin gene to cell death during starvation, we have generateddeletion plasmids for each gene using standard biochemical techniques such as PCR, cloning, transformation, and restriction digest. The deletion plasmid is composed of a vector and insert that lack the gene; the plasmid will be taken up by *M. xanthus,* forcing the bacterium to act without the gene, possibly changing its behavior. We have also generated FLAG-tagged plasmids to determine when the *holin*genes are expressed and plasmids that can express the *holin* genes under the control of an inducible promoter to determine if *holin* gene expression leads to cell death. The experiments will allow us to determine if the Holin protein contributes to cell death during starvation.

Comparing the Catalytic Cycles of Myoglobin and Hemoglobin in Oxidative Environment. Jason Lam, Naomi Shohet, Gabriel Chadi, Christine Ishanyan, Chana Ariel, Jorge Ramos and Uri Samuni, Queens College, Flushing NY.

Heme proteins such Myoglobin (Mb) and Hemoglobin (Hb), are crucial for oxygen delivery and storage to the tissue. Surprisingly, under conditions of oxidative stress such as during inflammation, Mb and Hb are capable of acting as catalysts of redox reactions with important implications for the mechanism and propagation of oxidative damage. We studied the catalytic cycle of Mb and Hb in the disproportionation reaction of hydrogen peroxide under different experimental conditions, varying [Mb] and [Hb], [H2O2] and pH. Although the heme proteins act as catalysts, overtime, the protein itself can undergo structural degradation and the catalytic cycle is broken. We used UV/ vis spectroscopy to follow the oxidation state and concentration of the heme proteins as they shuttles between the met and ferryl forms and to determine the rate of the protein's degradation. We employed colorimetric assay and oximetry to follow the concomitant rates of hydrogen peroxide depletion and oxygen evolution. Further insight into the protein's degradation mechanism was explored by investigating the effects of Nitroxides, a class of potent antioxidants. Our data yielded the corresponding rates of heme protein degradation and hydrogen peroxide depletion and allowed to determine the number of catalytic cycles a heme protein can go through until it undergoes degradation. We use the results to compare the catalytic cycles for the different heme proteins (Hb vs. Mb). This work was supported by the PSC-CUNY Research Award Program.

Hitchhikers in Honey: An Investigation of the Inhibitory Mechanisms of Bacteria Found in Honey. Emma Letcher and Davida Smyth, The New School, New York City, NY.

Honey has a stable physiochemical composition that contributes to its long shelf life and has been noted as an antimicrobial substance for centuries. Although it is common knowledge that honey affords some antimicrobial properties, the specific mechanisms behind this remain elusive. This paper hypothesizes that the microorganisms in certain raw honeys contribute towards their antimicrobial properties. In our study, we analyzed several raw and processed honey samples to determine their microbial constituents. The antimicrobial potential of the isolated microbes was tested using several clinically relevant bacteria including *Escherichia coli, Staphylococcus aureus, Staphylococcus epidermidis* and *Pseudomonas*

aeruginosa. Of the tested honeys, Manuka (New Zealand) and Wildflower honey (Tennessee, USA) contained microorganisms exhibiting antimicrobial activity. All the isolated colonies grew on MacConkey and Mannitol agar and generated bands for the 16S rRNA gene implying that they were bacteria. This paper concludes that bacteria isolated from honey could be a new area of research within the topic of antimicrobial honey samples.

Exploring the Influence of pH on Assembly of Thermoresponsive Protein Hydrogels. Bonnie Lin, Michael Meleties, Priya Katyal and Jin Kim Montclare, New York University, Brooklyn, NY.

Self-assembling biomaterials have proven to be useful in biomedical applications including drug delivery, gene delivery, and tissue engineering. More recently, self-assembled hydrogels exhibiting thermoresponsive sol-gel behavior have been gaining traction as carriers of small molecule therapeutics. Our lab has developed a hydrogel based on a single coiled-coil protein, Q, which is an engineered variant of the coiled-coil domain of cartilage oligomeric matrix protein (COMPcc). The surface charge of the parent protein was re-distributed by swapping the N- and C-termini of COMPcc about a central glutamine (Q54) residue, allowing for lateral fiber assembly. Here we demonstrated that Q can further assemble into nanofibers that can physically cross-link to form hydrogels at low temperature. We further explore the effect of pH on self-assembly and gelation properties of Q. The secondary structure, fiber assembly and gelation properties of Q will be characterized through the use of circular dichroism spectroscopy, transmission electron microscopy and rheology, respectively. Our results indicate that fiber formation is necessary for gelation, with higher pH leading to faster gelation. Future studies will focus on investigating the encapsulation and release of a small hydrophobic molecule for drug delivery purposes.

Improving the Gag-iCre Assay to Identify Drugs that Block HIV Entry. Trisha Livera[1], Sophia Philippe[1], Andrew Madea[1], Benjamin Chen[2] and Anthony Esposito[1,2], [1]New Jersey City University, Jersey City, NJ and [2]Mount Sinai School of Medicine, New York, NY.

HIV hijacks the body's immune system by fusing with CD4+ t helper cell's plasma membrane and injecting its genetic material. In order to detect HIV entry into cells the Gag-iCre assay was previously developed. To further improve the Gag iCre assay, luciferase will be used instead of GEP to signal when HIV infects a t helper cell. Since the floxed-luciferase plasmid had a detective backbone, we decided to insert the luciferase gene into the lentiCRISPR V2 backbone. Using the DNA cloning method, we were able to successfully complete a restriction digest using enzymes Xba1 and Pme1, which cut the plasmids into fragments, perform gel electrophoresis, which separated the fragments by band size, and gel extraction, which separated the agarose gel from the desired fragments. In continuation with the past summer's progress, we adjusted the restriction digest protocol, loaded more sample during electrophoresis, modified steps during electrophoresis, and used a 2:1 vector ratio during extraction to successfully transform bacterial cells. Future steps include transducing into mammalian cells in order to potentially create a new cell line. This project received support from US Education Department Title III Part F HSI-STEM grant # P031C160155.

Variation in Reproductive Traits Among Mice Adapted to Different Regions of the Americas. Tiffany Longo, Jesse Bragger, David Grossi and Megan Phifer-Rixey, Monmouth University, West Long Branch, NJ.

Although house mice, *Mus musculus domesticus*, are not native to the Americas, they have quickly adapted to a wide range of climates. For example, body size and nesting behavior are two traits linked to fitness that vary among populations from different latitudes, and those differences have been shown to have a genetic basis. Reproductive traits have a direct impact on fitness and life history theory predicts that both body size and climatic seasonality have the potential to affect reproductive investment. Here, we investigate whether litter size and pup weight vary among mice from different climates using new wild-derived mouse strains originating from New York, Brazil, Arizona, Florida, and Canada. We find significant differences in litter size among laboratory bred mice from these populations, both in early and later generations of inbreeding. Preliminary data also suggest differences in pup size among mice derived from these locations. Overall, mice from higher-latitude locations tend to have larger litters and larger pups. These findings suggest that reproductive parameters may be either directly or indirectly selected on as populations of house mice adapt to more seasonal, temperate climates. To identify additional phenotypic and genotypic variation, two new projects are being launched, a survey of local populations in New Jersey and a study testing differences in activity levels and behaviors typical of predator avoidance.

Evaluation of Sporicidal Effects of Natural Formulations Containing Lipophilic Green Tea Polyphenol. Sabrina Lopez and Tinchun Chu, Seton Hall University, South Orange, NJ.

Derived from the leaves of *Camellia sinesis*, green tea is widely consumed and has been known for its distinct health benefits. Studies have shown that the popular drink has been associated with the prevention of infections and infectious agents. Green tea polyphenols (GTP) found in the tea leaves contain antioxidant, anti-inflammatory, and anti-microbial properties. The major active ingredient in GTP is epigallocatechin-3-gallate (EGCG). This study focuses on the sporicidal effect of lipophilic GTP, epigallocatechin-3-gallate-palmitate (EGCG-P) as the water-soluble EGCG is unstable. Several EGCG-P based formulations were used to evaluate its anti-germination

activity on a Gram-positive bacterium, Bacillus cereus (B. cereus) with the time-kill assay. Different concentrations of ethyl alcohol, 70%, 78%, and 85%, have been included as positive controls for this study. The results showed that the EGCG-P based formulations were able to reduce spore germination by up to > 4 log10. It suggested that antiseptics with an EGCG-P base should be more effective than consumer-antiseptics containing ethyl alcohol as their main active ingredient, ranging from 62% to ~80%.

Glutathione Determination in Chinese Hamster Ovary Cells Exposed to Nickel and Chromium. Angèle Louis-Jean, Rickesha Morris and Spiros Katsifis, University of Bridgeport, Bridgeport, CT.

Nickel and chromium are widely recognized as carcinogens and mutagens. Previous studies report their cytotoxic effects in mammalian cells; however, their mechanism of action remains poorly understood. To analyze the process involving nickel and chromium toxicity, Chinese Hamster Ovary cells were treated with soluble salts of each metal alone and in combination to which the glutathione (GSH) concentration on each metal was recorded. In biological systems, glutathione (GSH) maintained an antioxidant activity where it is oxidized to GSSG as scavenger of reactive oxygen species (ROS). Both heavy metals should induce toxic effects in cell culture. Our results indicate with increasing chromium concentration, from 0.5 to 5μM, the concentration of glutathione increases as well. On the other hand, nickel treatments indicate an increase of GSH concentration for nickel treatments from 1-10μM and a decrease at 25μM of nickel treatments. For the combined treatments of the two heavy metals, the concentration of glutathione increases then decreases at high chromium concentration. For the combined treatments with 0.5μM – 2.5μM Cr with 1 and 5μM nickel, the GHS concentration was found at a slight increase compared to the control. However, at higher levels of Cr (2.5μM) and Ni at 1 or 5μM, the GSH concentration decreases from 3.69μM to 2.14μM. These observations will provide information for further studies required for the elucidation of the mechanism(s) involved in previously reported antagonistic interaction of Ni (II) and Cr (VI) observed in vitro and epidemiological studies.

The Role of Purinergic Receptors in HIV Entry. Andrew Madea, Sophia Philippe, Trisha Livera, Benjamin Chen and Anthony Esposito, New Jersey City University, Jersey City, NJ and Mount Sinai School of Medicine, New York, NY.

Purinergic receptors are transmembrane proteins that respond to purine binding and are involved in a variety of pathways. It has recently been shown that chemical inhibitors of purinergic receptors block entry of HIV into cells. Specifically, inhibitors of the P2X1 and P2X7 receptors blocked entry. In order to assess the role of these proteins in HIV entry, plasmid constructs are being made for both the overexpression and deletion of these genes. So far the P2X7 construct has successfully been created and the other constructs are in the process of being made this experiment. This project received support from US Education Department Title III Part F HSI-STEM grant # P031C160155.

***D. takahashii onecut* Gene Mapped to dot Chromosome. Nabil Mahmoud and Cindy Jo Arrigo, New Jersey City University, Jersey City, NJ.**

Ortholog onecut, a homeobox gene involved in transcriptional activation, was observed in the dot chromosome of an uncharacterized genome of *D. takahashii* on contig36. Both isoforms of the gene were mapped and custom gene models were used to compare the polypeptide sequences. The two sequences are 76% identical, with a high similarity of 84.6% to *D. melanogaster*. Onecut's homeobox and cut properties are supported through RNA-Sequence, with an overwhelming preference to mixed embryos over adult males and females.

Juveniles and Their Carapaces: What Can They Tell Us About the Population of American Horseshoe Crabs (*Limulus polyphemus*) on Plumb Beach. Kera Mansfield and Christina Colon, Kingsborough Community College, Brooklyn NY.

Juveniles American Horseshoe Crabs (*Limulus polyphemus*) and the shed carapaces they leave behind tell researches a lot about the population size and distribution on nursery beaches along the East Coast. Adult American Horseshoe Crabs come ashore to spawn each spring on Plumb Beach (Jamaica Bay, Brooklyn, NY), showing preference for the undisturbed eastern segment. Juveniles emerge in June to forage, shedding their exoskeleton as they grow. In 2018 hundreds of these carapaces were found, possibly indicating higher than usual growth and survival. Therefore, it was hypothesized that juveniles would be larger in 2019 compared to 2018, and there would be fewer carapaces in 2019 than 2018. It was also hypothesized carapace size and counts would reflect the juvenile population. If so, carapaces could serve as a surrogate for estimating juvenile population size and structure. Bi-weekly timed visual surveys at low tide were conducted to count juveniles, while carapaces were collected opportunistically along the wrack line. In the summer of 2019, it was found that the juvenile horseshoe crabs median size was only 12.5 mm while 2018 measured 25.5 mm, thus not supporting the first hypothesis, perhaps due to high recruitment in 2019. While in the summer of 2018 we observed 615 carapaces on Plumb Beach, in 2019 we observed only 155, which supports the hypothesis that the high 2018 counts were an anomaly. While the carapace data and the juvenile data should go hand in hand, this was not observed. The juvenile data was skewed towards smaller juveniles such as young of the year while the carapaces were skewed towards the larger (older) individuals not directly observed.

We can conclude that carapaces and juvenile counts are both needed to get a more accurate assessment of the population dynamic of juvenile crabs on nursery beaches. This work was supported by grant 2R25GM06003 of the Bridge Program of NIGMS and by grant 0537-19-1091 of the CSTEP Program of NYSED.

Investigating the Interaction of CaMKII with Neuronal Protein GRIP. Isabella Mattingly and Reed Carroll, New Jersey City University, Jersey City, NJ.

Synaptic signaling occurs when one neuron releases a chemical signal that is received by a neighboring neuron, generating an electrical current. Synaptic plasticity is the ability of synapse signaling to strengthen or weaken over time in response to an increase or decrease in activity, possibly by changing the number of postsynaptic receptors. Ca^{2+}/calmodulin-dependent protein kinase (CaMKII) activation has been found to play a crucial role in several forms of synaptic plasticity. CaMKII is thought to play an essential role in learning and memory storage due to its ability to increase the strength of excitatory responses as well as regulate inhibitory responses. CaMKII controls excitatory responses by interacting with N -methyl-D-aspartate (NMDA) receptors and localizing at excitatory synapses. The mechanisms by which CaMKII regulates inhibitory synapses remains unknown. This experiment tested the hypothesis that CaMKII regulates inhibitory responses by interacting with the protein GRIP. This was tested using several activated mutant CaMKII constructs including E139K and T286D/T305D/ T306D. It was found that the cells expressed both the kinase and GRIP, and co-expression levels.

Identification of Protein Interaction Partners for the N-terminus of Cytoskeletal Element BacM. Brittney McLarty and David Zuckerman, Iona College, New Rochelle, NY.

The cytoskeletal element BacM in *Myxococcus xanthus* has been characterized using protein gel electrophoresis to be expressed as both 13 kDa and 16 kDa proteins. Therefore, BacM can be expressed as two isoforms: large and small. The large isoform has been found to contain 23 additional amino acids at the N terminus. The present research was conducted to identify interaction partners of the BacM-N-terminus domain in bacterial species *M. xanthus*. We hypothesize that the N-terminus of Bac-M is targeted to the bacterial cell membrane through protein-protein interactions. PCR was used for the amplification of the N-terminal sequence of BacM and molecular cloning techniques were used to fuse this sequence with the GST gene. Plasmids encoding the BacM-GST fusion or GST alone were transformed into chemically competent *E. coli* BL21 cells and induced to express protein. The proteins were then isolated from the cells and purified for further analysis. The purified protein will be examined for interaction partners.

Anti-Biofilm Properties of Flax, Chia, and Hemp Seed Oil Extracts. Jessica Menjivar and Meriem Bendaoud, New Jersey City University, Jersey City NJ.

Worldwide, pathogenic bacteria and yeast have been gaining antibiotic and antifungal resistance. This is a critical problem for public health as millions of people acquire infections from gram-positive and negative pathogenic antibiotic resistant bacteria/yeast like *Staphylococcus epidermis, Staphylococcus aureus, Candida albicans* and *Pseudomonas aeruginosa*. For many years now, scientists look for natural alternatives like herbs, oils, and seed extracts to fight off infections and support better health. Chia, Flax, and Hemp seed oil extracts have been found to have health-promoting benefits properties. However, very little research has been done to determine their effects on the growth of gram-positive and negative pathogenic bacteria/yeast. The purpose of this study is to test these oil seed extracts for antimicrobial properties against pathogenic bacteria and yeast. Using the biofilm assay we were able to show that Chia Seed Oil Extract and Hemp Seed oil had the most effective antibiofilm properties against two strains of P. aeruginosa and S. epidermis. Future research will focus on isolating different compounds of these oils and determining what compound has antibiofilm properties. Additionally, by producing the seed extract directly from the seeds, I would be able to identify potential inhibitory effects as well.

A Comparison and Contrast of Present-day *Crassotrea virginica* oyster shells with those from a shell midden in Croton Point Park. Joshlyn Mensah and Kathleen A. Nolan, St. Francis College, Brooklyn, NY.

There has been a recent revival in interest in oysters in New York City, as has been seen through the Billion Oyster project. St. Francis College has been tangentially involved with this project, and there has been a successful attempt to grow oysters in the East River in conjunction with the Brooklyn Bridge Park. This information combined with the 'discovery" of an oyster midden in June 2019 in Croton Point Park has lead us to test hypotheses as to what the differences are between modern-day shells and old shells. (Six oyster shells from middens in Riverdale Park that were C-14 dated were over 3000 years old, so we are making an assumption that shells from the midden are in that same age cohort.) As present-day oyster shells can be difficult to obtain, we turned to a seafood restaurant, AquaGrill, for help. They have provided us with 75 oyster shells of which we have measured the length, width, and mass. These measurements have been compared to those of the shells found in the midden, and a rate of deterioration has been calculated. The pH of the soil in Croton Point Park was also calculated, and compared to pH's of soil in general. Climate change and/ or change in pH levels might affect deterioration of shells and archaeological artifacts in the future, as well as affect the health and longevity of present day oysters.

Plasmolysis and Stomata in *Ceratopteris richardii* (C-ferns). Joshlyn Mensah and Kathleen A. Nolan, St. Francis College, Brooklyn, NY.

Ceratopteris richardii (C-ferns) have been traditionally used to study genetic crosses and have also been used for that purpose in our genetics laboratory courses. The hermaphrodites produce a heart-shaped flat, single-cell layer gametophyte and the males produce a club-shaped structure. When concentrated NaCl or sucrose solutions (5% or greater) are added to these structures, plasmolysis can be quickly observed. Since these plant forms are only a single-cell layer thick, they offer a clear, actually easier to view, model to observe and study plasmolysis in plants than the traditionally used Elodea leaves, which are two-cell layers thick. Even the next generation of C-ferns, the sporophyte, is one-cell layer thick. These sporophytes make a rosette type clump, but "leaves" can be easily pulled from the multi-leaved structure and make a two-dimensional sheet on a microscope slide on which plasmolysis (and/or turgor) can be observed. An additional mutant, the polka dot, contains chloroplasts that have a clustered appearance under the microscope so adding concentrated solutions does not greatly change the phenotype. Stomata are also easily observed in C-ferns. We varied the concentrations of both NaCl, and added them to the C-fern gametophytes and sporophytes. We timed and observed differences in appearance of these plant structures and captured these images with phone and/or Motic cameras.

Seed Germination Rates from Laboratory Propagated Plant *Brassica rapa* Under Varying Seed Preparation Protocols. Chiara Ximena Mercado, Gerald Gabinete, Brandy Garrett-Kluthe and Rebecca Conley, Saint Peter's University, Jersey City, NJ.

Seed propagation and germination in the laboratory setting is essential for plant studies as well as is an important topic for our ecology. Maintaining seed stock that has a high germination percentage is important in experimental plant studies. In order to maintain this high stock, germination is necessary and a high seedling yield of germination is imperative. Seed collection, storage, and planting preparations can lead to higher germination rates based on the practices used. It is proposed that the maximum germination percentage in seeds collected in laboratory-grown plants can be determined. Seeds were collected from mature Brassica rapa plant seed pods that were grown in a laboratory under self-fertilizing conditions. The seeds were divided into two groups with one group stored fresh in a refrigerator while the other group was completely dried. Each of the seed types were then separated into three different pre-germination treatments that included planting directly into soil, soaking the seeds to test moisture levels in combination with light exposure, and planting and subjecting the seeds to alternating temperature conditions to mimic a day and night climate. Seeds or seedlings were monitored for evidence of germination on a regular basis. The results obtained were recorded and analyzed statistically through the Mathematics department. For the soil, treatment is was determined cold-stored seeds presented lethargic germination rates in comparison to that of the dry stored seeds. The seed moisture trial on paper towels showed the quickest germination results, both light and dark trials showed germination the next day. The slowest bearing results came from the temperature variant trial, these seedlings even after a week of exposure to trail have not germinated. The results indicated that pre-germination treatments do have an impact on germination percentages. It is also important to note the germination rates were also significantly different between treatments. The results of this experiment provide valuable information on the storage and seed handling methods needed to obtain higher germination percentages which is important for plant propagation research. The results of treatment effects on germination rates and percentages prove the hypothesis.

Testing the Effect of Unknown Bacterial Extracts on Different Pathogenic ATCC Bacteria and Biofilm Formation. Mariana Metry and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

Antibiotic resistance in bacteria is a growing global health concern. Biofilm formation is a major source of this resistance. Bacteria can form biofilm by attaching to surfaces and to each other. Trying to overcome this problem using an alternate approach is our goal. The purpose of this study is to test naturally produced agents for antibiofilm properties. Bacteria can work against each other through secreting natural substances that could kill or inhibit biofilm formation. Water samples were collected, and several unknown bacteria were isolated and tested against different pathogenic ATCC strains of bacteria through disc diffusion assay. Cell-free extracts of unknown bacteria were prepared and tested against biofilm formation of many pathogenic bacteria using a biofilm assay. Results showed that unknown bacterial extracts were able to kill one of the pathogenic strains, while the others inhibited the biofilm formation of other strains such as *Escherichia coli* and *Enterococcus faecalis*. Sequencing of unknown bacterial DNA is the next step to identify these unknowns. Furthermore, in a trial to understand the effect of soil bacteria on crops, different types of seeds were used in another study. Seeds were sterilized and grown with and without bacteria in 12, 24, and 48 well plates. Results showed that bacteria affected the development of seeds compared to the control. In future study, these unknown compounds will be tested for their ability to protect the seeds.

Peeling Back the Layers: The Hidden Hazards of the Walls Around Us. Molly Metz, Natalie Vegas and Davida Smyth, The New School, New York, NY.

The rise of superbugs has led to the development of products marketed to consumers as being antimicrobial. Today, these products are saturating the market and consumers are lead to believe they are the safest option for their health. There are concerns that the pattern of resistance and consumer habits could lead to emergence of further resistance amongst organisms which could, in turn, affect human health. One of these products on the market is antimicrobial wall paint for homes, industrial and commercial spaces. Paint companies have used several strategies to create a bacteria and mold killing paint. Our research is focused on two such antimicrobial paints and a standard paint. Our hypothesis, based on preliminary results from previous experiments, is that the antimicrobial paint will not be able to kill 99.9% of bacteria on the surface of the paint over the course of one month. To conduct this experiment, foam boards covered in three layers of each paint were mounted in six locations around the The New School which were determined to be low, medium and high traffic. The paint boards were mounted in these locations for one month to see what microbes, if any, were able to survive on the surface of the paint. After one month, the paint boards were removed and sampled in the lab. Using nutrient agar contact plates we isolated each colony of growth that was living on the surface of the paint. In addition the paint boards were swabbed to collect the DNA on the surface of the paint. A selection of the total colonies were isolated and sent for DNA sequencing. The results showed that although the antimicrobial paints showed less bacterial growth, there still was growth despite the label's claims. These results raise questions about the manufacturers' claims. In addition there are harmful chemicals in the paint which could pose additional threats to human and ecosystem health which can be explored in future experiments.

Transgene Insertion Increases Temperature-dependent Dark Respiration Rates in the American Chestnut (*Castanea dentata*). Sashoy Milton[1], Anuli Onwumelu[2] and John E. Drake[2], [1]St. Joseph's College, Brooklyn, NY and [2]SUNY ESF Department of Forest and Natural Resources Management, Syracuse, NY.

The American chestnut (*Castanea dentata*) was a keystone species of Eastern U.S. forests until it was rendered nearly extinct by a fungal pathogen (*Cryphonectria parasitica*). Recently, the American chestnut has been genetically modified to increase its ability to resist the impacts of girdling caused by the pathogen. We tested the hypothesis, transgene insertion increases the maintenance metabolic costs of the blight-tolerant American chestnut, by measuring the leaf dark respiration rate (R) across a range of temperatures. We found that the rates of R for the transgenic trees were increased by an average of 39% across a range of temperatures from 15-30 °C. The increased rate of R has the potential to reduce the growth rates thus impacting its successful integration into the natural ecosystem. Future work should address the consequences of this higher rate of R on American chestnut growth across a range of growing conditions.

Oxidative Stress is a Potential Regulator of the Volume Regulated Anion Channel Subunit LRRC8A. Joseph Minkler, Billy Nguyen, Stephanie Saintil, and Renee Haskew-Layton, Mercy College, Dobbs Ferry, NY. and Westchester Community College, Valhalla, NY.

Volume Regulated Anion Channels (VRACs) are activated in response to cell swelling to defend cells against cellular lysis. VRACs contribute to excitotoxic glutamate release in stroke and are therefore potential therapeutic targets for decreasing ischemic brain damage. VRACs are primarily composed of the leucine-rich repeat-containing protein 8A (LRRC8A), which is ubiquitously expressed in all cell types. The precise mechanisms leading to VRAC activation in stroke are yet to be fully elucidated. Previous studies show that direct oxidation of LRRC8 subunits can hinder or strengthen VRAC currents. We hypothesize that oxidative stress, which occurs in stroke, increases LRRC8A transcription, thus potentiating excitotoxic glutamate release and damage in stroke. To test our hypothesis, qPCR was carried out to monitor changes in LRRC8A mRNA expression following the treatment of chick embryo primary astrocytes and neurons with the oxidant hydrogen peroxide. Our results provide preliminary support for our hypothesis by showing that hydrogen peroxide indeed increases LRRC8A mRNA levels. However, the variation of LRRC8A expression in response to hydrogen peroxide suggests that a stronger level of oxidation or duration of hydrogen peroxide exposure may be required to induce consistent increases in LRRC8A.

Characterization of Engineered Supercharged Protein for Efficient Gene Therapy. Julia Monkovic[1], Joseph Thomas[2], Kamia Punia[1], Priya Katyal[1] and Jin K. Montclare[1,3], [1]New York University, Brooklyn, NY, [2]SUNY Downstate Medical Center, Brooklyn, NY and [3]New York University Langone Health, New York, NY.

The therapeutic delivery of nucleic acids provides a potential method to correct a disease at its most basic level, yet the successful insertion of the material into the cell is hindered by the absence of a safe and effective delivery vehicle. Nucleic acids are highly susceptible to degradation by nucleases, leading to difficulty reaching a high transfection rate while maintaining low toxicity. Protein engineering techniques have emerged due to their specificity in terms of structure and assembly, biodegradability, low toxicity, and environmentally-friendly production. Our group has created a protein-lipid hybrid to act as a novel delivery vehicle, in which the protein binds nucleic acids and is then complexed with a cationic liposome. A library of proteins has been designed, based on a parent coiled-coil supercharged protein, with varying

positive surface charges and terminally-located histidine sequences to maximize the structural and functional capabilities of this component of the vector. Here we report characterization of protein secondary structure, thermostability, and capacity for plasmid DNA binding. Structure, thermostability, and binding capabilities are disrupted upon insertion of a C-terminal histidine tag while optimized by the insertion of an N-terminal histidine tag. A highly positive surface charge also contributes to the protein's successful plasmid DNA binding ability. Such properties can aid in stabilizing the nucleic acid cargo of the delivery vehicle, thus more effectively enhancing its expression in cells.

Synthesis of an RNA-Therapy to Alter Overly-Expressed Tyrosine Kinase Receptors in Glioblastoma Multiforme. Reina Montero and Martin J. Hicks, Monmouth University, West Long Branch, NJ.

Tyrosine Kinase Receptors (TKRs) are key players in the proliferation and development of glioblastoma multiforme (GBM), a prominent form of brain cancer that originates in the astrocytes or oligodendrocytes of the central nervous system. GBM has a mortality rate of 15 months due to treatment limitations by the blood-brain barrier, and resistance to current medical treatments. Examples of TKRs include, vascular endothelial growth factor receptor (VEGFR) and epidermal growth factor receptor (EGFR). VEGFR is responsible for the formation of new blood vessels while EGFR signals for the proliferation of tumor cells. Transcription of DNA occurs within the nucleus to produce pre-mRNA that is modified through splicing, polyadenylation, and capping to form mature mRNA. Our strategy aims to deliver a gene therapy that encodes a functional antisense RNA which blocks splicing motifs and alters splicing patterns of EGFR. My hypothesis: Can the G-quadruplex binding motif of our RNA therapy vector bind to the hetero-ribonucleoprotein H (hnRNP H)? To ensure that our therapy interacts with hetero-ribonucleoprotein H and blocks splice site recognition, I performed multiple electrophoretic mobility shift assays (EMSAs) to verify RNA-protein binding affinity and the formation of RNA-protein complexes. Mammalian HEK 293T cell cultures were grown and transfected with a DNA plasmid that encodes hnRNP H. Cells were lysed; the protein was isolated and then dialyzed. RNA therapy was generated by T7 transcription, followed by RNA extraction and purification. Therapeutic RNAs were incubated at various concentrations with hnRNP H. Reactions were run through a non-denaturing gel to separate molecules and verify the formation of RNA-protein complexes. Preliminary experiments demonstrate a shift in therapeutic RNA upon binding with hnRNP H. We will continue to further analyze the interactions between the RNA H-binding motifs and the hnRNP H protein.

Anaylsis of the Mps1-PP1 Interaction I*n Vivo.* Gina Moretti, Steven Almazan, Janet K. Jang, Kim S. McKim, Elizabeth A. Manheim, Rutgers University and Kean University, NJ.

Meiosis and mitosis rely on the formation of a bipolar spindle to segregate chromosomes and complete cell division successfully. Many of the Drosophila spindle assembly mutants, including Protein Phosphatase 1 (PP1-87B) and monopolar spindle-1 are either embryonic lethal or exhibit elevated levels of chromosome nondisjunction and abnormal spindles. PP1-87B is known to be an essential regulator of the attachment of microtubules to the kinetochores, likely via its interaction with monopolar spindle-1 (mps-1) (Moura, 2017). mps-1 is a serine/ threonine protein kinase member of the spindle assembly checkpoint (SAC) mechanism (Althoff, 2012). Mps1-null human and Drosophila cells enter anaphase upon completing spindle formation, without allowing enough time for the chromosomes to orient correctly and segregate to their respective poles. Moura et al., (2017) found that altering the Protein Phosphatase 1- (PP1-) binding domain of mps-1 (KVLF to AVLA) prevents timely metaphase exit in human and Drosophila mitotic cells in vitro, indicating the importance of this domain to the function of mps-1. Our project is the investigation into whether mutating the KVLF domain of Drosophila mps-1 will interfere with the mps1-PP1 interaction in vivo. We have found that wildtype transgenics build normal spindles and the mutant ones are embryonic lethal, supporting the in vitro data. This poster will present our genetic and cytological analyses of the wild type transgenics, confirming the ability of transgenic mps1 to bind to PP1 and maintain the SAC in vivo, while demonstrating sensitivity to overexpression.

Active Drawing of Genetics Mechanisms as an Undergraduate Learning Tool. Laine V Morris and Martin J Hicks, Monmouth University, West Long Branch, NJ.

Many students navigate undergraduate biology courses through the use of a passive learning approach, relying on memorization techniques to learn material. However, genetics and molecular biology topics and associated mechanisms can be best learned through diagramming, drawing, and explaining. This unique pedagogical design unites the minds of students in the classroom by encouraging participation and inquiry. Can active drawing of complex molecular biology topics in lecture, group recitation, and instructor led collaboration sessions increase student understanding and learning success in undergraduate genetics coursework? The basis for this learning approach is based off the fundamental topics of the Genetics Society of America which are integrated into the lecture structure of the course. Topics are covered in three main sections - nature of genetic material along with gene expression, transmission and genetic variation, and patterns of inheritance complexed with evolution and population genetics. Active stepwise drawing and discussion of concepts is followed by the use of novel disease examples

to connect ideas. Hand-drawn illustrations are created in a precise comprehensible format. Strategies include reductionist point of view from theoretical macroscopic down to molecular. Students are then exposed to reinforcement through recitation and weekly group collaboration sessions led by lecture coordinators before being assessed on concepts. With this active learning approach, students can increase understanding and develop an expanded knowledge base in order to successfully master material with improved retention. Student growth and comprehension using hand-drawn illustrations is measured through concept inventory assessments and student feedback to demonstrate efficacy of active drawing. Genetics concept-based hand drawings will serve as a learning tool for the genetics and molecular biology community after peer review and preparation for publishing.

Molecular Investigations of Distyly and Self-Incompatibility in *Primula vulgaris*: Distribution of Style- and Pollen-Specific Proteins. Agata Movsisyan and Farshad Tamari, Kingsborough Community College, Brooklyn, NY.

Distyly is a dimorphic reproductive system, where two floral morphologies exists within a given species. Shorts have short styles and long stamens and the opposite is true for longs. Distyly, together with its associated self-incompatibility, serves to prevents inbreeding depression. While the genetics of distyly and self-incompatibility is well understood, the molecular control of this interesting breeding systems is largely unknown. To investigate the molecular biology of distyly and self-incompatibility in Primula vulgaris, we examined the proteins within reproductive and non-reproductive organs of short- and long-styled plants. We hypothesized that there exists morph-specific protein profile differences using SDS-PAGE, which is what we used to compare protein profiles of shorts and longs for styles, ovaries, anthers and sepals. The protein profiles for both reproductive and non-reproductive tissues look very similar, however, there may be slight differences. For example, short-styled plants appear to have a morph-specific protein at around 25kD, which is absent in long-styled plant. This is consistent with findings in other species, where short-specific proteins such as polygalaturonase and alpha-dioxygenase have been identified. Future studies will be conducted to confirm our results. This work was supported by grant0537 -19-1091 of the CSTEP Program of NYSED.

Examining Microglia Structure through Extrinsic Manipulation. Sara Mroziuk[1], Alicia C. Barrientos[2], Juan E. Muñoz[1], Saleha Tahir[1] and Joshua C. Brumberg[1,2], [1]Queens College, CUNY, Queens, NY and [2]The Graduate Center, CUNY, New York, NY.

Sensory deprivation (SD) during the critical period of development results in behavioral and cognitive abnormalities in mammals. The C57BL/6 mouse is a useful model for studying the neural mechanisms of SD. Each whisker provides sensory information analogous to the human fingertips and aligns with a corresponding barrel structure in the primary somatosensory cortex. A key component of neuroplasticity during development are microglia (MG). MG modulate how neurons communicate. In addition to expressing molecular markers, activated MG take on a primed or ameboid shape: rounder somas and shorter, thicker processes. Homeostatic MG have a ramified phenotype: smoother, smaller somas and longer, thinner processes. Previous studies from the laboratory showed that SD via whisker trimming leads to activation of MG across cortical laminae. The current study uses pharmacological manipulation to activate or inhibit MG during the critical period. We randomly assigned litters of C57BL/6 mice with IP injections of saline (control), minocycline (a MG inhibitor in adult mice) and lipopolysaccharide (LPS; an inflammatory agent) until post -natal day 30. We hypothesized that LPS-treated mice would show significantly more primed or ameboid MG phenotypes relative to control mice, while the minocycline-treated mice would show fewer activated MG relative to LPS-treated and control mice. We labelled IBA-1 to identify MG and examined their morphology in the somatosensory cortex. Preliminary data shows the most significant changes in MG morphology in the minocycline-treated mice, which suggests that minocycline alters the cortical environment and influences MG behavior differentially than LPS. Further research is needed to determine whether these alterations in MG interact with other neural structures within the somatosensory cortex that aid in experience-dependent plasticity. Examining changes in MG morphology helps us understand their contribution to healthy and abnormal brain development. This work is supported by NIH #2T34GM070387 to Zahra Zakeri and #SC3GM122657-02 to JCB.

"Adropin"- Setting Fire to Fat. Umit Muradi, and Sarbani Ghoshal, Queensborough Community College, Bayside, NY.

Introduction and Background:Adropin, which literally means "setting fire to fat" was discovered by Prof Andrew Butler in 2008. It is a 76 amino acid peptide encoded by Energy Homeostasis Association (Enho) gene, a small two exon gene on human chromosome 9. This peptide was originally identified as a secreted factor expressed in liver that regulates peripheral metabolic processes affecting diabetic and obese conditions. While adropin may be expressed at various levels in peripheral tissues including liver, analysis of gene and protein expression using mouse and human tissue samples indicated it is most abundant in the nervous system. The present research is part of a major study being conducted in Prof Butler's laboratory in Saint Louis University (SLU) with liver-tissue specific adropin knock-out mice (AdrLKO). Hypothesis:Given adropin's specific role on obesity, our present study hypothesized that deletion of the gene encoding adropin in liver will lead to less fat accumulation in AdrLKO, when such mice were fed a diet rich in fat (HFD). Methods: Liver tissues were collected from AdrLKO and control mice

(WT) both on HFD and haematoxylin-eosin staining was done by Department of Histology, SLU. Scanning of those slides were thereafter done using a compound microscope in Queensborough Community College. Slides were coded to prevent observer bias and a score of 1 to 5 was given to each slide based on the amount of fat droplet accumulation, with 1 showing least fat and 5 showing maximum fat droplet accumulation. Results:Our analysis of liver samples shows with Enhogene deletion in liver mice accumulate more fat than corresponding control animals, when both groups were fed HFD. Conclusion: Liver is a major organ regulating metabolic diseases. Fat accumulation in liver can lead to serious complications including liver cirrhosis. Our data is valuable in indicating a role of adropin in attenuating hepatic fat accumulation.

Effects of Organic Compounds on the Spinach-DFHBI Aptamer Fluorescence. Kaitlyn Murtha, Danielle Guillen and Jonathan Ouellet, Monmouth University, West Long Branch, NJ.

Light-up RNA aptamers bind specifically to a compound to enhance fluorescence. The Spinach RNA aptamer can bind to DFHBI to produce green fluorescence, similarly to GFP. The discovery of the light-up RNA aptamers have been successful in tagging RNA to produce live-cell imaging by the use of fluorescence, providing a translation-free system. As for Green Fluorescent Protein (GFP), the RNA aptamers can be used to monitor the expression, interaction, localization and role of RNAs in cells. Although very little functional studies are known, a high-resolution crystal structure is available and identifies several key components. The most notable feature of the 98-nucleotide long RNA is the RNA G-quadruplex, onto which the DFHBI stacks to be stabilized. Further studies engineered a smaller Spinach RNA, called Baby Spinach RNA, of 51 nucleotides. In order to learn about the Baby Spinach RNA aptamer folding, fluorescence melting studies are performed. Currently, the melting point of Baby Spinach-DFHBI was found to be 41°C. Furthermore, the addition of several organic compounds will contribute to either the stabilization and or destabilization of the RNA structure. Currently we have preliminary results with a T_m at 35°C, indicating a destabilization, accompanied to a 3-fold fluorescence reduction. The outcomes can have significant impact in aging and cancer treatments.

Analyzing the Expression Level of $GABA_A$ Receptor Genes in *Gallus gallus* Chick Tissues Through Embryonic Development. Taylor Nason and Cathryn Kubera, Monmouth University, West Long Branch NJ.

Fetal Alcohol Spectrum Disorders (FASD), which arise from fetal ethanol exposure, are a prevalent group of disorders impacting as much as 5% of the US population. This ethanol-induced environment can lead to mental deficits and lack of motor skills in the developing fetus due to the activation of GABA neurotransmitter receptors within the developing granule cell precursors. The composition of these pentameric GABAA receptors include a wide variety of subunit combinations that yield to different overall behaviors of the receptor. Because the subunit composition of GABA receptors changes depending on developmental time point and location in the brain, we hypothesized that GABAA subunit expression would differ among tissue types and time point in an embryonic chick model. The expression levels of nine different GABAA subunits, including alpha types 1-6 and beta types 1-3, will be analyzed at six key time points in chick embryonic development (E7, E9, E11, E13, E15, E17) within four sample groups of the Gallus gallus chick species (cerebellum, forebrain, optic tectum, and liver). After RNA isolation, the GABA receptor transcripts will be assessed and quantified using RT-qPCR with specifically designed primers for each GABAA subunit type. Expression of the tested GABAA receptor subunit genes were consistent throughout all brain tissue types and only showed a slight variation level of expression when it came to the different developmental timepoints of E7-E17. Based on the collection of all the data gathered it can be concluded that different GABAA subunit genes are expressed throughout the chicken embryonic timeline. The persistance of GABAA receptor subunit expression points to having potentially substantial influence of ethanol on the developing brain in the chick model. In future experiments, it may be important to identify where GABAA receptor subunits are expressed on a cellular level to better understand how alcohol might adversely affect individual cells in the developing circuit.

***Haplosporidium nelsoni* was Not Found in Eastern Oysters (*Crassostrea virginica*) from Delaware Bay. Lenise Muso Nkwain, Lilja Nielsen and Craig Hinkley, Kingsborough Community College, Brooklyn NY.**

The Eastern oyster, *Crassostrea virginica*, is native to the east coast of North America and the Gulf of Mexico. In addition to its economic importance, oysters are filter feeders, and can improve water quality for other organisms by removing sediments and pollutants from the water. Oyster reefs provide shelter for other marine organisms and can act as barriers to prevent coastal erosion. In the 1950's, MSX (Multinucleated Sphere X) was discovered in eastern oysters in Delaware and Chesapeake Bays. Over the next 35-45 years, MSX contributed to the devastation of the oyster populations and led to a loss of hundreds of millions of dollars to the oyster market. MSX is a disease caused by the protozoan parasite *Haplosporidium nelsoni*, which causes a gradual disruption of the digestive tubule epithelium, and infected oysters appear emancipated and exhibit no new shell growth. The complete lifecycle of *H. nelsoni*, as well as its mode of transmission, are still unknown. No transfer of MSX between oysters has been observed, nor are infection rates affected by oyster density, suggesting that there might be an intermediate host for transmission. The overall goal of this research is to determine if there is an intermediate host and to identify that host. Firstly, we want to identify geographic regions that harbor *H. nelsoni* and we decided to test oysters from Delaware Bay since MSX was initially discovered there. My hypothesis is that *H. nelsoni* will be present in oysters from Delaware Bay. To test this hypothesis, we used DNA extracted from gill or

mantle tissue of twelve Delaware Bay oysters to PCR-amplify a region of the small ribosomal RNA subunit of *H. nelsoni*. The amplified DNA was then run on a 2% agarose gel to verify it was the correct size. Using the *H. nelsoni* primers, we did not obtain a PCR product from either gill or mantle DNA for any of the oysters that were tested. In order to make sure we had amplifiable DNA in our gill and mantle samples, we PCR-amplified a region of the *C. virginica* cytochrome-c-oxidase I gene. Agarose gel electrophoresis confirmed that we obtained PCR products of the correct size from all twelve oysters. Taken together, these results do not support our hypothesis and instead indicate that *H. nelsoni* DNA was not present in the tissues of the oysters we tested. A possible explanation is that infections are known to correlate to both seasonal water temperatures and salinity, and perhaps the oysters we tested were collected during periods where conditions were not ideal. In addition, the oysters we tested were collected from commercial oyster beds, which might have lower MSX infections than naturally occurring oyster beds. In the future, I would like to test more oysters from this study's area of Delaware Bay, as well as oysters collected from natural beds. This work was supported by grants 2R25GM06003 of the Bridge Program of NIGMS and 0537-19-1091 of the CSTEP Program of NYSED.

Transient Copper Exposure Results in Decreased Cell Survival and Misrouting of Axons in the Embryonic Zebrafish Retina. **Amani Ortiz, Joseph Pagnotta, Ashley Shields and Alison Dell, St. Francis College, Brooklyn, NY.**

It is widely known that early exposure to lead disrupts brain development and impairs learning and fine motor coordination later in life. However, the molecular underpinnings of neurodevelopmental defects caused by exposure to other metals have not been well studied. The embryonic zebrafish has emerged as a powerful model system for toxicology studies and developmental genetics. Our aim was to use this system to dissect cell signaling events that translate exposure to environmental pollutants into neuronal developmental defects. We previously report generalized developmental and behavioral deficits in zebrafish embryos transiently exposed to low levels of copper ions during development. We hypothesized that these deficits could be caused by cell survival defects, or by defects in neuronal connectivity as axons extend towards their synaptic targets. Here, we report that cell numbers in copper-treated retinae are significantly reduced compared to controls, and retinal axons misproject en route to their destination. To discover the molecular and cellular basis of copper toxicity we identified potential gene targets of copper by analyzing open source gene expression datasets GEO2R datasets, and refined our candidate list to GPCR signaling components expressed in the retina as neurons are born, and extend axons to their targets. We conclude that copper exposure may contribute to neuronal behavioral defects by decreased cell numbers, as well as misrouting of axons.

Mapping the Spread of the Invasive Pest Insect, *Lycorma delicatula* (Spotted Lanternfly) Using Data Generated in the Crowd-Sourced Data Application, iNaturalist. **Niko Panagiotopoulos, Elena Tartaglia and John Smalley, Bergen Community College, Paramus, NJ.**

Lycorma delicatula (spotted lanternfly) is a recently-introduced pest insect in the United States. The insect is native to China and threatens several commercially important crops, including stonefruit, hops and wine grapes. Mapping the distribution and spread of invasive species to minimize risk is a difficult task but is vitally important to establishing control and eradication protocols. Crowd-sourcing data is becoming an increasingly-used tool for mapping biodiversity. One platform for aggregating crowd-sourced data is iNaturalist, a smartphone application established in 2008 by UC Berkeley as a means of making species identification accessible to the public. Given that users geotag data for accurate identification, the app is also proving useful for generating range maps for a variety of species. For this study, we investigated whether iNaturalist is a useful tool for tracking the spread of non-native species. We used research-grade observations of *L. delicatula* submitted to iNaturalist to generate an observation map for this species and compared it to the official USDA *L. delicatula* county quarantine map. USDA county quarantine maps and iNaturalist generated maps overlapped, but iNaturalist indicated the presence of *L. delicatula* in areas not currently within the USDA quarantine. We also used mathematical models to extrapolate data to predict likely areas of future areas of invasion by the insect. Crowd-sourced data, when verified, can be a useful tool in mapping the spread of invasive species.

Identification of Telomere Regulating Genes in *Drosophila melanogaster.* **Patrick Elysee, Sydney Sieh-Takata, Murad Kaid, Billy Nguyen, Isabella J. Hanesworth, Allaysia Bradley, Chad E. Jacob, Besjan Kelmendi, and Chun Zhou, Mercy College, Dobbs Ferry, NY.**

Telomeres are the natural ends of linear chromosomes and contribute to the maintenance of chromosome stability. Without the capping effect of telomeres, broken chromosomes can undergo the breakage-fusion-bridge cycle which may cause cancer. In *Drosophila melanogaster*, telomeres are extended by telomere-specific non-LTR retrotransposons which serve as an alternative, yet similar approach to the telomerase. Previously, we described a genetic factor called Telomere elongation (Tel) on the third chromosome of fruit flies that can enhance telomere elongation. Another telomere-elongating gene was also identified in the similar chromosomal region in *D. melanogaster*. In the present study, we used a bioinformatic approach to identify the genes in this chromosomal region that have the potential to influence chromosomal stability in Drosophila. We hypothesized that the genes with the function of modulating chromosomal structure could have the potential to regulate telomere length or structure. We

extracted genomic DNA from the fly strains in which one of these identified candidate genes had been mutated. Using real-time PCR, we are analyzing the telomere length among different mutant strains with the Oregon-R wild-type strain as the control. In addition, to probe whether or not the disruption of these candidate genes causes a structural defect of telomeres, we have performed polytene chromosome staining. The results will help identify the genes that play a role in regulating telomere length and/or structure.

Are There Ethnic-Specific Variants of the Breast Cancer Gene BRCA1? Ryan Pearson, Zouberou Sayibou and Rajendra Gharbaran, Bronx Community College/CUNY, Bronx, NY.

In the US, 1 in out of every 8 women in the U.S. will develop breast cancer. But studies are now showing that the rate of cancer emergence is different among ethnic lines. One of the ways to track these differences is through genetic variants of mutations in the BRCA 1/2 (Breast Cancer Type 1 & 2 Susceptibility Proteins), DNA repair proteins. To do this, we studied clinical data from Breast Cancer Information Core (BIC) available through the BRCA Exchange which collects BRCA1/ BRCA2 data from several other databases. Our specific focus for this project was, in regards to pathogenicity, are there genetics variants that show differences in racial and ethnic differences in breast cancer patients? Of the 745 mutations, available from the BIC database in regard only to the BRCA 1 gene, we found 109 genetic variants (in 4245 individuals) were common to only minority populations, approximately 353 variants among Caucasians (in 5166 individuals), and approximately 95 were found in both minority and Caucasian populations (in 2638 individuals). The other 188 were unable to be attributed to any specific groups. Some of those connections among minority populations were broad, like Asians and some were very specific, like the Berbers from Morocco or the Pakistani. However, the number of individuals with each mutation varies widely. Most of the variants appear to be of germ line mutations. Identification of ethnic-specific BRCA1 genetic variants may help to enhance screening for breast cancer risk, especially among minority populations.

Molecular and Physiological Characterization of *Microcystis aeruginosa* under Zinc Stress. Jose L. Perez and Tinchun Chu, Seton Hall University, South Orange, NJ.

Cyanobacterial Harmful Algal Blooms (CHABs) are environmental biomasses found in increasing climate change conditions, eutrophic conditions, and aqueous environments contaminated with heavy metals. Certain cyanobacteria can also release toxins that are detrimental to animals and humans. Metallothionein (MT) is a cysteine -rich, metal-binding protein often upregulated as part of the stress response mechanism. This study focused on the characterization of zinc stress in Microcystis aeruginosa UTEX 2385 (toxic) and 2386 (non-toxic). Cells were monitored at various ZnCl2 concentrations (0, 0.1, 0.25, and 0.5 mg/L). Flow cytometry and phase contrast microscopy were used to evaluate the morphological changes. Molecular assays and bioinformatic analysis were carried out to characterize the expression of metallothionein under zinc stress. The results showed that the minimal inhibitory concentration (MIC) was 0.5 mg/L while the half maximal inhibitory concentration (IC50) was approximately 0.3 mg/L ZnCl2 for both strains. Flow cytometry and phase contrast microscopy indicated that toxic MA2385 average cell size was significantly larger than MA2386 average cell size when comparing 0 mg/L ZnCl2 with 0.25 mg/L ZnCl2 by days 5 and 8. The concentration of Chlorophyll-a decreased significantly by day 5 for both strains under ZnCl2 stress. Toxic 0.5 mg/L ZnCl2-treated MA2385 showed an overall higher concentration of chlorophyll-a from day 5 to day 15 when compared with MA2386 cultures. Multiple sequence alignment (MSA) results indicated that the MT proteins contain conserved cysteine-rich domains in positions 8-16 (N-terminus) and 53-55 (C-terminus). Phylogenetic analyses exhibited five clades among the selected MT sequences. The structure alignment results displayed the conserveness of the zinc-binding domain at the N-terminus.

Use of Enzymatic Ethanol Assay to Evaluate a *Gallus gallus* Model of Fetal Alcohol Syndrome. Samantha Perez, Nadine Khalil, Noelle Kubinak and Cathryn Kubera, Monmouth University, West Long Branch, NJ.

Fetal Alcohol Spectrum Disorder (FASD), which results from prenatal exposure to alcohol, is a wide-spread condition impacting 2-5% of infants in the United States. Distinctive craniofacial abnormalities and symptoms that develop from FASD include widening of the eyes, flat nose, thin upper lip, learning disabilities, and heart defects. In the brain, the cerebellum controls mobility, coordination, balance and speech, all of which may become impaired as a result cellular apoptosis in the cerebellum following embryonic alcohol exposure. Here we use a Gallus gallus model to study FASD. We hypothesize introduction of alcohol in ovo or ex ovo at the onset of cerebellum development will result in measurable changes in egg-white alcohol content and spontaneous embryonic motility. On embryonic day seven (E7), when cerebellum development begins, 20% ethanol, 50% ethanol or PBS was injected into the air sac of the egg during the in ovo method, whereas in the ex ovo method 20% ethanol, 50% ethanol or PBS was added topically. In our FASD model, tissue and egg white samples were harvested on E8.An enzymatic Ethanol Assay was performed on egg white samples from ethanol- or PBS-treated eggs to determine alcohol concentration. The Assay measured reduction of NADH from nicotinamide-adenine dinucleotide (NAD+) through two separate enzymatic reactions: aldehyde dehydrogenase mediated

oxidation of ethanol to acetaldehyde, followed by alcohol dehydrogenase mediated conversion of acetaldehyde to acetic acid. The Cytation 5 plate reader was used to collect readings of NADH absorbance of 340 nm, which is directly related to the amount of ethanol in the sample. Preliminary assay results indicate successful detection of ethanol in positive controls and standard curves, as well as in egg white samples collected 24 hours post ethanol treatment. In addition, chicks developing ex ovo were video recorded to observe the effects of alcohol on the intrinsic spontaneous behavior that developing chicks begin to display on E6. Pre- and post-treatment movies will be assessed for frequency and duration of activity bouts to determine the effect of alcohol on embryonic movements.

THZ1 Synergizes With ABT263 To Induce Apoptosis in Cultured Glioblastoma Cells. Azariel Perry and Enyuan Shang, Bronx Community College, Bronx NY.

Cancer is a disease that has plagued human existence for centuries and is the second leading cause of death globally. Glioblastoma (GBM) is the most common and the most malignant glial brain tumors and its very poor prognosis has not significantly improved despite the development of innovative diagnostic strategies and new therapies. Recently a group of small molecule compounds that target cancer cells intrinsic apoptosis program, the BH3-mimetics, have been developed. However, cancer cells can generate resistance by upregulate the expression of Bcl2 family proteins. So what we are trying to do is to combined drugs that can down regulate Bcl2 family proteins with BH3-mimetics to enhance death of cancer cells. The BH3-mimetic ABT263 was combined with THZ1, a CDK7 inhibitor that downregulate Mcl1, a member of Bcl2 family proteins. Our results showed that both ABT263 and THZ1 inhibit the proliferation of GBM cells. However, the combination of ABT263 and THZ1 dramatically enhanced the apoptosis of GBM cells. We used FITC Annexin V and PI (Propidium Iodide) staining and Flow cytometry showed that the cancer cells died through apoptosis. We also used TMRE (Tetramethylrhodamine ethyl ester) staining, a mitochondrial membrane potential indicator, to show that THZ1 synergizes with ABT 263 and cause a greater induction of apoptosis. Collectively, these results showed that the combination of two drugs has an enhanced effect compared to each individual inhibitor alone. And as a result indicate that in order for tumors to not become resistant to a single treatment, the synergy of inhibitor drugs may be the most viable method for the treatment.

Characterization of Microbial Communities Responsible for the Biodegradation of Cellulose in Soils. Lisa Pincus, Stephania Vazquez, Adelajda Turku and Luis Jimenez, Bergen Community College, Paramus, NJ.

Cellulose, a B-(1,4) homopolymer of glucose, is the most prevalent biopolymer on the planet. Cellulose can be a renewable and greener source of energy which can meet the high-energy demand of the world. Furthermore, cellulases are used in major industrial applications such as textiles, household products, animal feed, food processing, peppermills, etc. The microbial hydrolysis of cellulose requires the action of different enzymes such as endoglucanases, exoglucanases, and B-glucosidases in a synergistic manner so that cellulose is converted to simple sugars like glucose. Different soils were analyzed by PCR for the presence of microbial cellulases genes belonging to glycoside hydrolases (GH) families 1, 5, 6, 7, and 48. DNA fragments for each specific gene were detected in all positive soil samples. Microbial cellulases genes belonging to GH1 and GH7 were detected in all samples while GH5, GH48, and GH6 genes were detected in 46%, 39%, and 31% of soils, respectively. The amplified DNA fragments of GH7 (mold) and GH48 (bacteria) genes 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. Unknown genes of GH7 (90%) and GH48 (65%) cellulases were the predominant members of cellulose degraders in the tested soils indicating undiscovered diversity of cellulose biodegradation genes in soils.

Use of Quantitative Polymerase Chain Reaction to Assess Expression of Erythromycin and Penicillin Resistant Genes in the East River and Coney Island Creek. Daniel Pintor, Muminakhon Nazarzoda, Mariah Allen, Robert Buchanan and Victoria E. Ruiz, St. Francis College, Brooklyn, NY.

Inappropriate use of antibiotics in human and veterinary medicine and animal agriculture have led to increased levels of antibiotics and associated metabolites in landfills and its leachates, including soil and water. Antibiotic levels in these various leachates may persist long after antibiotic use and promote the presence of antibiotic-resistant bacteria and antibiotic-resistant genetic elements. Enterococci are gram-positive bacteria that are commonly used to assess water quality. Enterococci species are reservoirs of antibiotic resistant genomic elements. Previous work has demonstrated high Enterococci levels in Coney Island Creek compared to East River sites (DUMBO, Pier 2, Pier 4). We hypothesize that Coney Island Creek contain higher levels of antibiotic resistance genes. To test this hypothesis, we extracted DNA from water samples collected from Coney Island Creek, Pier 2, and Pier 4 using the DNAEasy PowerWater

Kit. Relative gene expression of erythromycin resistance gene, ErmB and Beta-lactam resistant gene (BlaTEM) were measured. Samples were normalized with 16srRNA gene. Coney Island Creek had higher amount of ErmB compared to both East River sites (Pier 2 and 4), while East River contain higher level of BlaTEM. Existence of antibiotic resistant organisms in water may have direct health hazards for humans and animals.

Examining the Prevalence of Salmonella Bacteria in Standing Water Using Loop-Mediated Isothermal Amplification Method, an Alternative to Polymerase Chain Reaction. Kaylynn Pubill and Andrew Nguyen, Queensborough Community College, Bayside, NY.

Salmonella bacteria cause salmonellosis, an infection with symptoms of diarrhea, chills, fever, and occasionally vomiting. Though most commonly spread through contaminated food and water, waterfowl can also transmit Salmonella. Effective detection of Salmonella bacteria can serve as a prevention method to lower the rate of outbreaks and infection. The goal of this project is to detect the prevalence of Salmonella bacteria, and more specifically *Salmonella enteriditis* in standing water around New York City. The new and inexpensive LAMP (loop-mediated isothermal amplification) method was used as an alternative to PCR (polymerase chain reaction). LAMP uses only primers, free nucleotides, a buffer solution, and bst enzyme in a single temperature of 65ºC for one hour. To detect the presence of Salmonella spp., we amplified the fim-Y gene while the detection of the sdf 1 gene was linked to the presence of *S. enteritidis*. Our preliminary results indicate that LAMP can amplify the fim-Y gene in the isolated samples of *S. typhimurium, S. enteriditis, S.Heidelberg, S. Newport*, but not Staphylococcus aureus, *S. faecalis, Proteus vulgaris, or Serratia marcensens*. We have optimized the reaction and are in the process of testing and monitoring water samples in surrounding areas of Queens and the East River of New York City. In conclusion, the LAMP method is specific, yet inexpensive making it ideal for the detection of Salmonella spp. in environmental samples.

The Volume Regulated Anion Channel Protein Subunit LRRC8A is Expressed in Chick Neuronal Primary Cultures. Alison Quijano, Jonathan Ungania, Isabella Hanesworth, Julius Vargas and Renee Haskew-Layton, Mercy College, Dobbs Ferry, NY.

Volume regulated anion channels (VRACs) play a role in cell volume homeostasis, proliferation, and apoptosis. In the brain, VRAC activation contributes to cell death in stroke and Alzheimer's disease. The main protein subunit of VRACs is the leucine rich repeat containing protein 8A (LRRC8A). Our aim is to understand the mechanisms that modulate LRRC8A protein expression in stroke and Alzheimer's disease using a chick embryo primary brain cell model. While our lab has successfully measured LRRC8A mRNA levels, we are optimizing methods for detecting LRRC8A protein levels in chick brain cells. We hypothesize that LRRC8A protein is ubiquitously expressed in chick brain cells, as is found in mammalian cells. To monitor LRRC8A protein levels, we used both Western Blotting and immunocytochemical techniques. Our preliminary results show that LRRC8A protein is expressed in chick primary neuronal cells. The ability to monitor LRRC8A protein expression in primary brain culture will allow us to further determine mechanisms of LRRC8A modulation in stroke or Alzheimer disease, leading to potential therapeutic interventions aimed at decreasing neuronal death.

Bacterial Diversity and Community Composition of Cyanobacteria and Cyanophages in Barnegat Bay, New Jersey. Roksana Rahman and Tinchun Chu, Seton Hall University, South Orange, NJ.

Cyanobacterial harmful algal blooms (CHABs) has increasingly become a threat to animal and human health with its higher frequency due to eutrophication. Increasing nitrogen levels at Barnegat Bay has put it at higher risk for CHABs. In this study, the focus was on the detection and identification of cyanobacteria and cyanophage populations within Barnegat Bay. Water samples were obtained from 12 sites in Barnegat Bay and filtered through a 30- and a 0.4-mm polycarbonate filter sequentially. Genomic DNA extraction, polymerase chain reaction (PCR), and gel electrophoresis were then performed with four primer sets 27F/785R, PSF/UR, CYA359F/CYA781R, and MSF/MSR. Flow cytometry was conducted on the 0.4 - 30 mm filtrate. Viral plaque assays were carried out on the < 0.1 mm filtrate to detect the presence of cyanophages. Nextera XT DNA Library Preparation Kits were used to prepare for the library and next generation sequencing (NGS) was performed on an Illumina MiSeq platform. Microbial community profiles were generated and analyzed by CLC Genomic Workbench. Flow cytometric results exhibited the water samples contained a wide range of cyanobacteria, including *Microcystis aeruginosa*, Synechococcus sp. IU 625, Cylindrospermum spp., and Anabaena spp., ranging from 3.16 to 8.17 x 107 cells/L. PCR-based assays indicated that though phyto-specific species and cyanobacteria were present for all sites, no toxin-producing M. aeruginosa was detected. Viral plaque assays showed that cyanophages were detected in all 12 sites, ranging from 2.5 x 102 to 5.0 x 105 PFU/mL. Metagenomic analysis depicted that the genera ranged from 474 (Forked River Lagoon) to 918 (Forked River Route 9).

TFIIIB Isoform Expression in Zebrafish. Jason Ramdeo, Carlo Belifore and Laura Schramm, St. John's University, Queens NY.

Transcription of DNA into RNA requires a multi-submit enzymatic complex termed RNA polymerase (pol). In eukaryotes, there are three RNA pols which transcribe genes with varying promoter structures. RNA pol I transcribes rRNA genes. RNA pol II transcribes mRNA,

miRNA, snRNA, and snoRNA genes. RNA pol III transcribes ribosomal 5S rRNA, tRNA and other small untranslated RNAs such as snRNA and miRNA genes involved in a variety of cellular activities including development, immunity, and oncogenesis. RNA pol III, like all other eukaryotic polymerases, cannot recognize its target promoters directly, and requires a multi-subunit complex termed TFIIIB. Human RNA pol III initiates transcription from both gene internal (tRNA and VAI) and external (U6) promoters. To initiate transcription from gene internal promoters, RNA pol III requires a form of TFIIIB containing TBP, BRF1, and BDP1. Transcription from gene external promoters requires a form of TFIIIB comprised of TBP, BRF2, and BDP1. Alternatively spliced variants of human TFIIIB have been identified but the isoforms roles in health and disease remains elusive. The TFIIIB subunits TBP and BRF2 have been linked to a variety of human cancers. Recently, alterations in BRF1 have been linked to neurodevelopmental issues. Zebrafish (Danio rerio) is a model organism for human aging and disease and may prove to be a useful tool to study TFIIIB isoforms in the context of aging and disease. Thus, we examined isoform expression of TFIIIB subunits BRF1, BRF2, and BDP1 in zebrafish using bioinformatics approaches. Herein, we report a high degree of gene sequence homology between human brf1 and zebrafish brf1b with a GOC score of 50 and WGA coverage score of 54.33, meeting the threshold necessary to classify the two genes as orthologues. Protein alignments of human BRF1 (677aa) and zebrafish BRF1B (693aa) reveal the proteins are 64% and 65% identical, with 97% and 94% coverage, respectively. We then compared the conserved regions between the orthologues. Within the Zn ribbon domain human and zebrafish protein sequences are 80% identical. The first and second TFIIB imperfect repeats in human BRf1 and zebrafish BRF1B are 91% and 94% identical, respectively. Together, these data suggest that human BRF1 and zebrafish BRF1B are orthologues. As such, we believe zebrafish could potentially be used as a model to study RNA pol III transcription from gene internal promoters requiring TFIIIB complexes containing BRF1 in the context of human aging and disease.

Carnosine Reduces the Neurotoxic Effect of Manganese on the Physiological Response of a Cilio-Inhibitory Dopaminergic System. Christopher Ramirez[1], Janette Quintuna[2], Edna Georges[1], Margaret A. Carroll[2] and Edward J. Catapane[2], [1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY.

Manganese, a neurotoxin causing manganism a Parkinson's-like disease, involves disruption of dopamine neurotransmission. The mechanism by which manganese produces this dysfunction is not fully resolved. Lack of effective treatment for manganism has been a major obstacle in its clinical management. Gill lateral cell cilia of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervations from their ganglia. Dopamine (DA) is cilio-inhibitory, while serotonin is cilio-excitatory. Previous work of our lab showed acute and short-term manganese treatments block the cilio-inhibitory effect of DA, and this neurotoxic action of manganese was reversed by the drugs p-aminosalicylic acid and taurine. Recently, reports suggest the dipeptide carnosine (*beta*-alanyl-L-histidine) may be worth investigating as a neuroprotective agent for manganism because of its anti-oxidative and chelating abilities, and its efficacy in other neurodegenerative diseases. We hypothesize carnosine would reduce the neurotoxic actions of manganese on the cilio-inhibitory effects of DA in *C. virginica* gill. To test this we conducted acute experiments testing DA dose responses on excised gill treated with manganese (10^{-4} M) for 10 minutes in the presence or absence of carnosine (10^{-4}M). Cilia activity of gill lateral cells was measured by stroboscopic microscopy and expressed as beats/min ± sem. Cilia of control lateral gill cells that were first activated by serotonin (10^{-5}M) responded normally to the dose response to DA (10^{-6} - 10^{-4} M) with the appropriate decrease in cilia beating rates from about 20 beats/second to about 0. Manganese treatments disrupted the DA induced cilio-inhibitory dose response of gill lateral cells and carnosine treatments reduced this neurotoxic effect, generating a cilio-inhibitory response similar to that of DA without manganese present. We also conducted short-term experiments in which *C. virginica* were treated for 2, 3 and 5 days with manganese (100 μM) with or without carnosine (100 μM). Control animals were sham treated. For each treatment period, the effect of co-treating animals with carnosine and manganese reduced the neurotoxic effect of manganese on the physiological response of the oyster cilio-inhibitory dopaminergic system, generating cilia responses similar to control animals that were sham treated. This physiological study showed carnosine to be effective in reducing the neurotoxic effect of manganese on the cilio-inhibitory dopaminergic system in *C. virginica*. These findings are helpful in furthering the understanding of the mechanism of manganese neurotoxicity and provides evidence suggesting carnosine needs to be further investigated as a potential therapeutic agent for manganism. Supported by NIGMS grant 2R25GM06003, NIH grant K12GM093854-07A1, PSC-CUNY grant and 62344-00-50 0537-19-1091 of the CSTEP Program of NYSED.

Spawning Location Selection for The Atlantic Horseshoe Crab (Limulus polyphemus)on Plumb Beach, Brooklyn, NY. Manuel Ramos and Christina Colon, Kingsborough Community College, Brooklyn, NY.

Horseshoe crabs are arthropods more closely related to arachnids than crabs, their origin traces back 450 million years. Plumb Beach is one of their spawning locations. This is important because there aren't many ideal locations for them to lay eggs, and due to their use in the medical field, we need their counts to rise. It was hypothesized that high egg densities in the prime spawning area will cause

an overflow in adjacent areas. Eggs were collected on the Eastern side of Plumb Beach and then sieved in our lab over the Summer. High egg counts in the prime spawning site seem to correlate with extremely low counts in the adjacent study plot, along with relatively high counts in a farther site. In eight out of nine years the data expresses this pattern. In six out of nine years we see BW also expresses a relatively high egg count when compared to BE. Our egg counts show that five out of nine years keep up with this pattern of high-low-high. Even in the year with our highest counts in 2011 we haven't seen our expected linear decline. The only year that followed our expected linear decline is 2016 that experienced a later peak in July rather than June. These findings do not support my hypothesis. Rather than selected sites being a function of relative distance to the prime location, it is likely there are other factors that influence the selection of a spawning location. Another study indicates that spawning females are more prone to disturbing the preferred spawning sites rather than selecting adjacent nest areas [Smith, 2007]. This work was supported by grant 2R25GM06003 of the Bridge Program of NIGMS, and by grant? 0537-19-1091 of the CSTEP Program of NYSED.

Investigating Autophagy and Inhibitory Plasticity Through Regulation and Modulation of GABARAP. Angely Rojas, Martena Grace and Reed Carroll, New Jersey City University, Jersey City, NJ.

The health of neuronal connections and their successful function is highly predicated on homeostatic maintenance through different processes. Autophagy is a cellular process in which damaged organelles and components are sequestered in autophagosomes for degradation. Autophagy plays a critical role in neuronal functioning, allowing detoxification and renewal. The disruption of this process has been linked with neurodegenerative diseases including Parkinson's and Alzheimer's. GABARAP is a protein that regulates autophagy by mediating the fusion of autophagosomes with the lysosome. GABARAP also plays a role in regulating synaptic plasticity in neurons by modulating the surface expression of inhibitory GABA receptors through its interaction with its □2 subunit. Inhibitory plasticity also has an effect in health and disease of neurons, playing a role in cellular homeostasis by allowing neuronal activity to stay at appropriate levels. In this research, a possible link between autophagy and inhibitory functioning were investigated through their common working protein GABABAP using HEK (human embryonic kidney) cells as model systems to study neuronal functions. Ongoing studies are investigating the effects of autophagy in regulating surface expression and clustering of $GABA_A$□2 receptor through its interaction with GABARAP.

Sexual Dimorphism in Asian Shore Crabs and Its Influence in Predation on Whelks. Prachi Saxena and Aaren Freeman, Adelphi University, Garden City, NY.

The Asian shore crab, *Hemigrapsus sanguineus* is native to the western Pacific Ocean, however, it became an invasive species to the east coast of North America in New Jersey by 1988. In the Northwest Atlantic *Hemigrapsus* preys on native dog whelks *Nucella lapillus*. Generally, co-evolution between gastropods and their crab predators has resulted in gastropods with more robust, thicker shells and narrower apertures, while crabs have modified their foraging strategy to more effectively feed by "winkling" (i.e. probing by the crab to remove gastropod tissue without breaking the shell). *Hemigrapsus* applies the foraging strategy of winkling to consume *Nucella*. Crabs consuming relatively large gastropods through winkling is well-documented, however, the impact of sexual dimorphism on gastropods being winkled has been reported in a few studies. Therefore, we hypothesize that *Nucella* with a large aperture width and lower unoccupied volume may become more susceptible to winkling. Since female *Hemigrapsus* has smaller claws relative to a male *Hemigrapsu*s we hypothesize that female crabs may be more efficient in winkling *Nucella*. So, we measured *Nucella's* shell length, shell width, aperture length, unoccupied volume, and aperture width, and *Hemigrapsus's* carapace width, claw length and claw height prior to each feeding trial. *Hemigrapsus* was kept in a perforated plastic cage with three different sizes of *Nucella*. Crabs were given a choice of three *Nucella*, ranging in size (approximately 15 – 30 mm). The trial was continued for 3 days and the results were recorded after every 24 hours as winkled (if a snail is found dead/no tissue/some tissue consumed) and not winkled (if the snail is found alive). Preliminary statistical analysis using R software suggests that *Nucella* with a larger aperture width is more susceptible to winkling and female *Hemigrapsus* are more efficient in winkling *Nucella* relative to its male counterpart.

Implementing the Theophylline Riboswitch in Riboswitch Conversion. Mika Schievelbein, Lauren Lucia, Sonia Dadlani, Toni Zangrilli, James Tilton and Jonathan Ouellet, Monmouth, West Long Branch, NJ.

Fluorescence Activated Cell Sorting, or FACS, is a method that was used to convert the theophylline aptamer into a riboswitch. This method could theoretically be used to convert other discovered aptamers into riboswitches, however it is a costly method and is only available to those with access to these high-tech, expensive machines. The theophylline riboswitch was previously discovered by implementing the theophylline aptamer, with random sequences linking it to the expression platform, into a specifically-designed plasmid, and then using a FACS machine to sort the cells. We can structure a new system that would select only the correct sequence, containing the theophylline riboswitch out of a pool, without the use of a FACS machine. To do so, we place the pool of sequences

containing the aptamer, linked to the Shine Dalgarno by eight randomized nucleotides, into a newly designed plasmid, placNEO, and transform the plasmid into bacteria cells. Then, the use of replica plating along with screening will select the cells that only contain the plasmid with the correct riboswitch sequence. By doing so, we confirm that this system is efficient in converting aptamers into riboswitches without the need for a FACS machine. After an aptamer has been successfully converted into its riboswitch, the system of ratiometric fluorescence will allow for testing of the riboswitch's function. This is done by designing a plasmid, pTRFlac, that contains genes for red and green fluorescence proteins, mCherry and GFP respectively, on either side of the inserted riboswitch. A PCR product encoding for mCherry, the riboswitch, and GFP will be inserted downstream of the lactose operon in pUC18. Ratios of the fluorescence intensities of the two florescent proteins will provide the ability to measure the riboswitch's function through fluorescence readings.

Study of G Protein-Coupled Inwardly-Rectifying Potassium Channel (GIRK) and the Control of Lateral Cell Membrane Potential and Ciliary Response in Gill of *Crassostrea virginica.* Shatema Small[1], Alecia Johnson[2], Mohamed Eid[2], Margaret A. Carroll[2] and Edward J. Catapane[2], [1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY.

Crassostrea virginica gill lateral cell (GLC) cilia are controlled by serotonergic-dopaminergic innervations. Our lab showed dopamine (DA) causes cilio-inhibition and hyperpolarization of the plasma membrane, and serotonin causes cilio-excitation and membrane depolarization. The DA receptors in GLC are D2-like G-protein coupled receptors. While activation of the D2 signal transduction pathway opens G Protein-Coupled Inwardly-Rectifying Potassium channels (GIRK) causing hyperpolarization, it is unknown if GLC have GIRK and if the hyperpolarization aspect is involved in the cilio-inhibitory effect of DA. In this study we hypothesize GIRK is present in GLC and its activation results in hyperpolarization and slowing of GLC cilia beating. To test this we conducted immunohistofluorescence (IHF) studies with GIRK antibodies to visualize GIRK in GLC and tested a GIRK inhibitor and activator on changes in plasma membrane potential while simultaneously measuring cilia beating rates. Cilia beating was measured by stroboscopic microscopy and expressed as beats/min. Plasma membrane potential was measured using the fluorescent dye $DiBAC_4(3)$ and a microspectrum analyzer. IHF showed GIRK is present in GLC. Application of the GIRK activator ML297 hyperpolarized the membrane but had no effect on cilia beating rates. Application of the GIRK inhibitor barium chloride ($BaCl_2$) had no effect on membrane potential or cilia beating rates. However applying DA after $BaCl_2$, decreased cilia beating rates but membrane hyperpolarization did not occur indicating $BaCl_2$ was effectively blocking the GIRK channel. In other experiments gills were treated with manganese (Mn), a neurotoxin causing a Parkinsons-like syndrome in humans, and shown to interfere with the cilio-inhibitory effect of DA in *C. virginica*. Previous work of our lab showed Mn treatment blocked both the hyperpolarization and cilio-inhibitory effects of DA in GLC. In the present study Mn had no effect on the actions of either the GIRK activator or inhibitor, suggesting the toxic effect of Mn on the DA system is not involved in altering GIRK activity, but rather the activation of the D2 receptor. This study helps differentiate the steps of the D2 signaling pathway involved in controlling cilia beating from those controlling plasma membrane potential. While GIRK influences membrane potential this study showed it had no effect on cilia beating rates. The study also showed Mn does not affect GIRK activity in these cells. This is important because the mechanism how Mn produces neuro-dysfunction is not fully resolved and lack of effective treatment for Mn toxicity (manganism) in humans is a major obstacle in its clinical management. These findings are helpful in furthering the understanding of the D2 signaling pathway mechanisms as well as Mn neurotoxicity and provides evidence to guide future studies of potential therapeutic agent for manganism. Supported by NIGMS grant 2R25GM06003, NIH grant K12GM093854-07A1, PSC-CUNY grant 62344-00-50 and 0537-19-1091 of the CSTEP Program of NYSED.

Chemical Analysis of Melanin Inhibition in *Cryptococcus neoformans.* Tasnia Tabassum, Fu Dong, Orrette R. Wauchope and Helene Eisenman, Baruch College, CUNY, New York, NY.

Melanotic fungi are a major cause of morbidity and mortality around the world. *Cryptococcus neoformans* is a species of fungus harmful to human health and is particularly harmful to those with compromised immune systems. Exposure occurs via inhalation of spores into the lungs. If the immune system cannot contain the infection, *C. neoformans* will disseminate to the central nervous system and elsewhere in the body. Melanin production increases the fungi's virulence by helping it evade killing by phagocytic cells. Understanding how fungal melanin production may be inhibited has significance for the development of more effective treatments for cryptococcosis and other fungal infections. Melanin is produced in *C. neoformans* through L-dopa oxidation, catalyzed by laccase. *In vitro*, autopolymerization of L-dopa results in the formation of dark pigments resembling melanin. We hypothesized that the reducing agents, ascorbic acid and glutathione, will inhibit melanin production in *C. neoformans.* Fungi were incubated in the presence of L-dopa +/- glutathione or ascorbic acid and melanin production was monitored visually. Upon initial experiments, ascorbic acid and glutathione appeared to inhibit *in vivo* melanin production in *C. neoformans* when grown in culture. This also appeared to be true *in vitro* as well, suggesting that the inhibition occurred via chemical modification of L-dopa. Mixtures of L-dopa plus glutathione or ascorbic acid were analyzed by HPLC to test whether modified species were observed.

Regulation of Motor Neuron Innervation and Muscle Attachment in the *Drosophila* Embryo. Sharon Tang, Basya Buchbinder and Krista C. Dobi, Baruch College, New York, NY.

Drosophila melanogaster, commonly known as the fruit fly, have two sets of muscle systems: larval muscles and adult muscles. Since many developmental pathways are conserved between *Drosophila* and humans, seeing how muscle development and neuron innervation of muscles occur in the organism can provide valuable insight for similar processes in vertebrates. In fact, studying *Drosophila* has provided insight on human muscle and neuromuscular diseases such as muscular dystrophy and spinal muscular atrophy. Like humans, *Drosophila* muscles have individual characteristics, like unique sizes, shapes, orientations, attachment sites, and innervation patterns by motor neurons. These properties are encoded by a group of transcriptional regulators that are expressed in specific muscle subsets. Currently, there are twenty known transcription factors required for the development of the 30 distinct larval somatic muscle and specification of muscle properties. We are examining transcription factor mutants for defects in particular muscle characteristics. We are using genetics, immunohistochemistry, and fluorescent microscopy to study motor neuron innervation and muscle attachment. We will examine how neuron defasciculation and innervation occurs by testing how mutations in muscle-specific transcription factors affect innervation of a specific muscle subset, the lateral transverse muscles, by the segmental nerve. We hypothesize that mutant genotypes, which display defects in muscle patterning, will also disrupt motor neuron innervation. In addition to studying the motor neuron pathway across the lateral transverse muscles, our experiment aims to quantify and identify various connective tissue structures, such as integrins, within the *Apterous* genetic mutant. We have collected and stained 3 genotypes and are currently examining the architecture of the segmental nerve. This work will identify muscle-specific factors that regulate the process of innervation and muscle attachment.

Effects of Extreme Weather Patterns on the Soil Microbiome of New York City. Wes Thomason and Davida Smyth, The New School, New York, NY.

Extreme weather events are taking place across the globe, particularly impacting islands and coastal areas. Urban centers on the coast have and will continue to experience environmental changes due to such extreme weather events associated with climate change. As these extreme weather events become more frequent, it is important to understand their impact on microbial ecosystems such as the soil microbiome of both natural and manufactured urban green spaces. For our study, we studied an urban green roof and public park. Our goal was to compare the effects of simulated “flooding” and “drought” in a manufactured urban microbial ecosystem and a natural urban microbial ecosystem. Soil samples were taken from a green roof and a public park and plated on Tryptic Soy Agar to test for microbial growth before and after treatments. Two treatments were employed. The first involved saturating the soil with varying amounts of water based on the mass of the sample to simulate flooding. The second, involved drying the sample at 100°C for 100 minutes to simulate drought. Untreated soil samples served as controls. Samples were allowed to stand for 3 days. The control samples exhibited significantly higher colony forming unit counts (CFUs) for the public park sample than the green roof sample. By plating onto Mannitol Salt Agar and MacConkey Agar, both control samples were shown to contain gram positive as well as gram negative, fermenting and non-fermenting bacteria. This implies that while the park had greater numbers of bacteria, both samples were similarly diverse. It was found that 20% saturation of both the park and green roof samples resulted in the maximum number of CFUs. Samples that were dried to simulate drought had significantly less CFUs, the green roof had no CFUs and the park only 2. Results of this preliminary investigation suggest that water volumes higher than 20% of the soil mass reduced the CFUs in representative samples for both the public park and green roof locations. Further investigation will include sampling from additional urban NYC public parks and green roofs to verify the preliminary results. Our work is significant due to recent NYC legislation that mandates the installation of green roofs on all new buildings. If confirmed, our results would suggest that these green roofs should be designed to be able to withstand water content higher than 20% of its soil mass as well as drought conditions in order to maintain the microbial populations.

The Influence of Catecholamines in Broken Heart Syndrome. Hannah Rose Toussaint and Rochelle Nelson, Queensborough Community College, Bayside, NY.

Takotsubo syndrome, a stress-derived apical ballooning of the heart found predominantly in post-menopausal women, was thought to be the result of varying sex hormone levels. However, many of these hypotheses have been rejected. This study aims to further the scientific community’s knowledge of the cause(s) and mechanism of this syndrome by exploring the possible etiologies linked to the over-expression of specific X-chromosome escapee genes. To do this, primary endothelial cells were exposed to varying amounts of stress hormones. Total RNA and protein were then collected, and samples were analyzed using qRT-PCR and western blot gel electrophoresis. A change in the levels of several X-chromosome escapee genes was observed. This data provides further insight into a new possible mechanism of this syndrome while further elucidating the importance of gene expression balance between females and males. Hanna Rose Toussaint is a participant in the NIH Bridges to the Baccalaureate Program at Queensborouh Community College R25GM065096.

Microplastics and Plankton in the Bronx River. Stephanie Valencia and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

Pollution of microplastics in the Hudson Raritan Estuary has been a growing issue and has caused a negative impact in the food web (as it can be ingested by any organism, and accumulates up the food chain). Specifically, the Bronx River (NYC), which flows over several beds of mussels and restored oysters, has reported increasing marine debris and microplastics over the past years. The microplastics are abundant in the water column, where bivalves will filter feed; this means that the bivalves may unintentionally ingest plastics along with food particles. It is hypothesized that the water that is heavily polluted with plastic would cause an accumulation of microplastics in tissues of animals that filter feed. This experiment was done by using multiple plankton tows to collect zooplankton and microplastics along the Bronx River. The water samples were sorted and enumerated for different types of zooplankton as well as size/material classes of microplastics using a dissecting microscope. Ribbed mussels, which are common filter feeders in the Bronx River, were digested using the Fenton reaction to break down any organic material, leaving microplastics. Results showed that there were more microplastics present than zooplankton in the water column, and that microplastics were present in the tissues of filter feeding ribbed mussels, which supports the hypothesis.

Carnosine Reduces the Toxic Effect of Manganese on Mitochondrial Membrane Potential. Rosanne Wallach[1], Tenise Bowman[2], Edward J. Catapane[2] and Margaret A. Carroll[2], [1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY.

Manganese (Mn) is an essential metal that at excessive levels in brain produces extrapyramidal symptoms called manganism, which is clinically similar to Parkinson's disease. The mechanism of action of Mn toxicity is not fully understood and currently there is no effective treatment. Proposed mechanisms suggest Mn causes cellular oxidative stress and mitochondrial dysfunction leading to damage to dopaminergic neurotransmission. Previously we showed Mn reduced mitochondrial oxygen consumption in gill of *Crassostrea virginica* and this deleterious effect was reduced by EDTA or p-aminosalicylic acid (PAS), two proposed treatments for patients with manganism. We also showed Mn disrupts mitochondrial membrane potential of *C. virginica* gill lateral cells (GLC). In this study we hypothesize the neurotoxic effects of Mn on mitochondria membrane potential in *C. virginica* GLC can be prevented by either PAS or carnosine, another antioxidant with possible neuroprotective properties. To test this we used the mitochondrial selective fluorescent probe TMRM (tetramethylrhodamine methyl ester perchlorate) to study the effects of these agents in protecting mitochondrial membrane potential in Mn treated GLC of *C. virginica.* Gill sections were placed on modified microscope slides holding 2 ml of artificial sea water and treated with 2.5μM TMRM. Gill sections were then exposed to Mn (125 μM) alone, carnosine or PAS (125 μM) alone, Mn with carnosine (125 μM each), or Mn with PAS, and compared to control gill sections. Mitochondrial fluorescence of GLC was viewed on a Leica fluorescence microscope with epilume illumination using a 50 watt HBO mercury excitation lamp fitted with Texas Red filters (Ex 560 nm, Em 630 nm). Photomicrographs were taken with a Leica DFC400 camera at 100X and 200X at 0, 10 and 20 min. All sections were photographed with the same camera settings. GLC mitochondrial fluorescence intensity (FI) was measured using ImageJ from NIH. Statistically significance was determined by ANOVA. Control gills not treated with Mn fluoresced brightly in the presence of TMRM indicating a strong mitochondrial membrane potential. Gills treated with carnosine alone or PAS alone had mitochondrial FI similar to controls. Mn treatment resulted in a 40% reduction in mitochondrial FI over the 20 minute period. Gills co-treated with Mn and PAS showed no loss of FI. Gills co-treated with Mn and carnosine had reduced FI compared to controls, but the loss was only 15% compared to the 40% reduction seen in gills treated with Mn alone. These differences were statistically significant. This study showed PAS and carnosine have protective effects against Mn toxicity on mitochondrial membrane potential, with carnosine being less protective than PAS. These findings should be of interest to those exploring possible therapeutic treatments for manganism. Supported by NIGMS grant 2R25GM06003, NIH grant K12GM093854 -07A1, PSC-CUNY grant 62344-00-50 and 0537-19-1091 of the CSTEP Program of NYSED.

Molecular Detection of *Legionella pneumophila* in Water Samples across Passaic County, New Jersey. Paul Yoon and Tinchun Chu, Seton Hall University, South Orange, NJ.

Legionella spp. are gram-negative bacteria that are found in a wide range of environments such as soil, lakes, streams, and manmade water systems. The number of cases of Legionnaires' disease, a severe form of pneumonia caused by Legionella, have been on the rise in recent years. *Legionella pneumophila* is responsible for most cases of Legionnaires' disease. Approximately 7,500 cases of Legionnaires' disease were reported to the Centers for Disease Control and Prevention (CDC) in 2017. Currently, water sources are tested for Legionella spp. through culturing, and while results may be accurate, they may take several days to determine the presence of *L. pneumophila*. In this study, water samples across Passaic county were filtered through a 0.4 μm filter. A chelex DNA extraction, PCR, gel electrophoresis, and qPCR were then used to determine the presence and concentrations of *L. pneumophila* within various water samples from public and private taps across Passaic County, New Jersey. Of the 62 sites that were tested, 27 sites (43.5%) were positive with Legionella spp. and 20 sites (32.3%) were positive for *L. pneumophila*. qPCR results showed that copy number of *L. pneumophila* can be detected as little as 5 copies. This study shows that by combining PCR, gel electrophoresis, and qPCR, we can rapidly determine the presence of *L. pneumophila* in water samples. The increased efficiency can greatly reduce the response times when *L. pneumophila* are tested.

Anti-Spore Activity and Potential Application of Theaflavin. Ayuni Yussof and Tinchun Chu, Seton Hall University, South Orange, NJ.

Bacillus genus can form spores under stressful condition including when it lacks nutrients. Bacillus spores are significant in the food industry as these spores are associated with food spoilage and food poisoning. Black tea polyphenol or theaflavin (TF) is extracted from the fermented leaves of *Camellia sinesis* has been shown to have beneficial properties like anti-bacterial, anti-viral and antioxidant. This study aims to determine the anti-germination and anti-sporulation effects of different Bacillus species. Three Gram-positive species were used in this study, which are *Bacillus cereus (B. cereus), Bacillus megaterium (B. megaterium)* and *Bacillus subtilis (B. subtilis).* Microplate assay was used to profile the effect TF on the planktonic cell while cytological technique and colony-forming unit (CFU) assays were used to determine the effect TF on the sporulation and germination process of the selected bacteria. The data obtained from the microplate assay showed the minimum inhibitory concentration (MIC) is 0.1% TF while the Inhibitory Concentration 50 (IC50) is 0.025% TF. The cytological technique showed 1% TF can inhibit 99% of the sporulation for all three species after 6 hours of the incubation period. CFU assay showed 0.25% TF inhibits 99% of spore from germinating while 0.125% TF inhibits about 50% of spore from germinating. In summary, TF can be a promising food preservative agent that can inhibit sporulation and germination in Bacillus spp.

Biochemical and Spectroscopic Charecterization of G-Quadruplex Stabilization by Small Molecules. Adriana Zelaya, Christopher Bentsen, Massimilano Lamberto and Davis Jose, Monmouth University, West long Branch, NJ.

Telomeres are repetitive Guanine rich sequences at the ends of chromosomes that play a crucial role in protecting critical gene coding proteins from getting attacked and lost through cell division. The human telomere consists of a sequence of nucleotides, TTAGGG, that starts near the end of the duplex DNA and continues as a single strand. This single strand intrudes into the duplex DNA to form a T-Loop, which resembles a cap. Inside the cap, the Guanine rich sequence forms a G-Quadruplex structure, which is where our research is focused. The two important abnormalities that are directly correlated to the malfunction of telomeres are cancer and premature aging syndromes. The malfunctioning of telomeres results from many factors and the stability of the G-Quadruplexes is one of them. In the current research, we are introducing several types of small molecules, one of which is the porphyrin-based class of small molecules, to study the effect of ligand-induced stabilization/ destabilization of these non-canonical DNA structures. Incorporation of several classes of ligands have been introduced in two ways. Ligands under study were either incubated with the annealed DNA for 1 hour and or annealed with the DNA. Depending on the way these ligands are introduced has shown variances in the thermal stability of the G-Quadruplex. As the next step, we will introduce fluorescent probes either on the DNA or on the ligands to identify how the ligands bind to the DNA and the structural changes caused by it. The final test will be the introduction of a helicase to analyze the true stability of the G-Quadruplex. This study will be useful in developing new therapeutic methods for treatment of diseases including cancer and genetic diseases such as Bloom syndrome, Werner syndrome, and Fanconi anemia.

Lessons Learned from Students, Faculty and Near-Peer Leaders of a Structured Learning Assistance Model in Science Courses.

Irina V. Ellison and Christian F. Lucio, Mercy College, Dobbs Ferry, NY.

Introductory courses in the sciences historically act as a filter instead of a pump for science majors, often impacting student retention and graduation rates (Steen, 1988). One of the strategies to address this challenge at Mercy College is the implementation of recitation using a structured learning assistance (SLA) model. The goal of SLA is to support student success through structured opportunities for interactive group learning led by near-peers who can model success strategies. SLA activities can support both content learning as well as improvement of study skills by providing students with additional time outside of the traditional class to process material and collaborate with other students. At Mercy College, SLA is strategically paired with courses that have historically high rates of failure and withdrawal. These include developmental courses/gateway courses and courses necessary in a sequence. The Department of Natural Sciences has required SLA in all of the following courses: Anatomy and Physiology (Nursing Program students only), General Biology, General Chemistry and Organic Chemistry. SLA is weight bearing and is included in the final assessment of each student for that course. In order to assess the perceptions of SLA, faculty, near-peer leaders and students partaking in SLA across two campuses were asked to reflect about their experiences. Reflective data from faculty, near-peer leader and students partaking in PLA will be shared as well as feedback for improvement of SLA moving forward.

The Effect of Titanium Dioxide Nanoparticles on Marine Fish Fitness.

Kestrel Perez, St. Joseph's College, Brooklyn NY.

The presence of nanoparticles in everyday products is increasingly common, due to their small size and unique properties. In particular, titanium dioxide nanoparticles are widely used in sunscreens as a transparent UV blocker. The effect of titanium dioxide ($nTiO_2$) nanoparticles on the marine environment, however, is not well understood. I will discuss a research project that evaluated the impact of $nTiO_2$ on marine fish growth, survivorship, swimming ability, and feeding behavior. These traits are commonly measured indicators of fish fitness.

Effect of Marijuana on the Detection of Mitochondria Integrity in Adenocarcinoma Cells of the Colon: Significance of the Drug Transport System.

Steven M. Lipson[1], Darcy Rodriguez[1], Kirsten Casares[1] and Ronald E. Gordon[2]. [1]St. Francis College, Brooklyn NY and [2]Mt. Sinai Med. Ctr., New York, NY.

Abuse of cannabis [a.k.a. marijuana (MJ)] due to the drug's increasing availability to the general populace, has been associated with patients presenting with severe intestinal cramps, diarrhea, vomiting, and headaches [viz. cannabis hyperemesis syndrome (CHS)]. Fatalities have been recognized as well. A need exists to understand the mechanism of CHS activity on the cellular level, especially among those cells of the intestinal tract. Human adenocarcinoma of the colon (HT-29) was used as a model enteric system. Mitochondrial viability/toxicity was determined using a fluorescein conjugated monoclonal antibody clone 113-1 recognizing a 60 kDa non-glycosylated component of the *intact* organelle. Varying concentrations of MJ [encompassing a ratio of 20:1 tetrahydrocannabinol (THC) to cannabidiol (CBD)] were diluted in cell maintenance medium (MM) and dimethylsulfoxide (DMSO) from 0.025 to 5 mg MJ/ml, followed by inoculation onto monolayers of HT-29 cells. As determined through immunostaining, the preparations had no effect on mitochondrial loss of antigenicity. We ascribe our findings to the immiscible state of the commercially obtained MJ. Homogenization of MJ in MM proved effective in altering mitochondrial membrane integrity in the cultured epithelial cell monolayer. Light microscopy suggests that homogenization of MJ [ca. 20,000 rpm (OMNI homogenizer)] of 0.025 mg MJ/ml, produced "soluble" micelle-sized particles, capable of entering the HT-29 cells by endocytosis or a pinocytosis-like mechanism. MJ was found detrimental to mitochondria integrity, although cell monolayer gross morphology appeared unaltered. Importantly, the utilization of an appropriate MJ delivery system is critical in avoiding false negative results, as suggested in the current work.

The Flora on the High Line, New York City, New York, a Seventeen Year Comparison.
Richard Stalter, Amanda Garcia, Umair Khalid, Demetri Limperopolous, Rahema Nasary, Nicholas Scott, Khadija Yousuff, Luke Renda, Hayden Dimaio, Jingjing Tong. St. John's University Jamaica NY.

The lichens, mosses and vascular plant species on the abandoned High Line rail line collected in 2002 were compared with those collected by the author on a three block High Line remnant between 30th (40 15' 15"N 74 00' 20""W) and 33rd St. and 12 Ave. in 2019. The original High Line study identified 16l species within 122 genera and 48 families. The 2019 study included 105 species within 81 genera in 45 families. Ten lichens were identified in 2019 while 5 were identified in 2002. We attribute the difference in lichen numbers due to the competence and diligence of NYBG lichenologist, James Lendemer, who accompanied the author on a collection foray, May 2019. The number of mosses remain the same, 5 species. The loss of vascular plant species on the old High Line in 2019 is a function of the original High Line's reduced size, a 3 block remnant of the original site. Few invasive taxa can invade and persist on new High Line Park because of the aggressive eradication of invasive taxa at the park.

Does Intuitive Thinking Reinforce Biology Students' Misconceptions?
Regina Sullivan[1], Michal Fox[2] and John Coley[2], [1]Queensborough Community College,Bayside, NY and [2]Northeastern University, Boston, MA.

General Biology courses are challenging for U.S. college students. In most colleges, including Queensborough Community College (QCC), General Biology I is deemed a gatekeeper or gateway course. The grade a student receives in this course has a significant impact on their retention in STEM and STEM related fields. Successful completion of General Biology can either open or close the “gate” to higher level required courses and achievement of students’ career goals. Statistically, 30% of students in these courses earn a grade of F, W or WI. This is particularly true of students from underrepresented groups in STEM. Therefore application of interventions that increase our students’ success is imperative. We studied the effect of interventions that are designed to dissect the relationship between misconceptions in biology and intuitive thinking. Misconceptions are not based on scientific knowledge and lead to misunderstandings and perhaps failure of the course. There is a body of evidence to suggest that common misconceptions are tightly linked to types of intuitive thinking specifically teleological, essentialist and anthropic thinking. Several interventions were implemented to identity these types of intuitive thinking in QCC General Biology I&II classes. Further, interventions were also implemented that served to inform students about these types of intuitive thinking. The students were shown examples of how such thinking can reinforce science misconceptions. The methodology, examples of student’s responses and results will be discussed.

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