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Water Quality Analysis Infuses Environmental Health into the Biology Curriculum

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Abstract

Neuronal and cardiac birth defects are correlated with water pollution by chemicals associated with agriculture and industry. Infectious diseases, such as cholera are transmitted through contaminated water. Human exposure to these contaminants may occur through drinking water, during contact with surface water in recreational areas, or as a result of flooding or other natural disaster. However, the role that environment plays in health is largely absent from the typical undergraduate biology major. We present a model for incorporating topics of environmental justice and environment and health throughout the undergraduate biology curriculum. Our aim was for students to perform research that was relevant to human health and their daily lives while adhering to the cell and molecular biology concepts that form the foundation of the pre-health curriculum. Studies of local water sources were used as a model for study in first year as well as in upper level and independent study projects. A project that focused on Newtown Creek was included in molecular biology and bioinformatics courses. First year biology students conducted a microbiology project to assess the efficacy of homemade and commercially available filters in removing bacteria from different surface water sources. Finally we seek to connect our students with social change and environmental organizations outside of the classroom. Independent study summer students partnered with The River Project, a local NGO, Citizens Water Quality Testing program as part of a citywide endeavor to monitor bacterial levels in Hudson River water.

Introduction

Health workers may be the first to recognize and report occupational and environmental hazards. However, discussion of environmental health is curiously absent from the pre-medical curriculum, as environmental justice courses often center around social science or environmental science departments[1]. Biology faculty have an opportunity to engage future scientists and health care workers with environmental health issues in their communities. This is particularly true of colleges and universities in environmental justice areas like New York City, especially commuter schools, where ties to home communities are strong[2].

We present a model for incorporating environmental justice topics into the undergraduate biology curriculum. To broaden the possible application of this type of study, we chose local recreational water sources as the focus for our course. The water testing methods we propose are straightforward and can be done by students with minimal supervision using inexpensive commercially available kits. At St. Francis College, we have used water quality as an entry point to discuss topics related to microbiology, developmental biology, neurobiology, and gene expression. The projects described here tap into institutional framework and college wide adoption of a "sustainability curriculum," based on the United Nations Sustainable Development Goals[3].

In order to investigate the roles of common environmental pollutants on neuronal development, undergraduates collected and analyzed samples from sites along Newtown Creek, one of the most polluted waterways in New York City and designated Superfund Site[4,5]. The students assessed each water sample for chlorine, copper, iron, hardness, nitrate, pH, and phosphates and cross-checked and augmented this data set with data from the US EPA[6]. Students used bioinformatics tools to predict the molecular targets of these pollutants and assessed the effects of observed pollutants on the gene expression and neuronal development of a vertebrate model system, the embryonic zebrafish. The example we present here examines copper, based on elevated levels of this metal measured at a site close a student's home. This initial finding resulted in an independent study led by that student, fulfilling one of the most important Jemez Principles, "let people speak for themselves[7]."

In the second case, students conducted a microbiology project (Battle of the Water Filters) to design and test the ability of homemade filters to limit bacterial contamination in samples from various bodies of water; compared to a commercially available LifeStraws to filter *Enterococci spp.* from water. Through actively visiting and conducting experiments on New York waterways, our students incorporate their course materials in the context of society. We conclude by reporting on extramural student participation in water research with a local none governmental organization (NGO), The River Project, laying a framework for our students to be citizens and scientists after graduation.

Neurons in Newtown Creek: Using a Local Environmental Justice Case Study for Cell and Molecular Biology

In recent years, New York City's urban shorelines have undergone dramatic change concurrent with its Vision2020 Waterfront Plan, turning away from industrial and towards residential and recreational use[8,9]. Newtown Creek, an estuarine waterway in New York City forms a border between Brooklyn and Queens. It is one of the most heavily polluted areas in New York City and has been designated an US EPA superfund site as a result of its 100 year history of industrial manufacturing including refining, processing, and storage of petrochemicals, fertilizers and coal[5,10–12]. Combined Sewage Overflows (CSOs) associated with the Newtown Creek water treatment facility discharge raw sewage along the waterway during heavy rainfalls[12]. The area is further contaminated by a large underground oil spill, resulting in a major lawsuit and subsequent settlement between the US EPA and ExxonMobil[4]. Even as the creek maintains active industrial use, rapid development, a new ferry service, and odor abatement measures from the water treatment plant have all increased activity and community engagement in and around Newtown Creek. The settlement from the lawsuit created the Greenpoint Community Environmental Fund (GCEF), which has financially supported community engagement and environmental awareness and education around the creek[13].

Health risk to those who live near the creek is a point of contention and mistrust between community members and government agencies[14,15]. Epidemiological analysis, typically correlated with postal codes adjacent to the creek does not directly measure exposure to the creek's contaminated water, soils or sediment[16]. For example, analysis correlating emergency room visits for asthma with postal codes suggest higher asthma rates in some areas adjacent to the creek[16,17]. For residents within half a mile of the waterway, the New York Department of Health observed an increased rate of central nervous system birth defects compared to the city as a whole[18]. As these defects are rare, this increase was not found to be statistically significant. The same study recorded significant increases in the rates of lung and liver cancer in individuals living in close proximity to the creek. However other cancers typically associated with environmental toxins, such as kidney cancers, were not increased.[18] These and other ongoing investigations highlight the complexity of how long term combinatorial exposure affects health[19–21].

Materials and Methods

Water collection and analysis for basic water quality testing: Water sample of 0.5-1L were collected by hand and analyzed using LaMotte Water Monitoring Kit (5971-02). Teams of students measured Ammonia Nitrate, Nitrite, Chlorine, and Phosphate and Dissolved Oxygen (DO). If more than 24h had elapsed since collection, DO analysis was not performed.

Water collection and analysis for coliform bacterial tests: Coliform Bacteria culture tests were performed according to the manufacturer's protocol in LaMotte's Urban Water Quality Test Kit (Lamotte 5918).

Water collection and analysis for the Citizens Water Quality Testing (CWQT) program: Students collected water samples weekly from the Main Street Beach at Brooklyn Bridge Park; and transported the samples to the River Project's lab for analysis.

Zebrafish maintenance: Fish were maintained at 28.5 degrees on a 12h light/dark cycle. The day before embryos were to be collected, adult mating pairs were separated in mating boxes, either at room temperature, or in an incubator at 28.5. Zebrafish were analyzed at 1,2 and 3dpf using a Moticam Camera and with its accompanying software.

Identification of candidate genes: Candidate genes were identified using GEO datasets G2RTop250 analysis, after searching for parameters, pollution, PCBs, PAH, and organophosphate[22].

Dose response toxicology studies: Embryos were treated with (Copper II Chloride Dihydride) 1DPF in 4 groups: Control group (no treatment), 0.06%, .07%, and .08% Cu.
Students searched the literature to determine an appropriate dose range to generate a dose-response curve, and treatments were subject to approval by the SFC Institutional Animal Care and Use Committee (IACUC).

Water filtration efficacy studies: Students collected water samples and transported them to lab for filtration and subsequent serial dilution and plating of the water samples. Colonies were plated them on nutrient agar (non -selective), MacConkey agar (to select for gram negative bacteria), and Eosin Methylene Blue or EMB agar (also selective for gram negative bacteria).

Results

Newtown Creek and developmental defects

Here we describe how we used contaminants found in a local water body, Newtown Creek as a site of inquiry for undergraduate biologists. A full lesson plan with detailed methods is available upon request. Figure 1A presents an overview of the working process for this study. Briefly, students (1) collected water samples, (2) measured water quality, (3) verified results, (4) identified gene target candidates, and (5) predicted developmental defects from each pollutant. In tandem to lab activities, students read government reports on the site, and toured the Newtown Creek Wastewater treatment plant to better understand issues of water quality and treatment within New York City. Water samples were taken from several points along the creek. Sampling locations (Figure 1B) were chosen based on accessibility, which is limited by private property from

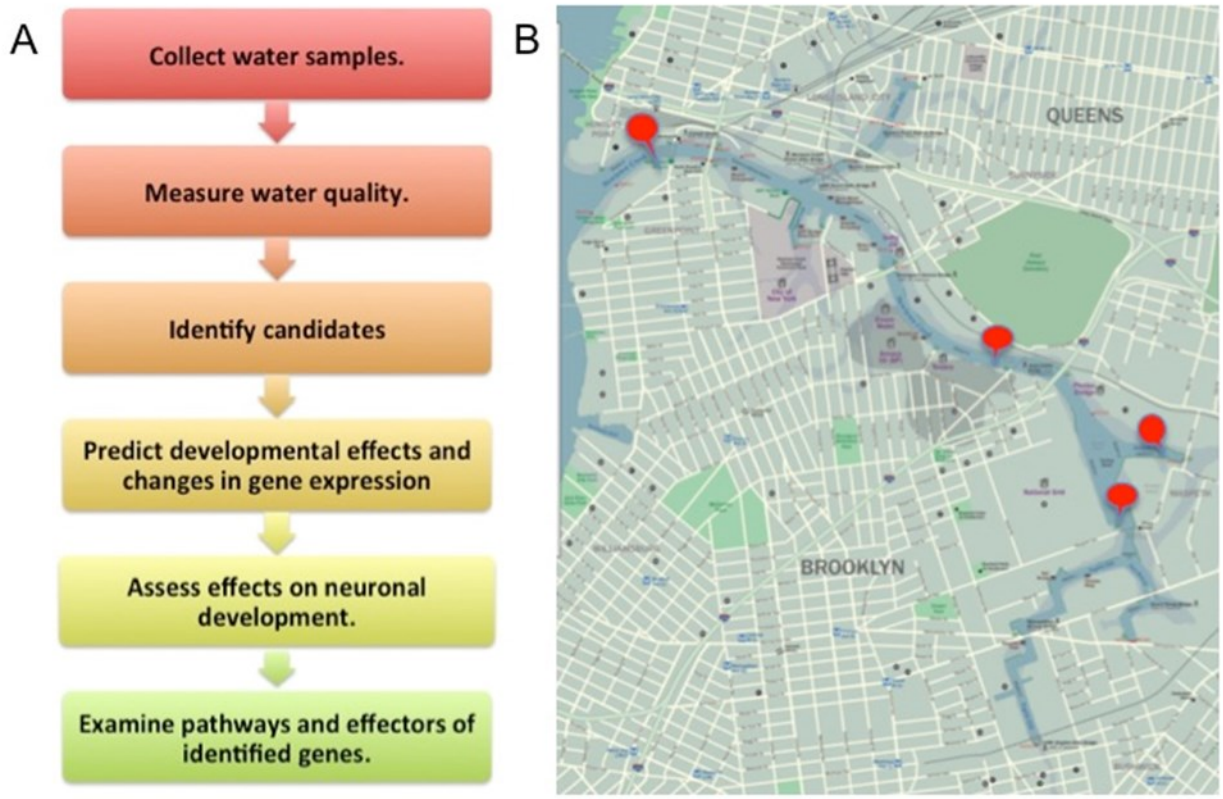

Figure 1: Newtown Creek Environmental Case Study Overview. A. Experimental overview, B. Map of sampling sites, from right to left, Manhattan Ave, Bridgewater, Maspeth, and Plank Road. Not shown, Grand Ferry Park (East River Control Site). Map modified from the Newtown Creek Alliance[10].

commercial enterprises along the creek and also by bulkhead (concrete barriers which line the waterway)[10,11]. After sampling, students performed analysis of basic water quality parameters including pH, Nitrates, Phosphates and Hardness (Figure 2,3) in addition to metals such as lead, copper and iron. Results were verified by consulting EPA and DEP data from matched sample sites along the creek[6,12]. It should be noted here that this exercise was meant to be a jumping off point for developmental analysis and prediction of gene targets not an end in itself; the GCEF has supported an extensive water quality project along the creek, SAMPLES, a partnership between the nonprofit Newtown Creek Alliance, and CUNY's LaGuardia Community College[23].

Elevated copper levels were measured at sampling points near Maspeth, Queens; near to a student's home. The measurement was confirmed by repeated sampling and by verification with EPA's sampling data[4–6]. Sampling sites were located near the Phelps Dodge Refining Corporation that refined copper and other metals from the mid-nineteenth to early twentieth century. After shutting down the refinery in the mid1980's, the property was sold to the Post Office[24]. However, the contamination at the site was so great that the Postal Service was able to force Phelps-Dodge to re-purchase the site[25]. Phelps-Dodge remains a responsible party in the cleanup of Newtown Creek and the site remains contaminated with metals, especially copper as well as other pollutants.

In order to determine the effect of transient low-level copper on development, students performed a basic dose response assay to assess for markers of general embryo health (Figure 4). For these studies we turned to the embryonic zebrafish, an established system for undergraduate research, developmental studies, and toxicology[26]. The students observed cardiac and neuronal developmental defects in embryos exposed to copper in a dose dependent manner. Rates of heart edema in copper exposed embryos were significantly higher compared to unexposed control embryos (Figure 4B,C,E). Significantly reduced mean body length could result from developmental delay as a result of copper exposure, inhibition of growth, or result from gene expression or

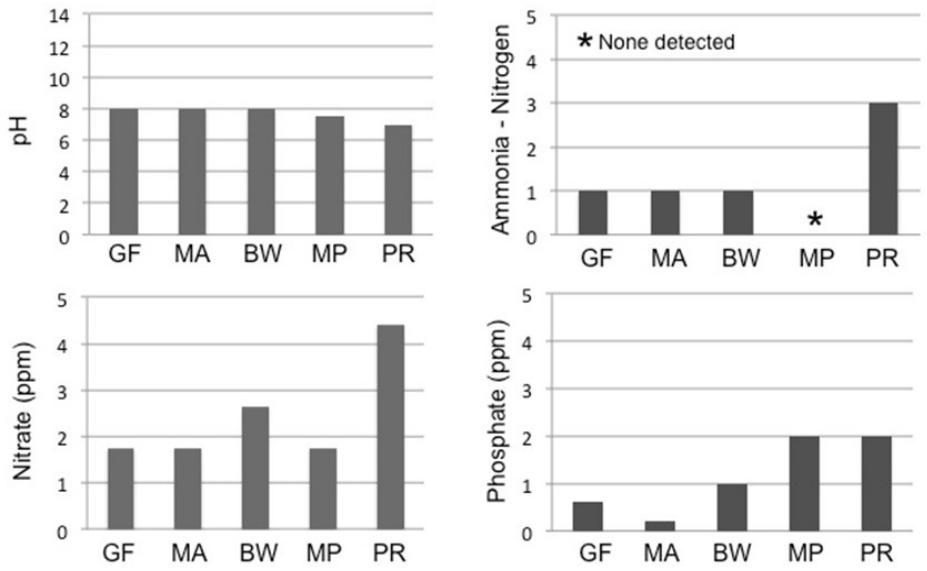

Figure 2: Water quality testing results for sampling sites along Newtown Creek. GF Grand Ferry Park (control), MA Manhattan Ave, BR Bridgewater 49th, MP Maspeth 48th , PR Plank Road. Results indicate that water quality worsened with distance from the east river.

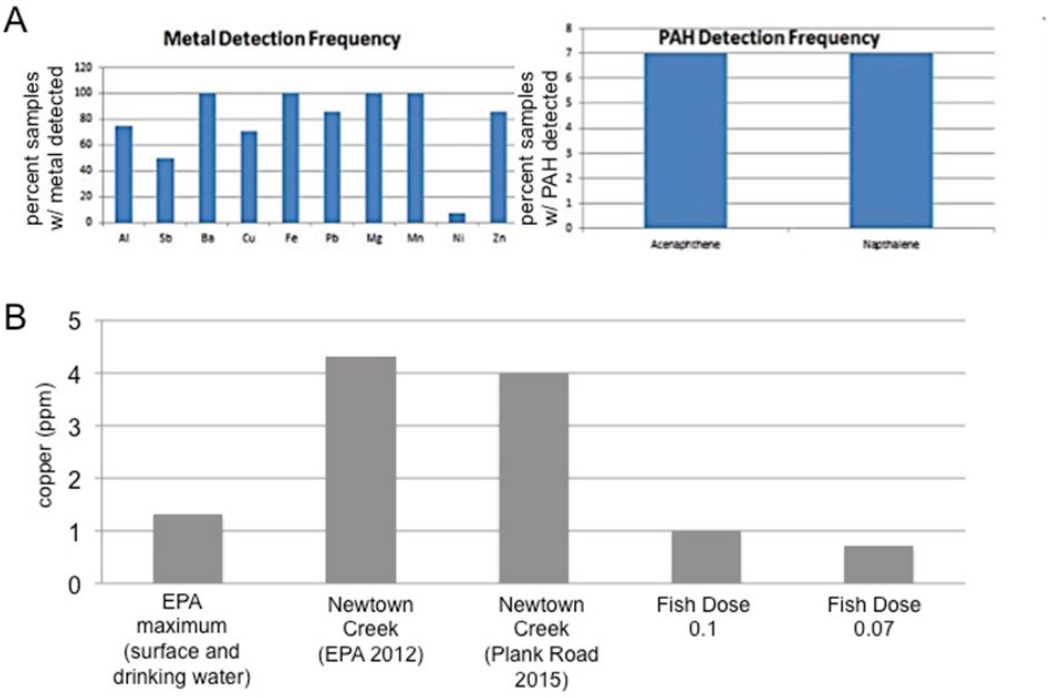

Figure 3: Student results were corroborated and extended by EPA results. A. Students analyzed EPA data to assess detection of metals as well as poly aromatic hydrocarbons (PAHs). Copper was detected in 60 of EPA samples. B. EPA maximum allowable limits of drinking water, compared to levels detected in Newtown Creek. We tested transient low-level copper exposure using a concentration similar to the EPA's allowable limits for drinking water.

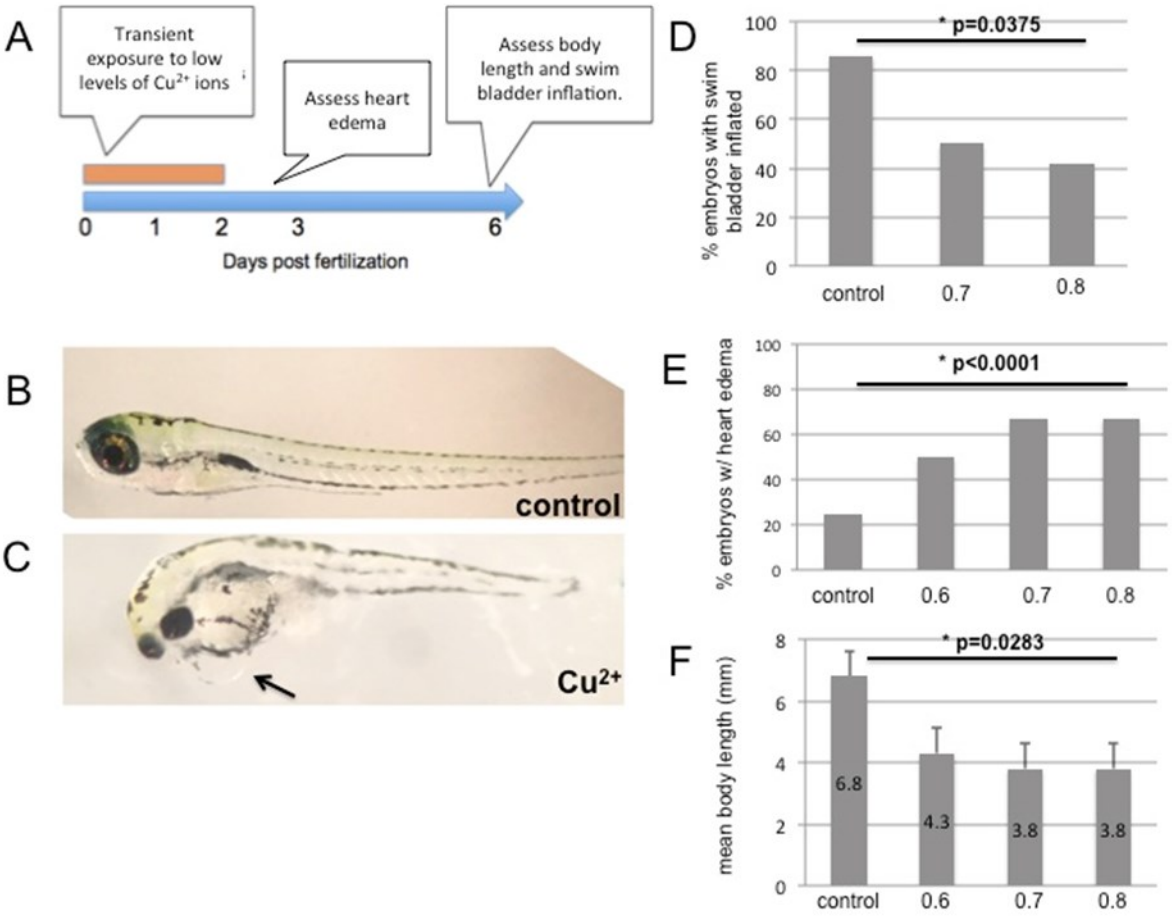

Figure 4: Transient low level exposure to copper results in cardiac and general developmental defects. A. Experimental overview showing time course of exposure and analysis. B,C. Representative control and copper exposed fish at 2.5 days post fertilization (dpf), arrowhead indicates heart edema; quantified in E. Visible blood pooling in Cu^{2+}-exposed embryos suggests heart defects persist. D,F. Dose dependent decreases in body length and swim bladder inflation suggests that copper exposure negatively impacts growth and development. Statistical comparisons in C and D were calculated using the Fisher Exact Test. Statistical Comparisons in B were calculated using a student t test (paired, two tailed).

redox changes in the developing embryo. Inflation of the swim bladder is a general marker of later development and embryonic health[27]. Copper treated embryos failed to inflate their swim bladders at an incidence significantly different than control. Taken together, these results suggest that low level transient copper exposure affects development generally, and results in a cardiac defect, heart edema.

Students selected candidate pollutants present in Newtown Creek from their own sample datasets or from EPA datasets with the aim of identifying molecular targets of these pollutants in keeping with the goals of the National Institute of Environment and Health and Department of Toxicology's Tox21[21]. Using open source bioinformatics tools candidate genes were identified using Gene Expression Omnibus (GEO) datasets G2RTop250 analysis, after searching for parameters, pollution, PCBs, PAH, organophosphate and copper. (Table 1). The National Center for Biotechnology Information (NCBI) provides a step-by-step tutorial for this resource, which helped students perform their analysis.[22] Some students also used the Toxicology Database Digital Infrastructure for Chemical Safety (DiXA) to extend their findings (data not shown)[28].

The Battle of the Water Filters

Waterborne illnesses including cholera are a major health burden in developing countries. The impetus for this project was based on a study by Huq *et al.*[29] who found that, upon returning to a village in Bangladesh, 31% of the women used a filter to filter their drinking water, and of that group, 60% used sari cloth filters for household water. This filtering was able to remove 70% of the *Vibrio*

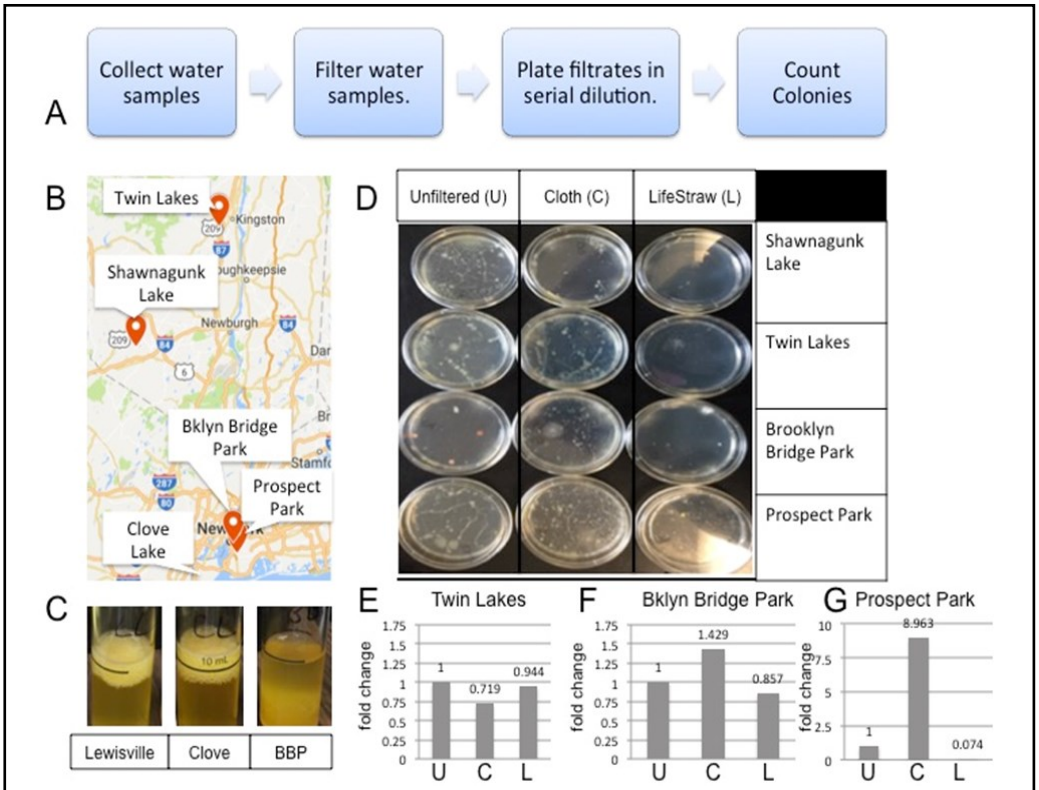

Figure 5: Textile filtration of surface water. A. Study Overview. B. Map of NY Sampling Sites, Lewisville Lake, TX sampling site not shown. C. Positive Coliform tests for unfiltered water from a control site (Lewisville Lake, TX), Clove Lake, Staten Island, NY and the East River in Brooklyn Bridge Park, NY. D. Colonies from filtrates or unfiltered control were plated in serial dilution and counted by hand. E-G. Fold change results for Twin Lakes, Brooklyn Bridge Park and Prospect park. Full counts for all conditions shown in Table 2.

Targeted Gene Symbols- Generated by GEO Analysis	
1. ahdA1c	6. TCEAL7
2. phnA2a	7.TPD52L1
3. bphA3	8.TEX15
4. bphB	9.H1FNT
5. bphC	10.GIT2

Table 1: Identification of Gene Targets Using open source gene expression datasets. Students performed GEO2R analysis to identify candidate neuronal genes that undergo a change in expression after exposure to polyaromatic hydrocarbons, persistent organic pollutants (POP), and organophosphates.

cholerae bacteria present. An even more effective filter, seasoned biosands, was used by Thompson and Gunsch (2015) that filtered up to 90% of Vibrio cholerae[30]. This was in response to the cholera epidemic that was associated with the environmental disruption caused by the earthquake in Haiti in 2010. In the first year biology laboratory, analysis of these studies evolved into a discussion about the disproportionate impact of environmental disasters on disadvantaged communities worldwide. Students responded by envisioning methods for water purification, especially for those who cannot buy fuel to boil water. Thus the Battle of the Water Filters was launched between two General Biology lab sections. Students filtered surface water through homemade textile filters such as denim cloth, and cloth from a t-shirt, and a homemade filter made of cotton and a sandy soil mix. As a control, students compared their homemade filters to a commercially available filter, Vestergard's LifeStraws. These portable, personal 0.2 μM filters remove bacteria and parasites from contaminated water[31,32]. These devices evolved from Nylon mesh cloth filters designed to filter out parasites, like the Guinea Worm; and have been adapted for use by hikers in the U.S., but remain predominantly in use in developing countries and in the wake of environmental disasters such as Hurricanes Harvey and Maria[33–35]. However, these filters are expensive and not always available; and textile filters could be as effective[36]. The first group of students did a

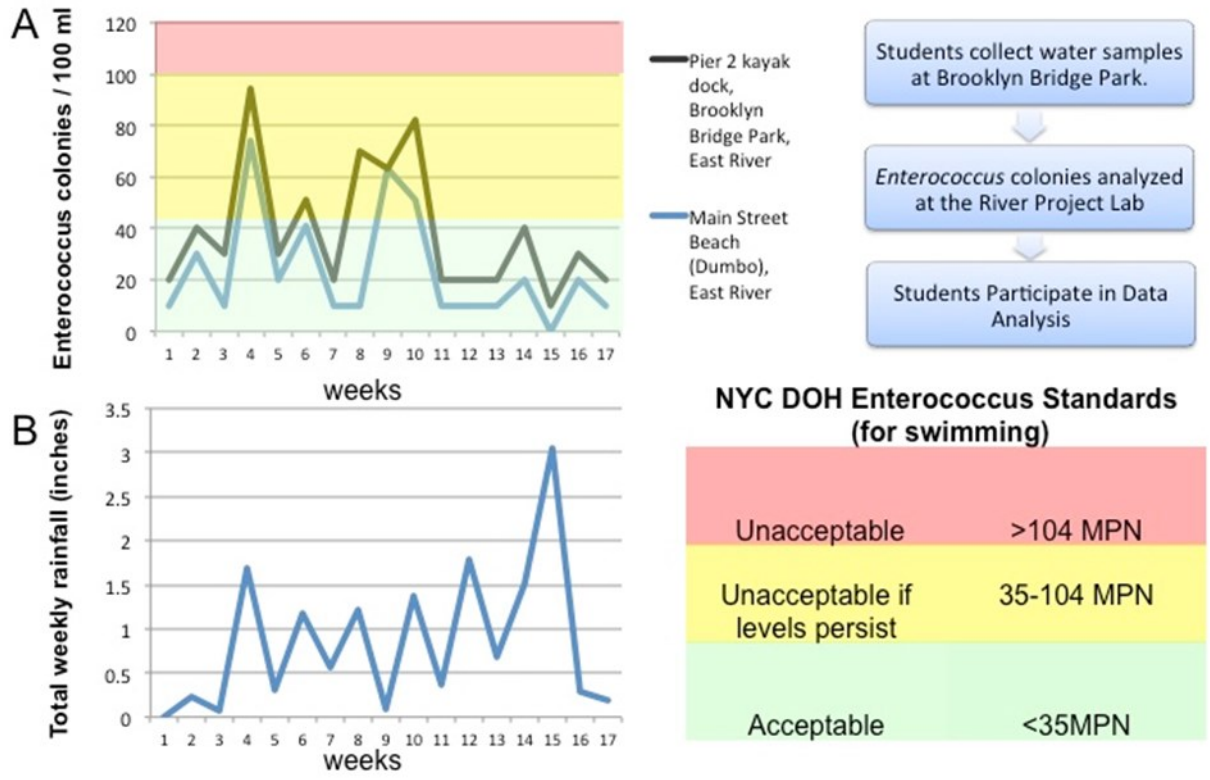

Figure 6: Summer independent study students partnered with local nonprofit The River Project's Citizens Water Quality Testing Program (CWQT) to monitor *Enterococcus* bacterial levels by collecting samples at Brooklyn Bridge Park from June-September 2017. A. *Enterococcus* colonies/ml in Brooklyn Bridge park correlate closely with each other, but only roughly correlate with weekly total rainfalls (B). Study overview and New York City *Enterococcus* standards depicted at right.

	Bacterial cell counts/ml			Fold change (vs. unfiltered control)		
Location	**Unfiltered**	**Cloth filter**	**LifeStraw Filter**	**Unfiltered**	**Cloth Filter**	**LifeStraw Filter**
Shawnagunk Lake	1000	258,000	95,000	1	258	95
Twin Lake	89,000	64,000	84,000	1	0.719	0.944
Brooklyn Bridge Park	7000	10,000	6,000	1	1.429	0.857
Prospect Park	27,000	242,000	2000	1	8.963	0.074

Table 2: Data for textile filtration experiments. Bacterial counts per milliliter were calculated for 1/1000 serial dilution plates; raw data is shown; as well as fold change vs. unfiltered control. Fold change data for Twin Lake, Brooklyn Bridge Park and Prospect Park and shown graphically in Figure 5E-G.

coliform test for water from Lewisville Lake, Texas (collected by the author KN), from Clove Lake in Staten Island, and the East River in the Brooklyn Bridge Park (Figure 6). They also made serial dilutions of the water samples, and plated them out on nutrient agar, MacConkey agar (this selects for gram negative enteric bacteria through lactose fermentation), and Eosin Methylene Blue or EMB agar (this selects for gram negative coliforms by killing gram positive bacteria). They used denim and cotton from T-shirts as their filters. There were no appreciable differences in the number of bacteria between the filtered and unfiltered waters. This could be because of improper sterile technique or because of cloth mesh size for the particular bacteria that lived in the water. (We did not test for cholera bacteria and we did not isolate for single bacterial species.) The second group used the LifeStraw filter and the homemade filter, and found that, even though the LifeStraw filtered the Prospect Park Pond the best, bacteria were still present. Pipetting water through the LifeStraw was a slow process during which additional contamination could have occurred. It is apparent that some of the filters may have actually introduced additional bacteria into the water.

Enterococcus, a gram-positive bacterium commonly found in feces; regularly contaminates New York's waterways either directly through runoff, or through untreated sewage discharged directly from via combined sewage overflow (CSO) system during rainstorms. During the summer months *Enterococcus* poses a human health risk when humans come into contact with contaminated waters during recreational water activities such as swimming, kayaking, etc. The River Project's Citizens Water Quality Testing (CWQT) program monitors *Enterococcus* levels at sites throughout NYC each summer[37]. This year two independent study students partnered with CWQT at a nearby site, Brooklyn Bridge Park. (Figure 6) Samples were collected each week from the Brooklyn Bridge Park Main Street Beach site in DUMBO and transported to the River Project's lab; where the samples were analyzed using a fluorometric assay to estimate *Enterococcus* contamination. The students' experience with CWQT illustrate that local NGOs are powerful partners to connect students with service learning projects that they care about and build connections with social change and environmental organizations outside of the classroom which can continue after graduation.

Discussion/Conclusions

The United States Environmental Protection Agency (US EPA) defines its goal for environmental justice such that all people will enjoy "the same degree of protection from environmental and health hazards" and "equal access to the decision making process to have a healthy environment in which to live, learn and work"[38].

Each of the inquiries described use water quality to incorporate environment and health issues with microbiology, developmental biology, and bioinformatics curricula, through a research experience relevant to students. When students studying Newtown Creek discovered their results were consistent with previously published data (Figure 2,3), this finding improved student confidence in their own results, as well as their respect and trust for state and local sampling efforts. The toxicology component of this learning paradigm could be applied to any common environmental pollutant – as long as the students and faculty agree that it is safe for the students to do the experiment. Marine invertebrates could be used instead of embryonic zebrafish at institutions without an IACUC. While one of the main benefits of the project is its "real life" application, student workers must be aware of real risks involved and work to minimize exposure to environmental toxins. A measurement of dangerously high levels of toxic substances should be reported to authorities and local NGOs. By using bioinformatics tools such GEO2R to predict the molecular targets of pollutants; abstract concepts of gene expression became more understandable. Through the Battle of the Water Filters project students learned about the principles of filtration and microbiology techniques, but also that clean drinking water is not to be taken for granted. Filtration techniques such as the ones students developed and tested are important given the prevalence of water-borne diseases such as cholera in developing countries, and that diarrhea is a leading cause of death, especially in youth, in these countries. Bacterial contamination of water, in this case surface water, became a focus for independent study students as they partnered with the CWQT project. In the future, we will continue to collaborate with NGOs to develop service-learning projects in which students work directly with their own local environmental groups. Climate change related storms and coastal flooding make New York's waterfront Environmental Justice Communities particularly vulnerable[2,8–10,39,40]. NGOs such as Newtown Creek Alliance, community groups and local colleges have contributed to sampling, mapping and rebuilding New York's waterways. These organizations also provide a local model for students, as they become citizens and scientists.

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MACUB 2017 Conference

Poster Presentation Award Winners

COMMUNITY COLLEGE

Biochemistry, Biophysics and Biotechnology

Decitabine Induction of Terminal Differentiation Markers on SV40 Transformed Human Keratinocytes
Olayinka Ajumobi-obe[1] and Mark Steinberg[2]
[1]Queensborough Community College, Bayside, NY and [2]City College, New York, NY

Ionic Liquid Mixtures with Single-Walled Carbon Nanotubes as Electrolytes for Dye-Sensitized Solar Cells
Rawlric A. Sumner[1], Tirandai Hemraj-Benny[1], Sharon Lall-Ramnarine[1] and James F. Wishart[2]
[1]Queensborough Community College, CUNY, Bayside, NY and
[2]Brookhaven National Laboratory, Upton, NY

Developmental Biology and Genetics

What is Lurking on Your Pocket Change?
Carolyn Curtis and Nidhi Gadura
Queensborough Community College, Bayside, NY

Signal Transduction and Activator of Transcription-3
Inhibits Osteoclast Differentiation
Stephanie Lochan and Dr. Andrew V. Nguyen
Queensborough Community College, Queens, NY

Environmental Biology and Ecology

Characterization of the First Auxin Conjugate Hydrolase-like Homologue
to be Isolated from Liverwort (*Marchantia polymorpha*)
and its Implications for the Evolution of Auxin Regulation in Plantae
Joy Bochis[1], John V. Smalley[1], Stephanie Kurdach[2] and James J. Campanella[2]
[1]Bergen Community College and [2]Montclair State University

Distribution of Leeches on the Eastern Painted Turtle (*Chrysemys picta*)
Arielle Hincapie, Ana De Sousa, Nichols Zelaya and Tony Pappantoniou
Housatonic Community College, Bridgeport CT

Microbiology and Immunology

The Protozoan Parasite *Toxoplasma gondii* Was Not Found in Eastern Oysters (*Crassostrea virginica*) from Jamaica Bay, New York
Manuela Aguiar, Gary Sarinsky and Craig S. Hinkley
Kingsborough Community College, Brooklyn, NY

Antimicrobial Characteristics May Lead to Antibiotic Resistance in Soil Bacteria
Kimberly Garcia, Salina Nawaz and Mangala Tawde
Queensborough Community College, Bayside, NY

Physiology, Neuroscience and Clinical

The Effects of Taurine on Manganese Accumulations in Gill of the Eastern Oyster, *Crassostrea virginica*
Rafael Santos[1], Emmanuel Agyei[2], Elvin Griffith, Jr.[3], Margaret A. Carroll[2] and Edward J. Catapane[2]
[1]Kingsborough Community College, Brooklyn, NY, [2]Medgar Evers College, Brooklyn, NY and [3]Notre Dame High School, West Haven, CT

Permethrin and High-mobility Group box1 Protein Pathway on Microglial Dysfunction
Miguel Vera, Mohammad Javdan
Queensborough Community College, Bayside, NY

MACUB 2017 Conference

Poster Presentation Award Winners

SENIOR COLLEGE

Biochemistry, Biophysics and Biotechnology

Native Free Radical Mediated Crosslinking of Functionalized PEGs as a Targeted Delivery Mechanism

Victor Manuel Suarez[1], David I. Shreiber[2] and Christopher Lowe[2]
[1]Kean University NJ and Rutgers, The State University of New Jersey

Regulation of the Class II Transactivator by 14-3-3β

Hagerah Malik and Drew Cressman
Sarah Lawrence College, Bronxville, NY

Developmental Biology and Genetics

Phosphorylation of Hexim1 is Critical for Prostate Cancer DU145 Xenograft Growth in Nude Mice

Sarah Sadik, Kristelle Pierre and Manya Mascareno
SUNY at Old Westbury, Old Westbury, NY

Genetic Delivery of RNA Molecules to Alter Expression of EGFR in Glioblastoma Multiforme

Nicole Sivetz, Sarah C. Falotico and Peter Nekrasov
Monmouth University, West Long Branch, NJ

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Environmental Biology and Ecology

Is Eating Behavior Affected When *Uca pugnax's* Competitior *Sesarma reticulatum* is Introduced?
Margaret Ramirez, Raysa Dominguez, Marily Ruiz
Julianna Jacobson and Allison Fitzgerald
New Jersey City University, Jersey City, NJ

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

Microbiology and Immunology

Strong Antimicrobial Activity Displayed by Newly Synthesized Hydroxamic Acids and Their Derivatives
Sonam Dosanjh, Jenique Klinkerth, Carrol Ellameh, Robert Aslanian and Meriem Bendaoud
New Jersey City University, Jersey City, NJ

Mesenchymal Progenitor Cells Influence Macrophage Phagocytosis Through Secreted Factors And Direct Contact But With Opposing Regulation
Anthony Morante, Anthony Ricigliano, Rachel Rex, Jillian Weiss and Jodi Evans
Molloy College, Rockville Centre, NY

Physiology, Neuroscience and Clinical

A Three-dimensional Culture Method to Assess the Role of Stress Hormone in Osteoarthritic Degradation
Christie Catterson, Liam Gallagher and Jodi Evans
Molloy College, Rockville Centre NY

The Effect of Ribosome Activation on Learning and Memory in Mice with Memory Deficits Due to rRNA Repression
Asuma Jalloh[1], Mathew Regier[2], Kim Allen[2] and Ivan Hernandez[2]
[1]Medgar Evers College Brooklyn, NY and [2]SUNY Downstate Medical Center, Brooklyn, NY

MACUB 2017 Conference

Poster Presentation Award Winners

GRADUATE SCHOOL

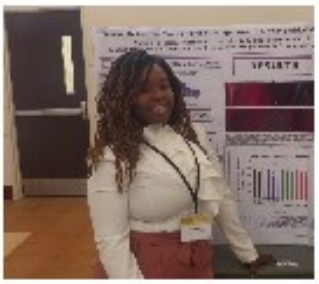
Flow Cytometric and Microscopic Analyses of Zinc-Stressed Cyanobacteria *Microcystis aeruginosa* and *Synechococcus* sp. IU 625

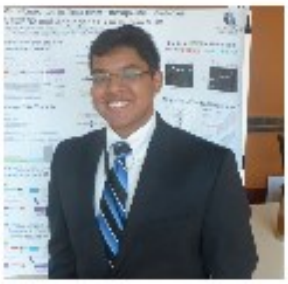
Jose L. Perez and Tinchun Chu
Seton Hall University, South Orange, NJ

Establishing a Method of MicroRNA (miRNA) Profiling Simultaneously with Comprehensive Chromosome Screening (CCS) in the Same Trophectoderm Biopsy

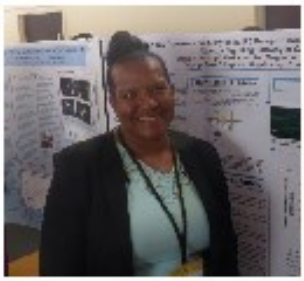
Jessica Rajchel, Xin Tao and Tinchun Chu
Seton Hall University, South Orange, NJ



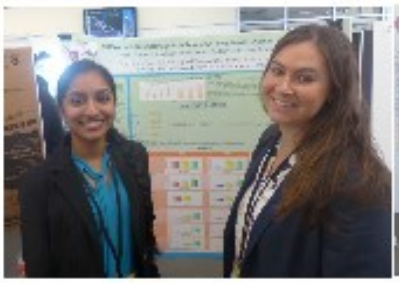




Conference Highlights







Identification of Metal Ion Transporters in *Phragmites australis.* Ramzy Abualteen, Constance Maurer and Yourha Kang, Iona College, New Rochelle, NY.

Phragmites australis, (common reed) is a wetland plant found throughout the U.S., specifically along the Atlantic Coast and the wetlands of northeastern United States. We have hypothesized that this plant contains genes that allow it to tolerate environments containing high amounts of heavy metals, including zinc, copper, and iron. In particular, we hypothesized that these genes would code for metal ion transport proteins that are involved in either moving metals out of the plant or sequestering them out of harm's way. The development of heavy metal tolerance in *P. australis* drives us to identify the genes that code for specific metal ion transporters. In order to do this, using a PCR-based method, we have used information from related species to amplify the DNA sequences of metal ion transporters in *P. australis*. Results of the PCR amplifications will be presented.

The Protozoan Parasite *Toxoplasma gondii* Was Not Found in Eastern Oysters (*Crassostrea virginica*) from Jamaica Bay, New York. Manuela Aguiar, Gary Sarinsky and Craig S. Hinkley, Kingsborough Community College, Brooklyn, NY.

Toxoplasma gondii is a protozoan parasite that infects most warm blooded animals. Cats are the primary host but there are many intermediate hosts including rodents, birds and marine invertebrates such as oysters. Humans can also be infected by *T. gondii* causing a disease called toxoplasmosis. Organisms typically become infected when they come in contact with feces from other infected organisms or if they eat undercooked contaminated meat. Since humans typically eat raw oysters and *T. gondii* has been found in eastern oysters (*Crassostrea virginica*) in several marine habitats, we wanted to test for its presence in eastern oysters from Jamaica Bay, NY. Our hypothesis was that *T. gondii* would be found in eastern oysters from Jamaica Bay. To test our hypothesis, we used the polymerase-chain-reaction (PCR) to amplify a 700-bp region of the oyster cytochrome-c-oxidase I (COI) gene from gill and mantle DNA. Agarose gel electrophoresis of the PCR-amplified product confirmed that it was the correct size. The PCR product was sequenced and BLAST searches with each of the sequences verified they were from the eastern oyster COI gene. To test for the presence of *T. gondii*, PCR was used to amplify a 791-bp region of the *T. gondii* GRA6 gene. A GRA6 PCR-product was not amplified from the gill or mantle tissues of the ten oysters tested, but a GRA6 product was amplified from a positive control. These results indicate there was no *Toxoplasma gondii* present in the oyster tissues. In conclusion, these results do not support our hypothesis that *T. gondii* would be found in eastern oysters from Jamaica Bay. In the future, I would like to test more oysters since only ten oysters from Jamaica Bay were tested. Supported by grants 2R25GM062003 of the Bridges Program of NIGMS and 0537171091 of the CSTEP Program of NYSED.

Decitabine Induction of Terminal Differentiation Markers on SV40 Transformed Human Keratinocytes. Olayinka Ajumobi-obe[1] and Mark Steinberg[2], [1]Queensborough Community College, Bayside, NY and [2]City College, New York, NY.

Abnormal growth and differentiation are the defining characteristics of cancerous cells. During the process of oncogenic transformation these cells lose the ability to regulate proliferation as terminal differentiation is blocked. The purpose of this study was to study the effects of the anticancer drug, 5-Aza-2'-deoxycytidine (5-aza) on the expression of genes involved in terminal differentiation in a line human keratinocytes transformed by the oncogenic virus, SV40 (SVHK). Gene expression was studied by quantitative Polymerase Chain Reaction (qPCR) in cells exposed to 5-Aza at concentrations of 0,2,5,10 and 20 μM for periods of 24, 48 and 72 hours. Our qPCR data showed significant positive modulation for Epithelial Cadherin, Junction plakoglobin, occludin and integrin beta -4, p63ß, cytokeratin 10 and transglutaminase genes that characterize keratinocyte differentiation. These findings suggest that 5-aza which has been used to treat leukemia may also have potential use as an inducer of differentiation in human skin cancers. Upregulation of integrin beta-4 implicates the wnt signaling pathway as a target of the drug as an effector of epidermal growth and differentiation. Olayinka is a participant in the NIH Bridges to the Baccalaureate Program at Queensborough Community College.

Testing Exogenous Rescue of Adventurous Motility in Slime Secretion Mutants of *Myxococcus xanthus.* Asia Alexander and Susan Gutekunst, Iona College, New Rochelle, NY.

Myxococcus xanthus is a non-pathogenic, Gram negative bacterium that is used as a model organism to study social interactions, biofilm formation, and motility. *M. xanthus* utilizes two distinct motility mechanisms: social motility, which involves groups of cells, and adventurous motility, a form of gliding motility that involves the movement of individual cells across a solid surface with no obvious extracellular appendages. While not completely understood, three hypotheses have been proposed for adventurous motility. The focal adhesion and

helical rotor models propose that secreted slime is used as an extracellular substrate, whereas the slime-extrusion model proposes that movement is generated via slime secretion at the lagging pole, propelling the cell in the opposite direction. Of these three models, only the slime extrusion model requires the cell itself to secrete slime in order to be motile, whereas the other two models only require slime to be in the environment. The GspD protein has been found to be necessary for cells to secrete slime, however, because gspD is an essential gene, it cannot be deleted from the genome. We engineered a mutant that expresses gspD under the control of a vanillic acid-dependent promoter, allowing for the conditional knock-down of the protein. Thus, GspD expression and robust slime secretion require the presence of vanillic acid in the media. To test the ability of slime-producing cells to rescue a motility defect, we developed an assay where mutant cells expressing GFP were mixed with wild type cells, and motility of the mutants was monitored via fluorescence microscopy. By testing the gspD mutant with this assay, we will be able to test the requirement for slime secretion on the motility of individual cells.

Immunohistofluorescence Study of the Actions of Manganese on the Phospholipase C Mechanism of Dopamine D2-Like Post-Synaptic Receptors in *Crassostrea virginica.* Peter Amoako, Mohamed Eid, Margaret A. Carroll and Edward J. Catapane, Medgar Evers College, Brooklyn, NY. Manganese causes Manganism a Parkinson's-like disease. Reports postulate the neurotoxic mechanism is related to dopamine neuron dysfunction, not degeneration. Gill lateral cell (GLC) cilia of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervations. Dopamine is cilio-inhibitory. Our previous work showed the dopamine receptors are D2 type (D2DR) and manganese disrupts the cilio-inhibition of GLC cilia, suggesting D2DR is a site of action in manganese neurotoxicity. The D2DR pathway involves inhibition of adenylyl cyclase and activation of phospholipase C (PLC). PLC hasn't been well studied in bivalves, nor have effects of manganese on PLC. e hypothesize PLC is visualizable in GLC by immunohistofluorescence, and if so we will determine if manganese effects its visualization. Gills were dissected, snap frozen, cryostat sectioned at 10 microns, fixed with EDAC (N-Ethyl-N'-(3-dimethylaminopropyl) carbodiimide hydrochloride) and incubated with 1° PLC antibodies, then 2° FITC antibodies. Sections were viewed on a Leica microscope with a DFC400 camera, 50 watt mercury lamps and FITC filters. All sections were photographed with the same camera setting. We found sections displayed green fluorescence in cytoplasm and along cell membranes indicating the presence of PLC. We then treated gills for 1 or 48 hours with 500μM of manganese or zinc. Zinc, which causes inhibition of various enzymes, was used for comparisons. Fluorescence intensity of GLC was quantified using ImageJ from NIH. Results show manganese treatments reduced fluorescence by 14 and 20% compared to untreated cells for the 1 and 48 hour treatments, respectively. Zinc treated gills showed no differences. The study shows PLC presence in GLC and manganese did cause a small, significant reduction in PLC fluorescence. This study provides new knowledge of manganese actions on D2DR pathway in bivalve gill. Our future experiments will test if manganese negatively effects physiological actions of PLC on GLC cilia activity. Supported 2R25GM06003 of NIGMS.

Evaluation the Effect of EGCG-S on Biofilm Formation with Dextrose and Sucrose in Seventeen Bacteria. Theresa Aponte and Lee H. Lee, Montclair State University, Montclair, NJ.

Over the years, a growing concern has been biofilm, which is the adherence of bacteria to a surface and to one another. Biofilm is an extracellular polymeric substance (EPS) that can protect the bacteria from adverse environments. Seventeen bacteria were used to determine their ability to form biofilm. The green tea polyphenol EGCG-S was then used to treat bacteria that could form biofilm. Congo Red Assay was used with different dextrose or sucrose concentrations to determine the effects of dextrose/sucrose on the formation of biofilm. The bacteria that were surveyed were: *Bacillus cereus*, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, *Enterococcus faecalis*, *Micrococcus luteus*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus mutants*, *Enterobacter aerogenes*, *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Serratia marcescens,* and *Mycobacterium smegmatis*. Each bacterium was incubated with different concentrations of dextrose or sucrose (0.1%, 0.5%, 1%, and 5%) respectively to analyze the effect of sugar on biofilm formation. The cultures with/without sugars were treated with EGCG-S (0, 100, 250 and 500 μg/mL) to determine if the formation of biofilm could be inhibited. The results indicated that Congo Red Assay with dextrose/ sucrose at 0%, 0.1%, 0.5%, did have growth but no biofilm was produced for several bacteria. Growth of nine bacteria were inhibited with 500 μg/mL of EGCG-S at all sucrose concentrations. Biofilm formation at 5% dextrose was inhabited in four bacteria with 500 μg/mL of EGCG-S. A Live/Dead BacLight assay was preformed to observe bacteria viability before and after treatment with 500 μg/ mL EGCG-S. There were no viable bacteria if the inhibition was observed. The data was further supported by the Colony Forming Unit (CFU) assay.This study suggests that EGCG-S could be used to inhibit biofilm formation in many bacteria.

Developmental Lead Exposure Reduces Encephalization and Cortical Quotients Resulting in Dysexecutive Functions in the Rat. Eddy Barrerra, Jourvonn Skeen, Jalen R. Bonnitto, Cyrus Jo, Jean-Martin Chrisphonte, Nimra Hameed, Samantha Rubi, Eric Khairi, Teddy F. Dacius Jr., Asma Iqbal, Youngjoo Kim and Lorenz S. Neuwirth, SUNY Old Westbury, Old Westbury, NY.

Lead (Pb) is a developmental neurotoxin that causes lifelong cognitive executive dysfunction. However, it is unclear how developmental exposure to Pb effects cortical volume and a variety of neurochemical signals which are responsible for not only regulating cognition, but also global brain excitability. Here we evaluated how Pb exposure alters cortical volume and neurochemical signaling in the adult rat brain following developmental exposure to Pb. We hypothesized that developmental Pb exposure would decrease cortical volume and increase brain excitability by reducing GABA levels and the ratio of GABA to other important neurotransmitters (i.e., glutamate, dopamine, norepinephrine, epinephrine, serotonin, and taurine) as a function of Pb exposure and sex. Results show that dependent upon the developmental time-period of Pb exposure and sex, that Pb differentially reduces cortical volume. The neurochemical analysis revealed differences in the patters of neurotransmitter profiles in specific brain regions (i.e., PrL = prelimbic cortex, IL = infralimbic cortex, OV = ventral orbital frontal cortex, OVL = ventrolateral orbital frontal cortex, dHP = dorsal hippocampus, & vHP = ventral hippocampus) dependent upon sex and developmental time-period of exposure. Our data suggest an emerging profile of which neurotransmitters in specific regions of the rat brain may contribute to cognitive dysexecutive functions and accompanying learning and memory problems associated with the attention set-shift task (ASST).

Dermo (*Perkinsus marinus*) is Not Found in The Tappan Zee, N.Y. Eastern Oyster (*Crassostrea virginica*). Kameca Baxter, Craig Hinkley and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.

As many locations along the Eastern Atlantic Coast became urbanized, water pollution, over farming and disease were responsible for significant declines in the Eastern Oyster (*Crassostrea virginica*) populations. In some locations, Jamaica Bay, NY, as an example, oysters disappeared in the 1920's. Dermo (*Perkinsus marinus*) is a pathogenic protozoan that was largely responsible for the demise of the oysters. The infected oyster's body decomposes, releasing infectious *P. marinus* parasites into the water looking for new hosts. Proliferation of the parasite, leading to infection is influenced by water temperatures above 20°C and salinities above 9 ppt. The Tappan Zee Bridge (TZ) is located in the Hudson River near Tarrytown, NY. Temperatures range from 18.3oC to 27.2oC and salinities range from 2.7ppt to 8.8ppt at the TZ location. Since water temperature and salinity values are not consistent with environments conducive to dermo, we hypothesize that the oysters tested from the TZ area will not be positive for dermo. Tissue was excised and DNA extracted from 10 oysters. The polymerase chain reaction (PCR) was used to amplify for the Mitochondrial Cytochrome Oxidase 1 (CO1) gene using Folmer's primer. The PCR product was subjected to gel electrophoresis and was sequenced. A NCBI Blast search confirmed that CO1 DNA was extracted from *Crassostrea virginica*. Extracted DNA, a sample known to be positive for dermo and a negative control (water) was amplified by using a PCR reaction with a dermo-specific primer. The products were subjected to gel electrophoresis to determine if the oysters were positive for dermo. No dermo DNA was amplified from the oysters tested. However, we were able to demonstrate the amplification of the positive dermo sample under the conditions used. The results of this experiment did support our hypothesis.

Characterization of the First Auxin Conjugate Hydrolase-like Homologue to be Isolated from Liverwort (*Marchantia polymorpha*) and its Implications for the Evolution of Auxin Regulation in Plantae. Joy Bochis[1], John V. Smalley[1], Stephanie Kurdach[2] and James J. Campanella[2], [1]Bergen Community College and [2]Montclair State University.

Both vascular and non-vascular plants regulate the balance of the phytohormone auxin, primarily indole acetic acid (IAA), through interactions among de novo synthesis, degradation, efflux, influx, and conjugate synthesis/ hydrolysis. IAA is stored in several conjugated forms, primarily thought not to be active. There are two major types of conjugated molecules: amide-linked IAA bound to one or more amino acids, and the ester-linked form mostly bound to sugar(s). These two types of conjugates are found at varying concentrations in the diverse tissues of Plantae (Domagalski *et a*l., 1987). Approximately 95% of the auxin in a plant is conjugated into these storage forms (Bandurski *et al*., 1995; Campanella *et al*., 1996). Previous research has demonstrated that auxin conjugate hydrolases are pervasive in the plant kingdom to help regulate auxin activity (Campanella *et al*. 2003). Our main goals in this study were to: a) examine the enzymatic activity of the liverwort enzyme, b) determine its substrate recognition for auxin conjugates, c) determine its phylogenetic/evolutionary standing relative to the other

"higher" plant hydrolases, and d) determine if its active site structure differs from vascular plant orthologues. We have discovered an unbroken line of orthologous IAA hydrolase genes from cyanobacteria up through Charophytic algae to liverwort. We believe the early orthologue (M20 peptidase) for ILR1 has been present in the Plantae evolutionary line since cyanobacteria. We have identified orthologues in algae (*K. flacciddum*) and cyanobacteria (*H. byssoidea*). Both cyanobacteria and the Charophytic algae appear to conserve the Leu176 residue needed for Mn^{+2}-binding. We conclude by proposing, based on the polymorphic structure and the limited amido-auxin conjugate hydrolysis of MpILR1, that the enzyme was conserved and eventually exapted into vascular Plantae evolution.

Spectral Sensitivity of Sensory Motor Integration of Gill Lateral Cell Cilia in the Bivalve Mollusc *Crassostrea virginica.* Reniece Buchanan[1], Johanne Jean-Pierre[2], Margaret A. Carroll[1] and Edward J. Catapane[1]. [1]Medgar Evers College and [2]Kingsborough Community College, Brooklyn, NY.

Gill lateral cells (GLC) of *Crassostrea virginica* are innervated by serotonin and dopamine nerves from their ganglia. Serotonin is cilio-excitatory and dopamine is cilio-inhibitory. The motor aspects of GLC innervation are well studied, but not the sensory side. We found sensory cues, including light, initiated a sensory-motor integration response between mantle rim tentacles or cerebral ocelli (with shells removed), and GLC cilia. They responded to light by slowing GLC cilia beating rates. We hypothesize light penetrates oyster shells and stimulates cerebral ocelli to initiate the motor response. We further hypothesize if light does penetrate shells, certain wavelengths will be more effective in stimulating sensory cells in ocelli and mantle rim tentacles. To test this we measured light transmittance through shells using a spectrophotometer and found red light (650+ nm) produced the greatest degree of transmittance through shells. Using animal preparations we found white light shown though shells stimulated ocelli to slow down GLC cilia beating. Repeating with blue light (405 nm), green (525 nm), amber (591 nm) and red (680 nm), we stimulated mantle rim tentacles and cerebral ocelli with the shell in place and found only red light caused a sensory-motor response that slowed GLC cilia beating. Cilia slowed from a basal rate of about 15 beats/sec to zero over a 20 minute period. This study further demonstrates the integration of photosensory signals in the control of GLC cilia in the bivalve *C. virginica*, and adds new knowledge demonstrating a spectral sensitivity of sensory cells in cerebral ocelli and mantle rim tentacle involved. This work was supported by grant 690340047 of PSC-CUNY, grant 2R25GM06003 of the Bridge Program of NIGMS and a Carnegie Foundation award.

Monitoring Resilience of an Ancient Oddity - The Atlantic Horseshoe Crab (*Limulus polyphemus*) on Plumb Beach, Brooklyn, NY. Naomi Campos and Christina Colon, Kingsborough Community College, Brooklyn, NY.

Plumb Beach serves as spawning habitat for the Atlantic horseshoe crab (*Limulus polyphemus*) and its intertidal flats support juveniles. Most adults spawn on the East side due to finer, oxygenated sediment, despite a 2012 sand replenishment project on the Western side. Egg density was monitored and counts compared to previous years on the undisturbed East side and the disturbed West side. A preliminary expedition revealed numerous adults on the East side compared to the West. It was thus hypothesized that egg counts would be higher in 2017 compared to previous years and egg counts would be higher on the Eastern side compared to the Western side. In six sampling zones a 15m quadrat was placed on each site parallel to the beach at the mid tide line. Using 20-cm. PVC pipes, ten core samples were randomly taken from each quadrat. In lab, sand samples were rinsed in a 1 mm sieve. Eggs were sorted and counted by hand. Egg counts for 2017 revealed 208 eggs/core. However, 2015 had the highest overall, with 279 eggs/core followed by 2011 which had 223 eggs/core. Most eggs were found on the undisturbed side with the highest counts found in the middle Eastern quadrat with a 2017 total of 7,685, followed by the Easternmost quadrat with 7,335 eggs. All Western Beach survey sites showed very few eggs, and totaled only 47 in all. Eggs seemed to be distributed throughout each Eastern site during the three surveys. The 2017 data support the first hypothesis in part since 2017 egg density was higher than four of the seven years of data collection. Counts appear to vary each year with no linear pattern. It was hoped that egg counts would be higher than previous years since no major disturbances occurred in 2017. The Western beach continues to be avoided by the horseshoe crabs.

The Effect of Methoprene on Larval Mortality. Lady Cardenas and Rebecca Spokony , Baruch College, New York, NY.

Juvenile Hormone (JH) is a hormone that plays a special role insect development; along with the hormone ecdysone, JH regulates the life cycle of insects. When both hormones are present it usually induces larval molting, sloughing into a larger larva until its big enough to undergo metamorphosis. However, when JH hormone production is stopped and only ecdysone hormone production remains, pupariation is induced and thus metamorphosis. JH therefore inhibits adulthood. A fruitfly's lifecycle has larval stages (called instar stages) followed by pupal formation to begin metamorphosis into an adult. A JH analog, methoprene, is used as an insecticide that disrupts metamorphosis preventing them from reaching adulthood. In this experiment 121 genotypes have been

treated with methoprene at the third instar larval stage and scored for dead wandering third instar larvae. It was found that there was variability in the percentage of dead larvae, the most being from DGRP line genotype 21 (put the % here). Genome-wide Association Study has been done on the percentage of dead larvae to find if there is correlation between mutations and methoprene sensitivity. The results show a total of about 1000 associated polymorphisms. To see if any of the polymorphisms fell within ecdysone or methoprene target genes, the results were then intersected with known Methoprene-tolerant and Ecdysone Receptor DNA binding sites from ChIP-seq analysis using the online program Galaxy. The results showed several regions overlapped with the Ecdysone Receptor DNA binding sites; one being close to the gene. There were also mutations within ecdysone pathway genes and ,(interacts and), (hemocyte differentiation, defining of the dorsal/ventral lineage) and . For further experiments, mutants of these genes should be tested individually for increased methoprene sensitivity.

Building a Better Phylogeny: Increasing *Drosophila melanogaster* Species Group Sampled for DNA Sequence from Cytochrome Oxidase II Gene Region. Brea Castro-Gambrell, Edwin Jacobellis, Josue Merida, Ines Muravin, Malika Sampson and Valerie Schawaroch, Baruch College, New York, NY.

Drosophila melanogaster is one of the most frequently used model organisms within genetics research. However, inconsistencies remain in the phylogenetic relationships between *D. melanogaster* and its close fruit fly relatives. This is indicated by the variations that occur across many publications. In order to start reaching a consensus with regards to these phylogenetic relationships, DNA sequences from the mitochondrial gene, cytochrome oxidase II (co II) was used. Perhaps extensive species sampling for this gene region could create a more substantiated phylogeny for these fruit fly species into their respective clades. DNA was isolated from single-fly representatives of species within the *D. melanogaster* species group and the out-group *D. obscura* species group. The sequence for the flies is unknown so general insect primers are used and the polymerase chain reaction annealing temperature is adjusted to optimize the reaction. Once a single, relatively bright PCR band is obtained of the correct length the PCR reaction was sent to Genscript®. Genscript® is a company that cleans up the PCR reaction and runs a PCR based Sanger DNA sequencing reaction. For each species, we compared the chromatograms from the right and left primers to generate a contig or consensus sequence. This newly generated species co II data is added to a previously generated dataset. Sequences were aligned then submitted to the computer program PAUP to generate a phylogeny using the maximum parsimony criteria. The results generated from this procedure were then compared to previous *D. melanogaster* species group phylogenies with regard to controversial clades and the stability of these clades. This research was supported by the Department of Natural Sciences, Baruch College and the Weissman School of Arts and Sciences Dean Romero.

A Three-dimensional Culture Method to Assess the Role of Stress Hormone in Osteoarthritic Degradation. Christie Catterson, Liam Gallagher and Jodi Evans, Molloy College, Rockville Centre NY.

Osteoarthritis (OA) is the most common form of arthritis. OA results from the degenerative changes in the protective articular cartilage of the moveable joints. There has been an increase in the development and use of 3D culture models in the study of disease. 3D models can accurately mimic the in vivo environment when compared to 2D cell culture. We sought to create a 3D culture model to define the role of stress hormones in osteoarthritic degeneration. A model was established through the chondrogenic differentiation of mouse mesenchymal stem cells in a synthetic hyaluron matrix. We grew them in the matrix for 28 days with chondrogenic medium. Cultures were assessed for chondrogenic differentiation at 14, 21, and 28 days through qPCR analysis of chondrogenic markers; day 21 was established as the peak. Hyaluronidase was introduced at day 21 to induce cartilage matrix damage to mimic first step osteoarthritis degradation. The hyaluronidase treated chondrogenic pellets were then paraffin embedded, sectioned, and morphology examined after Masson's Trichrome staining. Chondrocyte lacunae and a mesenchymal perichondrium were apparent, and degradation to the outer perichondrium was evident. After establishing the damage model, we examined the role of stress hormones through exposure to dexamethasone for 7 days following damage. qPCR analysis of chondrogenic markers RUNX1, RUNX2, SOX9 indicate that stress hormones can have significant influence on damage induced cartilage degradation. Using our newly established damage model, we will continue to assess the role of stress hormones in osteoarthritis.

The Effects of Ecological Parameters Such as Density and Bean choice on the Emergence and Survival of Bean Beetles. Diana Chaimov, Myar Dandash and Kathleen A. Nolan, St. Francis College, Brooklyn, NY.

The bean beetle or *Callosobruchus maculatus* (sometimes called southern cow pea weevil) has been used as an alternative to fruit flies to try and learn more about genetics and evolution. Usually they do not fly and are easy to maintain on mung beans. However, at high larval densities, they sometimes fly, which indicates a density-dependent mechanism for dispersal. Their life cycle takes place completely in the bean. They do not

need water, but need to be maintained at temperature of 25-30°C. We grew the bean beetles on five different bean types that they have been reported to grow on in the literature. These were mung beans, black-eyed peas, adzuki beans, small white beans, black beans, and pink beans. Mung beans with multiple eggs per bean and that also contained emerging beetles were added to each culture, along with an adult male and female. Generally, the beans other than the mung beans were not preferred by the bean beetle, although eggs were found on a few other types of beans. Additional density-dependent experiments will also be elucidated.

Immunohistofluorescence Study of the IP3 Receptor Mechanism of Dopamine D2-Like Post-Synaptic Receptor Signaling Pathway in *Crassostrea virginica.* Delilah Cummings[1], Maxine Jacobs[2], Margaret A. Carroll[1] and Edward J. Catapane[1], [1]Medgar Evers College and [2]Kingsborough Community College, Brooklyn, NY.

Crassostrea virginica lateral gill cell (LGC) cilia are innervated by dopamine and serotonin nerves. Dopamine is cilio-inhibitory, serotonin cilio-excitatory. Postsynaptic dopamine receptors are D2-like (D2DR), which inhibits adenylyl cyclase and activates phospholipase C (PLC). PLC synthesizes (IP3 activates IP3 receptors (IP3R) increasing intracellular Ca^{2+}. Manganese causes Manganism in people, a Parkinson's-like syndrome. Manganese disrupts dopamine cilio-inhibition of LGC in *C. virginica.* Our lab is showing manganese site of action are D2DR. We hypothesize IP3R are present in LGC and not affected by manganese. We tested this using immunohistofluorescence of gills treated with manganese or zinc. Zinc causes inhibition of some receptors. Briefly, tissues were dissected, snap frozen, cryostat sectioned at 10 microns, fixed with EDAC and incubated with 1° IP3R and 2° FITC antibodies. Sections were viewed on a fluorescence microscope with a Leica DFC400 camera and FITC filters. All sections were photographed with the same camera setting. Fluorescence intensity of LGC was quantified using ImageJ from NIH. Results show manganese reduced fluorescence intensity 22% compared to controls. Zinc caused no difference. Results show IP3R are present in LGC of *C. virginica* and contrary to our hypothesis manganese did effect fluorescence intensity. Although manganese reduced binding of IP3R antibody, other physiological work of our lab is showing manganese does not reduce the cilio-inhibitory ability of activating IP3R. Our alternative hypothesis that we will test in future experiments is manganese alters IP3R by impairing antibody binding, but not IP3R activity. This study provides new knowledge of the actions of manganese on D2DR signaling pathway and provides a foundation to further study the physiological role of IP3 in bivalve gill as well as the neurotoxic actions of manganese on the physiology of the D2-like receptors in gill. Supported by NIGMS grant 2R25GM06003 and the Carnegie Foundation.

Evaluation of Antibacterial and Anti-spore Properties of Theaflavins and Green Tea Extract. Emily Curran, *Nicholas DeCristofano, Ishani Rana, Christian Rios-Ruiz and Tinchun Chu. Seton Hall University, South Orange, NJ.

Many antibacterial drugs have become more ineffective, with many bacteria developing resistance to standard antibiotics. Tea, one of the most popular beverage around the world with reported antioxidant and antimicrobial activity, can be divided into fermented (black tea) and unfermented (green tea) category. Theaflavin is the major component of black tea extract. Disk diffusion assay and time course study were used to evaluate the antibacterial activity of both compounds against four bacteria - *Enterobacter aerogenes (E. aerogenes)*, *Escherichia coli (E. coli)*, *Bacillus megaterium (B. megaterium)*, and *Staphylococcus epidermidis (S. epidermidis)*. Sporulation and germination inhibition were also evaluated for the spore forming bacteria, *B. megaterium*. Disc diffusion assay results suggested both TF and GTE have antibacterial activities in all four selected bacteria. The amount of the spores were reduced when *B. megaterium* was treated with TF and GTE, showing that potential spore forming inhibition properties. Colony forming unit (CFU) assay also indicated that both TF and GTE can inhibit the spore germination in *B. megaterium*. GTE displayed greater inhibition on germination than that of TF.

What is Lurking on Your Pocket Change? Carolyn Curtis and Nidhi Gadura, Queensborough Community College, Bayside, NY.

The purpose of this project was to understand what different types of bacteria are on the coins in our pockets. Copper has long been known for its antimicrobial properties. Excess copper avidly binds to many biomolecules such as proteins, lipids, and nucleic acids, regardless of its valence state. Copper is one of the metal ions known to exert toxic effects on bacteria and other organisms. Since our coins have varying amounts of copper in it, we decided to test a hypothesis that we will find different types on bacteria on different types on coins. In this experiment, 100 random samples of coins ranging from pennies, nickels, dimes and quarters were collected. In addition to the coins, 100% Copper and Steel chips were used as the control group to understand and compare the different bacteria growing on copper, copper alloys, and non-copper material. Coins were swabbed and same swab was used to inoculate LB media overnight. Genomic DNA was then extracted. This was followed by amplifying specific DNA barcoding region using PCR with 16S rRNA primers that are well known in identified various bacterial species. PCR products were verified using gel electrophoresis and sequenced. Using bioinformatics, we could then analyze sequences to identify which bacteria is growing on what coins. We were in for a surprise to find various bacterial species on our coins. There was also a clear pattern that showed that increased copper content in coins led to lesser bacterial growth.

Monitoring Riboswitch Modulation Via Fluorescent Gene Expression. Sonia Dadlani, Toni Zangrilli, James Tilton and Jonathan Ouellet, Monmouth University. Monmouth NJ.

This summer, I continued a cloning project that was initiated by a former student, however there was missing genetic information in the sequencing. My main goal was to use the pHL 1278 plasmid to create a reporter system for the theophylline riboswitch. From this, a ratiometric fluorescent tool would be made to test the activity of the riboswitch. Upon completion, this project would provide a core tool used in other projects. A riboswitch is a structural domain rooted within a non-coding sequence of mRNA. It's in a position that interferes with the translation based on the presence of a specific ligand. Theophylline is a small molecule, similar to caffeine, that is used in inhalers for treatment of asthma. More importantly, to know if the RNA has bound to theophylline, an expression platform needs to be paired with the aptamer to observe the modulation of fluorescent gene expression.Through molecular cloning, PCR, DNA purification, etc., the DNA corresponding to a riboswitch that is known to bind to theophylline was inserted into the pHL 1278 plasmid between the mCherry and GFP fluorescent genes. The final cloned plasmid contained a promotor, mCherry gene, riboswitch and the GFP gene. Recently, the sequencing for this cloned plasmid was received and analyzed. A functional assay will be done to test the activity of the riboswitch. Upon induction, mCherry is constitutively expressed whereas GFP's expression is dependent on the presence of theophylline. This allows for a ratiometric fluorescent measurement to be made for mCherry vs. GFP. In the future, the GFP gene in plasmid pHL 1720 will be replaced with the Kanamycin resistance gene. The GFP gene allows for visual results whereas the Kanamycin resistance gene kills any unwanted bacteria, allowing it to be more accurate. Later, this system will be used to convert aptamers into riboswitches.

Distribution of Leeches on the Eastern Painted Turtle (*Chrysemys picta*). Arielle Hincapie, Ana De Sousa, Nichols Zelaya and Tony Pappantoniou, Housatonic Community College, Bridgeport CT.

Aspects of the leech population on the Eastern Painted Turtles (*Chrysemys picta*) from a local Connecticut farm pond were studied. The turtles were collected using 36" hoop traps baited with sardines. The captured turtles were measured, weighed, sexed, marked with a notch, and returned to their original capture site. The notches were filed in the scutes of the turtle shell and represent a unique code used to identify the turtles. Results of the study showed that the carapace and plastron were the most popular leech attachment sites for both the female and male population. The males averaged 15.1 leeches on their carapace and 4.6 on the plastron while the females averaged 5.3 leeches on their carapace and 4.3 on the plastron. This may be due to the fact that the shells supply the greatest surface area for attachment.

Constructing the SAE2 Disruption Cassette. Susan Dominguez-Mata[1] and Wilma Saffran[2], [1]Queensborough Community College, Bayside, NY and [2]Queens College, Flushing, NY.

Interstrand crosslinks (ICLs) prevent DNA replication and are lethal to cells. In order to prevent cell death, ICLs must be repaired. Homologous recombination (HR) is a major pathway in ICL repair, but can lead to DNA rearrangements and changes in gene copy number. is an endonuclease that plays a role in resolving DNA during recombination. Yeast strains with deleted genes were treated with psoralen plus UV light to induce ICLs, and the cell survival was measured. These strains showed sensitivities similar to those of repair proficient yeast, indicating that activity is not required for ICL repair. functions in DNA end processing at double strand breaks, and helps to generate intermediates in HR. Recombination between direct repeats in -deficient yeast cells showed that psoralen ICLs induce deletions in these strains at a higher frequency than in repair-proficient cells. This indicates that is required for the maintenance of genome stability in response to ICLs.

Strong Antimicrobial Activity Displayed by Newly Synthesized Hydroxamic Acids and Their Derivatives. Sonam Dosanjh, Jenique Klinkerth, Carrol Ellameh, Robert Aslanian and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

The increasing antibiotic resistance of pathogenic bacteria and decreasing availability of naturally produced antibiotics have made it crucial for researchers to design and synthesize new therapeutic agents with antimicrobial properties. Several chemical compounds including hydroxamic acids, and their derivatives were newly synthesized by the chemistry department and tested in our lab for antibacterial activity against eight different ATCC strains of pathogenic bacteria. The antimicrobial activity of each compound was evaluated using the disk-diffusion assay, liquid broth assay, and data derived from microtiter plate absorbance reading. While some compounds displayed a wide spectrum of antibacterial activity others did not have any effect on bacterial growth. These results enabled 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.

Does Myelin and Lymphocyte Protein (MAL) Function as *Clostridium perfringens* Epsilon Toxin (ETX) Receptor? Olawale Eleso[1], K. Rashid Rumah[2] and Vincent A Fischetti[2], [1]Medgar Evers College, and [2]SUNY Downstate Medical Center, Brooklyn, NY.

Epsilon toxin (ETX) is a β-pore forming toxin that is produced by *Clostridium perfringens* type B and type D. While *C. perfringens* is a member of the microbiota present in the human and ruminant gut, historically type B and D have been thought to be ruminant specific. In affected ruminants, ETX targets the central nervous system (CNS), causing symptoms with a striking similarity to human multiple sclerosis (MS). Interestingly, mounting pieces of evidence have recently supported the notion that *C. perfringens* may play a central role in the pathogenesis of MS, and that ETX may be the molecular trigger. Recent data suggest that Myelin and lymphocyte protein (MAL) may serve as a cellular receptor for the toxin. Our lab is interested in knowing if a physical interaction exists between MAL and ETX. To this end, we set to create a model capable of expressing a large amount of MAL. To accomplish this goal we use cell culture of the Tni insect cell lineage. These cells were cultivated to >95% viability and to a final concentration of 2 million cells/mL. They were then transfected using varying concentrations of MAL encoding baculovirus and incubated at 2 different temperatures for 48 and 72 hours. Tni cells were transfected with baculovirus, genetically modified for Green Fluorescence Protein (GFP), as positive control. Using fluorescence microscopy and Western blot, our preliminary results revealed that the Tni cells proficiently express both GFP and MAL proteins. Also, we determined that infecting the cells with a viral concentration of 1/20, and incubating the cells for 72 hours at 23oC results in the highest protein yield. In conclusion, our preliminary experiment creates a model capable of proficiently expressing MAL protein. The next phase of this experiment is to express and purify MAL for ETX binding studies via Microscale thermophoresis (MST).

Pathogenic Bacteria on the Rise in the Lower Hudson Raritan Estuary and Mussels to the Rescue. Carol Ellameh, Juliana Jacobson, Jenique Klinkerth, Allison Fitzgerald and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

Regular wastewater is a collection of rainwater runoff, domestic sewage, and industrial waste that collects to a sewage treatment plant, and discharges to a water body. Excess wastewater after rainfall leads to combined sewer overflows (CSOs) containing partially treated waste with high toxicity and increased pathogenic bacterial concentration. These CSOs have a high impact on water quality leading to impaired aquatic habitats, compromised drinking water, and endangered human health. Our project focused on testing the level of pathogenic bacteria at selected lower Hudson Raritan Estuary (HRE) as well as investigating the potential use of freshwater mussels to filtrate the pathogenic bacteria from contaminated water. Water quality testing was conducted for a period of 10 weeks in summer 2016 and 8 weeks in summer 2017 and the results show a strong correlation between high levels of pathogenic bacteria near CSOs after rainfall events. To address this problem, further studies were conducted in our laboratory using freshwater mussels, which have previously been reported to be able to filter contaminated water. Several beakers filled with water inoculated with high concentration of pathogenic bacteria in the presence or absence of a mussel, were monitored overnight for changes in bacterial concentration. After 18 hours, the levels of pathogenic bacteria decreased drastically in the presence of a mussel compared to the control. Future studies will focus on testing the level of bacteria in the guts of the mussels and determining the long-term effect of this filtration on mussels.

The Role of Drosophila SOCS36E in Linker Histone H1 -mediated Heterochromatin Formation and Tumor Suppression. Ki sum Fan[1], Andrea Mejia[1], Meghan Pfau[1], Nathan Doran[1], Amber Crockett[1], Arthur I. Skoultchi[2] and Na Xu[1]. [1]LaGuardia Community College, Long Island City, NY and [2]Albert Einstein School of Medicine, Bronx, NY.

The linker histone H1 is a key component of chromosomes and plays a major role in heterochromatin formation. However, how H1 executes these biological roles is largely unknown. Our recent studies showed that H1 interacts with three key factors involved in heterochromatin formation, Su(var)3-9, HP1 and STAT (Lu et al., 2009, Lu et al., 2013, Xu et al. 2014). We further discovered that the interaction of H1 and STAT plays an important regulatory role in JAK-STAT-induced blood tumor formation in flies (Xu et al., 2014). To further identify genes that cooperate with H1 in regulation of heterochromatin formation, we completed a mis-expression genetic screen. We ubiquitously mis-expressed 453 distinct genes in control and H1 knockdown flies, by using the EP collection of P-element insertions on the second chromosome. We then examined effects of their mis-expression on H1 knockdown-induced lethality. We identified a number of genes whose mis-expression either decreased or increased lethality induced by H1 knockdown. These genes spanned a wide spectrum of biological activities ranging from cell cycle regulators to chromatin remodelers. One of the suppressors identified in the screen is SOCS36E, a negative regulator of the JAK/STAT signaling. Our studies also showed that SOCS36E not only functions together with histone H1 in mediating fly lethality, but also is required for H1-mediated heterochromatin structure and function. Taken together, our results suggest a role for JAK/STAT signaling and SOCS36E in H1-dependent regulation of essential processes in Drosophila.

Activity-dependent Targeting of CaMKII to Inhibitory Synapses. Mohammad Fauzan, Zaki Minas and Reed Carroll, New Jersey City University, Jersey City, NJ.

In neurons, Ca2+/ calmodulin-dependent kinase II alpha (CaMKIIα) is a vital protein that regulates the strength of signaling at synapses. Activated CaMKIIα potentiates both excitatory and inhibitory synapses in neurons, however in response to different stimulus conditions. While the regulation of CaMKIIα at excitatory synapses has been well-studied, the physiological signals regulating the targeting of CaMKIIα to inhibitory synapses remains unknown. This investigation studied changes in colocalization and clustering of CaMKIIα protein at inhibitory synapses in rat cortical neurons, in response to low-frequency electrical stimulation to mimic real physiological conditions in the brain. The investigation was carried out by performing immunocytochemistry and calcium imaging in parallel experiments. Cells were stimulated with voltage pulses applied to stimulate action potential firing at 1Hz, 2Hz, and 5Hz. Effects on calcium levels were observed by live imaging pictures of Fluo-3 loaded neurons. In parallel, similarly stimulated cells were immunolabelled to detect CaMKIIα and VGAT (to mark inhibitory synapses). Results suggested that the 1 and 2Hz stimuli induced a slow increase in intracellular calcium levels. Furthermore, 2Hz showed a 40% increase in clustering of CaMKIIα at the inhibitory synapses while 1Hz showed slightly less clustering. Results suggest low-frequency activity in neurons can trigger the localization of CaMKα to, and possible regulation of, inhibitory synapses.

Taurine Reduces the Toxic Effects of Manganese on Mitochondrial Membrane Potential. Christina Florestan[1], Kelly Gazca[2], Margaret A. Carroll[1] and Edward J. Catapane[1], [1]Medgar Evers College and [2]Kingsborough Community College, Brooklyn, NY.

Manganese causes Manganism, which is similar to Parkinson's disease. The neurotoxic mechanism is not understood. Some propose manganese causes oxidative stress damaging dopaminergic systems. We showed manganese reduced oxygen consumption and depolarized mitochondrial membrane potential in *Crassostrea virginica* gill mitochondria, and these effects of manganese were reduced by EDTA and p-aminosalicylic acid. Our recent work with *C. virginica* shows taurine, which alleviate symptoms in a number of neurodegenerative diseases, reduced deleterious effects of manganese on cilio-inhibitory actions of dopamine on gill lateral cell (GLC) cilia. We hypothesize taurine can prevent neurotoxicity of manganese on GLC mitochondrial membrane potential. To test this we used the mitochondrial probe TMRM to study taurine in manganese treated GLC. *C. virginica* gills were placed in 2 ml of ASW (artificial sea water) with 2.5μM TMRM, and exposed to manganese (125 μM), taurine (125 μM), or manganese and taurine (125 μM each). Control gills had no manganese or taurine. Sections were viewed on a Leica microscope with DFC400 camera, 50 watt HBO mercury lamp and Texas Red filters. Photomicrographs were taken at 100 and 200X at 0, 10 and 20 min. All sections were photographed with the same camera settings. Mitochondria fluorescence was measured using ImageJ from NIH. We found control cells were brightly fluorescing indicating a strong mitochondrial membrane potential. Fluorescence of taurine treated was similar to controls. Manganese treated had a 40% reduction in fluorescence. Cells co-treated with manganese and taurine had reduced fluorescence compared to controls, but only half (20%) that of manganese treated. This study showed taurine protects against manganese on mitochondrial membrane potential. It support our physiology studies demonstrating taurine's neuro-protective ability against manganese on dopaminergic, cilio-inhibitory innervation of GLC cilia. These finding should be of interest to those exploring therapeutic treatments for Manganism. Supported by 2R25GM06003 of NIGMS.

Transcription Factor SOX9 Modulates Chemoresistance in Ovarian Cancer. Ryan Frank, Cassandra Greco, Casey Lievre, Laura Oliva and Rosemary Ritter, Molloy College, Rockville Centre, NY.

Ovarian cancer is among the most lethal of all malignancies in women. While chemotherapy is the preferred treatment modality, chemoresistance severely limits treatment success. Recent evidence suggests that deregulation of key pro- and anti-apoptotic pathways is a key factor in the onset and maintenance of chemoresistance. Furthermore, the discovery of novel interactions between these pathways suggests that chemoresistance may be multifactorial. SOX9 belongs to the SOX (Sry-related high-mobility group box) family and acts as a transcription factor that plays a central role in the development and differentiation of multiple cell lineages. Recent studies have demonstrated that SOX9 is required for the carcinogenesis in several cancer types. The aim of this study was to investigate the significance of SOX9 expression in chemoresistant and sensitive ovarian cancer cancer cell lines. SOX9 mRNA expression was detected by real-time quantitative RT-PCR assay in sensitive and resistant ovarian cell lines. After treatment with clinically relevant based platinum therapy, cells were assayed for various apoptosis markers. Therapy-induced damage of normal cells alter the tumor microenvironment, causing cellular senescence and bypassing the desired cellular apoptotic response to chemotherapy. We noted a decrease in cell proliferation which occurs as a result of the cells entering into a senescent-like phenotype. In summary, these data demonstrate the imperative functional role of SOX9 site as a molecular switch that regulates the DNA damage response after treatment with platinum based drugs.

Comparison of DNA Barcoding Reference Sets for the Identification of Fungi in 3 Distinct ITS Region Clone Libraries. Matthew Gardner, Joy Bochis, Theranda Jashari, Victoria Ellman, Jenifer Vasquez, Stephanie Zapata, Victorya Ramos, Tina Choe, Mahtab Tazehabadi and Luis Jimenez. Bergen Community College, Paramus, NJ.

Fungi are challenging to identify to species, as well as higher taxons, due to their microscopic and/or substrate-based forms, as well as because they frequently lack characteristics necessary for a detailed phenotypic analysis. Furthermore, there are large numbers of fungi that have never been isolated or identified. Molecular analysis and DNA barcoding is often the best, if not, only method of determining the species identity of most fungal life in environmental samples. Clone libraries from three separate samples (New Jersey soil, New York soil, and compost) were developed based on the internal transcribed space (ITS) region, which is the most widely used DNA sequence for fungal identification. These clone sequences were then run through four separate DNA reference sets including RDP UNITE Fungal ITS trainset 07-04-2014, RDP Warcup Fungal ITS trainset 2, NCBI Nucleotide BLAST (BLASTN), and the Mycobank.org pairwise alignment tool. Multiple reference sets were evaluated to compare the results across sources, as well as to develop best practices for clone identification. Among the four databases examined, the BLASTN set had the most species level matches above 97% homology. Cross-kingdom reference sets that include non-fungal sequences, such as BLASTN, are helpful in determining whether sequences are high homology (>97%) non-fungal matches rather than lower homology (<97%) fungal matches. Additionally, it was found that repeated evaluations of sequences over time are helpful because databases are frequently updated resulting in a likely increase in accuracy over time, which was seen with some of the compost clones evaluated in a prior study.

The Methodology of Keeping Crayfish and Assays of Behavioral Responses Influencing Molting and Neuropeptide Production. Christian Giraldo and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

The goal of this research is to observe behavioral responses to changes in the environment, which may lead to differences in neuropeptide production. It is hypothesized that changes in salinity would lead variation in behavioral responses related to feeding and aggression. Crayfish were housed in tanks and fed daily. Crayfish were kept alone, and then in groups, to test for aggressive behavior towards others. The results of the feeding test showed a significant difference in reaction time, with the fresh water crayfish reacting to the food drop and fighting more constantly. The salt water crays reacted less frequently and fighting was almost never observed. The tail touch demonstrated behaviors between dominant and submissive. After the assays, the crayfish were dissected, and ganglia and brains were removed to assess amount of neuropeptide. The results of these experiments and the method to housing crayfish will be used in future research.

FeederWatch: A Third Winter of Flurries and Feathers. Sara Gonzalez, Alaa Barbour, Abdul-Mumin Sanni-Adam, Sherane Raymond, Adewale Busayo, Lauren Chukrallah, Vasilios Orologas, Brittanie Fils, Gabriela Mosqueda, Naidel Montano, Dolly Basaldua, Vy Giang, Catalina Melendez, Frances Raleigh and Katherine Wydner, Saint Peter's University, Jersey City, NJ.

Project FeederWatch is a survey of winter birds that tracks their seasonal movements and reveals long-term trends in bird distribution and abundance across North America. For a third winter, a quadrangular space on the Saint Peter's University campus (Jersey City, NJ) was monitored by a team of observers on two consecutive days, Thursday and Friday, for 21 weeks between November 2016 and April 2017. Two suet blocks and a tube feeder containing birdseed were maintained on a pole next to Gannon Hall throughout this time. Following a protocol developed by Cornell University, data were collected on species of birds, highest number of each species, and environmental factors such as weather conditions and snow cover. Although our observations are informative in their contribution to the North American database, we have analyzed our local data and made comparisons between this season and previous seasons, 2014-2015 and 2015-2016. For all three seasons, the most abundant species was the House Sparrow (). Nine species were reported in 2016-2017 as compared to 6 species in 2015-2016 and 11 species in 2014-2015. Two species were reported for the first time this winter, raising the total species identified over three years to 13. One of the new species, a Wood Thrush represented a rare December record for the state of New Jersey. A unique leucistic female House Sparrow first identified during 2014 -2015 continued to visit the FeederWatch area throughout 2016-2017. Comparisons are made between our urban data and cumulative data reported for New Jersey.

Plant Pathogen Pressures on Seed Germination: Negative Feedback and Landscape Fragmentation. La Zhen Han, Elouise Schmidt, Hannah Richardson, Cathy Collins and Michelle Hersh, Sarah Lawrence College, Bronxville, NY.

Plants are subjected to a wide range of soil-borne pathogens that can affect plant diversity, species abundance, and growth. Of particular interest are the interactions between pathogenic fungi and seeds, including the host range and pathogenicity of different fungal strains. Our experiments sought to better understand the ways in which certain fungal strains affected the germination of seeds of different plant species, and the overall goal of this study is to assess whether patch size corresponds to particular pathogen pressures. We focused on the effects of Fusarium isolates on *Andropogon gerardii* and *Cassia chamaecrista*. These

strains were collected from the University of Kansas Habitat Fragmentation Facility by Dr. Cathy Collins and Dr. Michelle Hersh, where a variety of seeds were buried in landscape fragments of varying size and later exhumed. *A. gerardii* and *C. chamaecrista* seeds were grown on plates inoculated with the Fusarium isolates, and the rates of germination on inoculated and uninoculated control plates were then recorded and compared. The joint data indicated pathogenic behavior by Fusarium on *A. gerardii* seeds and not on *C. chamaecrista* seeds. This work is part of a larger ongoing study by Dr. Cathy Collins and Dr. Michelle Hersh that examines the ways plant diversity may be affected by pathogen pressure in fragmented landscapes through negative feedback systems.

In Search of Native Dwellers: The Rise and Fall of The Juvenile Atlantic Horseshoe Crabs *(Limulus polyphemus*). Kadijah Harry and Christina P. Colon, Kingsborough Community College, Brooklyn, NY.

Limulus polyphemus, the Atlantic Horseshoe Crab is essential for its ability to produce Limulus Amoebocyte Lysate, a substance that protects us from infections that could derive from contamination of surgical tools. It is also vital for migrating shore birds, that consume horseshoe crabs egg to survive migration. Juveniles crabs have declined on the Eastern side of Plumb Beach and are absent on the West, but appeared healthy in a nearby Tidal Creek refuge. It was hypothesized that the number and size of juveniles in a Tidal Creek in 2017 will be higher than counts in 2016 whereas average size and number on the undisturbed Eastern and restored Western Beach will remain similar to 2016. Timed visual surveys were done throughout the summer. Each crab was measured with calipers and returned. Results revealed that the total number of juveniles were lower than 2016. Tidal Creek numbers dropped while Beach East numbers increased compared to 2016. In both Beach East and the Tidal Creek juvenile average size increased from 2016. Only one crab was found on Beach West in comparison to none in 2016. These findings did not support the hypotheses because Tidal Creek numbers did not go up and Beach East and West did not Remain the same. However, the prediction that Tidal Creek average prosoma size would increase was supported. Predation and lowered egg count in past years could have contributed to observed declines. Water quality experts from the New York Aquarium confirmed that water quality was normal. Hope is not lost, as one cannot keep track of all juveniles, and while larger individuals move offshore, their shed carapaces wash ashore giving evidence of their presence. This work was supported by 1R25GM62003 of the Bridges Program of NIGMS and 0537-18-1091 of the CSTEP Program of the NYS Department of Education.

In the Search of Interactions of Phosphoprotein Enriched in Astrocytes 15 kD (PEA-15) Upon Phosphorylation at Ser^{104} and Ser^{116}. Sherouk Hassan, Sergio Crespo, Julissa Marrero and Yufeng Wei, New Jersey City University, Jersey City, NJ.

Cancers of all kinds are the predominant causes of early death today. Studies hitherto have shown that Phosphoprotein Enriched in Astrocytes (15 kDa), PEA-15, is involved in several cellular pathways along which it interacts with other proteins such as Fas-Associated Death Domain Protein, FADD. The interaction between PEA-15 and FADD happens only when PEA-15 is phosphorylated at two C-terminal tail residues, Ser104 and Ser116, leading to the inhibition of apoptosis in cancer cells. Yet, little is known about the structure of this protein-protein interaction which is a crucial step in the formation of the death inducing signaling complex (DISC). In our lab, PEA-15 and FADD are cloned into pET-28b(+) vector, and expressed in BL21(DE3) E. Coli competent cells. The proteins are purified using metal affinity (Ni^{2+} or Co^{2+}) chromatography followed by ion-exchange chromatography. Purified protein samples are then analyzed using SDS polyacrylamide gel electrophoresis. The protein structures and interactions are determined using NMR spectroscopy. Our initial results suggest that PEA-15 undergoes conformational changes depending on the phosphorylation states of the C-terminal serine residues, which allosterically controls the binding specificity of PEA-15.

Variance in Otolith Asymmetry in the Ontogeny of the Mummichog *Fundulus heteroclitus* in Great South Bay. Ronojoy Hem and Kestrel Perez, St. Joseph's College, Brooklyn, NY.

Variations in otolith asymmetry were studied across different stages of ontogeny of the *Fundulus heteroclitus* collected from the Great South Bay area in Long Island, New York. *Fundulus heteroclitus* are known for their ability to tolerate highly variable salinity, temperature and different levels of pollution. With an average lifespan of four years, this species can reach maturity in 36 weeks after hatching. Because of this, the *Fundulus heteroclitus* is a model organism to study in the field of ontogeny. For decades, the disruption of otolith symmetry has been negatively linked to fitness. In our experiment we investigate the relationship between fluctuating otolith asymmetry and fitness of *Fundulus heteroclitus*. Two test groups consisting of 29 individuals and 10 individuals that were collected approximately 20 days apart were studied for imbalances in otolith size in correlation to length and mass. Variation in otolith size has shown a positive correlation to length.

Expression of CX3CR1 in Tumor Associated Macrophages. Naomi Horowitz and Salvatore Coniglio, Kean University, Union, NJ.

Glioblastoma is a highly fatal cancer due to the likely recurrence of the cancer even after removal by surgery. The matrix of glioblastoma tumors contain macrophages, approximately 30% by weight, and have been associated with aiding the glioma cells in invasion of the surrounding tissue. The objective of this research was to utilize qPCR to determine if the gene, CX3CR1, was being expressed differently in tumor-associated macrophages compared to untreated macrophages. The threshold values attained for each qPCR were analyzed to determine the fold change in the treated media with or without drugs, compared to the untreated media. The first trial determined that the gene expression was lower in the macrophages treated with glioma conditioned media, with fold changes for the 4 hour treated and 24 hour treated being 0.2698 and 0.7897 respectably. The second and third trial found that gene expression in CX3CR1 was upregulated by a sizeable amount for all the treated samples, between 3.73 to 34.30 fold changes for all the media. Two drugs tested to determine their effect on gene expression resulted in the treated sample with no drugs, drug 1 which blocks the CSF1R receptor, drug 2 which blocks the CCR1 receptor, and a mixture of the drugs, containing fold changes of 25.63, 15.56, 17.27, and 9.51. Overall, it appears very likely that the CX3CR1 gene plays a role in glioblastoma tumors. Currently, testing is being done on 3-dimensional glioblastoma tumors to analyze the genetic expression of CX3CR1 using in-vivo conditions.

The Effect of Ribosome Activation on Learning and Memory in Mice with Memory Deficits Due to rRNA Repression. Asuma Jalloh[1], Mathew Regier[2], Kim Allen[2] and Ivan Hernandez[2], [1]Medgar Evers College and [2]SUNY Downstate Medical Center, Brooklyn, NY.

Previously we have determined that inhibition of RNA Polymerase I (Pol I), which explicitly synthesizes new ribosomal RNA (rRNA), disrupts the consolidation of long term memory. Since rRNA are essential components of the ribosomes our data suggests that “existing ribosomes” are not able to compensate for the loss of “new ribosome” synthesis required for memory consolidation. It is known that activation of mTOR pathway produces activation of protein synthesis in existing ribosomes, perhaps activation of those existing ribosomes would be able to compensate for the loss of new ribosome synthesis. To test this, we performed stereotaxic intrahippocampal cannulation surgery on adult mice. This cannulation facilitates the injection of a Pol I inhibitor directly into the hippocampus. We injected mice with Pol I inhibitor intrahippocampus, before habituation (see timeline), then we injected animals with mTOR activator (or vehicle) intraperitoneally, trained the animals and tested for memory 24h after. We are currently analyzing the data. If our hypothesis is correct, then mTOR activator will reduce the decrease in memory consolidation associated with Pol I inhibition.

Dermo (Perkinsus marinus) Was Not Found in the Eastern Oyster (*Crassostrea virginica*) at Woods Hole, MA. Kendall James, Craig Hinkley and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.

Dermo *(Perkinsus marinus*), a pathogenic protozoan, is a major factor responsible for the massive decline of the Eastern Oyster (*Crassostrea virginica*) along the Atlantic Coast. Its affect was first observed in Delaware Bay beginning in 1990. From there it spread to more northern locations. When infected, an oyster exhibits stunted growth and a decline in reproductive capacity. The protozoan spreads into the bloodstream and tissues of the oyster which eventually dies and is released into the water looking for a new host. Oysters reduce water turbidity through filter feeding and provide a habitat for other organisms. The health of oysters is vital to the sizes of annual harvests which affect sales, jobs and ways of life. Woods Hole, Massachusetts is an area near Cape Cod that has large populations of oysters. The purpose of this study is to determine if Woods Hole oysters are infected with Dermo. Our hypothesis is that the oysters will be infected with Dermo. Gill and mantle tissues were excised from twelve oysters collected at Woods Hole, MA. DNA isolated from the tissues and a positive control were amplified by PCR with dermo specific primers. The PCR products were verified by gel electrophoresis. Only the positive control was amplified and the twelve samples were not. The positive oyster control was sequenced and a NCBI Blast search verified that the DNA was *Perkinsus marinus*. To confirm that DNA had been extracted from all the oysters tested, the oyster CO1 mitochondrial gene was amplified by PCR utilizing Folmer primers and verified by gel electrophoresis. The CO1 gene was present in all twelve samples. Amplified DNA was sequenced and a NCBI Blast Search substantiated that the CO1 DNA was from *Crassostrea virginica*. Contrary to our hypothesis, the results showed that none of the oysters were infected with dermo.

Interleukin-17 and Gut Microbiota Axis in the Regulation of Metabolic Activities. Makheni Jean-Pierre[1] and Pawan Kumar[2], [1]Queensborough Community College, Bayside, NY and [2]Stony Brook University, Stony Brook, NY.

Non-alcoholic fatty liver diseases (NAFLD) is one of the major health problems in the developed countries. The exact cause of NAFLD is still unknown. Major risk factors contributing to NAFLD development include obesity, genetic predisposition, gut microbiota dysbiosis, pro-inflammatory mediators and insulin resistance. It has been demonstrated that interleukin 17A, (IL-17A), a pro-inflammatory cytokine, regulates gut microbiota and promotes the progression of NAFLD. However, how IL-17A modulates microbiota-dependent NAFLD development is unclear. We have recently reported that IL -17A plays an important role in regulating gut microbiota colonization as well as generation of microbiota-

dependent pro-inflammatory immune responses. We propose the central hypothesis that intestinal IL-17A signaling maintains homeostatic host-microbiota interactions, and the abrogation of IL-17RA signaling in the gut contributes to commensal dysbiosis, dysregulated inflammatory responses and predisposition to NAFLD. To study that, we have generated gut and liver-specific IL-17RA knockout mice. Our data shows wild type mice gained more weight than gut specific IL-17RA KO mice. In line with the weight gain data glucose level was higher in WT than gut specific IL-17RA KO mice. Our finding suggests that gut microbiota particularly Firmicutes composition is altered in gut specific IL-17RA knockout mice.Our data is useful to understand how intestinal IL-17A-dependent control of the gut microbiome regulates NAFLD, as this information will offer new therapeutic opportunities to treat liver diseases. This work was supported by NIH Grant GM050070 of the Bridge Program BioPrep.

A Role for Protein Kinase C in Gill Lateral Cell Activity of *Crassostrea virginica.* Alexcia Johnson[1], Krystle Ernest[2], Margaret A. Carroll[2] and Edward J. Catapane[2], [1]Kingsborough Community College and [2]Medgar Evers College, Brooklyn, NY.

Gill lateral cell (GLC) cilia of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervations. Dopamine causes cilio-inhibition, serotonin cilio-excitation. GLC dopamine postsynaptic receptors are D2-like (D2DR). The D2DR signaling pathway involves inhibition of adenylyl cyclase and activation of phospholipase C (PLC). PLC generates second messengers diacylglycerol (DAG) andintracellular calcium. DAG with calcium activates protein kinase C (PKC). While high cytoplasmic calcium slows GLC cilia beating, the role of PKC on GLC cilia has not been studied. We hypothesize PKC activation is involved in the cilio-inhibitory response caused by dopamine in *C. virginica*. The PKC activator SC9 [N-(6-Phenylhexyl)-5-chloro-1-naphthalenesulfonamide] and PKC inhibitor rottlerin were tested. Neither SC9 (10^{-6}–10^{-3}M) nor rottlerin (10^{-6}–10^{-4}M) applications to gill altered GLC cilia beating, nor did they alter cilio-excitatory actions of serotonin. However, rottlerin treated gills did not respond to dopamine, SC9 did not alter the cilio-inhibitory effects of dopamine. These finding indicate PKC is involved in dopamine induced slowing of GLC cilia in *C. virginica.* Inhibiting PKC prevents actions of dopamine, while activating PKC by itself did not significantly alter cilia beating rates. The study suggests PKC plays a role in cilio-inhibition caused by dopamine, but alone PKC activation is insufficient to generate the cilio-inhibitory response and other aspects of the D2DR signaling pathway also must be involved. These findings are helpful in furthering the understanding of the D2DR mechanism of GLC and provides a foundation for further research. This work was supported by 2R25GM06003 of the Bridge Program of NIGMS.

Hidden Truth: Survival Rate of Atlantic Horseshoe Crab (*Limulus polyphemus*) at Plumb Beach in Jamaica Bay. Kahli Grosvenor and Christina Colon, Kingsborough Community College, Brooklyn, NY.

The Atlantic horseshoe crab (*Limulus polyphemus*) is a marine arthropod found on the East Coast. Populations have declined at Plumb Beach in Brooklyn, NY, an essential spawning and nursery habitat. The purpose of this investigation is to quantify the progression from egg to juvenile and improve our understanding of hatchling survival. Researchers surveyed for eggs and juveniles during May through June. The 2017 data showed 17,655 eggs, 895 embryos and 46 hatchlings. Survival to embryo was 4.8%, to hatchling was only 0.2% the lowest since 2011. From 2011 to 2017, survival to embryos was on average 10%, and survival to hatchling was on average below 8%. Survival to juvenile on average 0.2%. No correlation was found between spawning adult females, eggs, embryos, hatchlings and juveniles. The only data that showed any correlation were growth rates at Tidal Creek and Beach East which progress upward, from 2016 to 2017. However, survival rates overall were higher than rates cited by Botton, Loveland and Tiwari (2003) Experts at the WCS Aquarium confirmed that all water parameters were normal in 2017. An important conclusion is that monitoring juvenile survival is a better indicator of survival than looking for eggs or spawning adults. In fact, juveniles show a clear linear relationship of between size and time, indicating healthy growth rates. Despite variations, the size trend in both areas is upward, whereas two small downward size trends in the Tidal Creek could indicate recruitment. Young individuals in Beach East represent recovery from a population crash in 2015. Further research on juvenile diet, sediment type, and food availability are underway to better understand these patterns.

Interrelationship Between C-SRC and SIT in the Regulation of Osteoblast Activity. Sydney Kauffman, Candace Morales-Wilde, David Cifelli, Samuel Sanchez, Joseph Tarr, Stephen Popoff, Nicole Rodstrom and Thomas Owen, Ramapo College, Mahwah, NJ.

Deletion of the c-src gene results in decreased osteoclast and increased osteoblast activity. Inhibition of c-src family kinases in calvarial osteoblasts or MC3T3 cells by the c-src inhibitor compound PP2 increases their differentiation. In Ros 17/2.8 osteosarcoma cells and in primary bone marrow cells though, PP2 results in a diminution of osteoblast phenotype markers, suggesting a differential role for the src family kinases in osteoblast function depending on the developmental origin. More recently, SIT (SHP2-interacting transmembrane adaptor) was described as a potential target for phosphorylation by src-family kinases in osteoblasts. When the SIT gene is deleted in mice, they show increased trabecular number, bone volume fraction, and connectivity density, as well as

decreased trabecular thickness and spacing. The intracellular portion of the SIT protein has three tyrosines in motifs which are known to mediate phosphorylation-dependent interaction with the SH2 domains of c-src family kinases. In T-cells, these tyrosines are phosphorylated following activation of the T-cell receptor and mediate binding to proteins including Grb2, SHP2, and Csk. Since the deletion of both c-src and SIT in mice results in increased osteoblast activity and they are known to interact in the immune system, it is reasonable to hypothesize that in osteoblasts, they interact to influence signaling pathways and ultimately regulate bone mass. We used the crispr-Cas9 system to independently target c-src and SIT in Ros 17/2.8 cells. Preliminary analysis of osteoblast phenotype marker expression in the antibiotic resistant pools following transfection of either c-src or SIT crispr-Cas9 shows that the levels of gene expression for OC, OP, DMP, and AP decrease as does AP enzyme activity. These data are consistent with our previous observations using PP2 in Ros 17/2.8 cells but also demonstrate that it is c-src itself and not a family member that is responsible for this activity.

Ribosome Rescue and Stalling Upon a Circular mRNA in *E. coli*. Dmitry Kharitonov and Devin Camenares, Kingsborough Community College, Brooklyn, NY.

Proper translation of genetic information into active proteins is vital to all organisms. Certain sequences and stress on the cell can cause ribosomes to stall during translation. Such stalling events are resolved by different rescue systems in some bacteria, which involve cutting the mRNA and subsequent destruction of the half-formed protein, enabling translation to continue on a separate molecule. It is not clear if this mRNA cleavage requires an exonuclease or endonuclease. To determine which is important, we are using a reporter system that creates a circular mRNA, which cannot be effected by an exonuclease. This reporter system utilizes a split intron, in which each half of the intron is located on the ends of the mRNA, and a blue chromoprotein (AmilCP-Blue) that can be placed upstream of the start codon. Once transformed into chemically competent E. coli, the blue color observed when the bacteria are cultured thus indicates the amount of circularization. Since rescue of stalled ribosomes will lead to degradation of the blue chromoprotein, we expect decreased expression when a stalling motif is introduced. In other words, we hypothesize that rescue will be insensitive to the circular nature of the mRNA, and that an exonuclease is not required. Surprisingly, we found roughly equal levels of chromoprotein expression between normal and stalling versions of the reporter. These hint that exonuclease activity may be important for the type of rescue that leads to protein degradation. These experiments can provide new insights into how ribosome rescue occurs, which can then be used as a target for the development of new antibiotics.

Identifying the Inflammatory Genes and Pathways Upregulated in LADMAC Cells Exposed to BCM7. Jaclyn Kirshbaum, Oumlissa Persaud, Kristen Deutsch, Eizle Bianca Salonga and Mary Kusenda, Molloy College, Rockville Centre, NY.

Casein is the main protein present in milk and other dairy products. Beta-casein is one of the 3 major proteins in milk and makes up ⅓ of the total protein in milk. Beta-casomorphin-9 (BCM9) was the original beta-casein protein found in milk, specifically cow's milk. However, a genetic mutation occurred and thhe 67th amino acid in the BCM9, proline, mutated to histidine (P67H) creating Beta-casamorphin-7 (BCM7). The protein BCM7 gets cleaved in the small intestine, making it readily absorbed in the body. In previous unpublished studies it was shown that LADMAC cells showed an increase in inflammation when exposed to BCM7, as compared to BCM9. LADMAC cells are murine leukocytes, specifically monocytes, in the immune system that produce cytokines. Cytokines are interferons that affect other cells in an inflammatory pathway. The specific aim of this experiment was to find out which of our 11 chosen genes (PTGS, PTGS1, PTGS2, TNF, IL12A, IL12B, IL1A, CXCL13, MAP3K11, MPO, NFKB) were turned on by BCM7 and the specific inflammatory pathway turned on. The quantitative Polymerase Chain Reaction (qPCR) method was used to identify upregulated inflammatory genes in the LADMAC cells exposed to BCM7, BCM9, Lipopolysaccharide (LPS, positive control) and Phosphate-buffered saline (PBS, negative control). Our results showed that none of the genes we studied were upregulated and although BCM7 has been proven to cause inflammation, these genes are not in the inflammatory pathway that causes the inflammation. This proves that the cyclooxygenase pathway does not lead to inflammation caused by BCM7.

Evaluating HIV Concern in Dominican Women in Washington Heights using Categorical Data Analysis. Steven Lawrence[1], Cassidy Mahor[2], Michelle Odlum[3] and Suzanne Bakken[3], [1]CUNY Medgar Evers College, Brooklyn, NY, [2]Amherst College, Amherst, MA and [3]Columbia University, New York, NY.

In this study we seek to address attitudes that Dominican women have regarding HIV/AIDS. Specifically, we wanted to address the attitudes of women aged 50 years and older because the aging population often underestimates their risk of contracting HIV. We sought to identify certain factors and attributes that influence how much Dominican women in upper Manhattan worry about getting HIV/AIDS so that future educational and preventative efforts can more directly target female populations that may be at high risk for HIV/AIDS. We used a subset of 851 participants of the WICER (Washington Heights/Inwood Informatics Infrastructure for Comparative Effectiveness Research) dataset to explore variables related to acculturation, sexual behaviors, relationship dynamics, and other factors. Programming languages such as “R” and “SAS” were used to perform

univariate analysis for frequency tables, demographics and variable distributions. Bivariate analysis and t tests for continuous variables with binary HIV concern outcome variable. From the 851 participants, 187 voluntarily answered a mail-in survey about sexual behavior. We used the same process to analyze this second category. Finally, we proceeded with model fitting using a logistic regression model with significant variables in bivariate analyses. Although our data has limitations in terms of bias and generalizability because it was a survey completed by convenience sampling, the preliminary results showed that i) women of age 50 and older worry less and the longer they live in the community the less they worry about HIV/AIDS ii) women who develop good communication with their partner worry less about the problem, and iii) interestingly, women who discuss freely about the use of condom with their partner worry the most. This exploration of survey data is one part of a larger look into aging and HIV, especially in different cultural subgroups, that must continue to develop.

Effects of the Psychoactive Drug Caffeine on the Behavior of Zebrafish (*Danio rerio*). Kevin Lipton and Brian Palestis, Wagner College, Staten Island, NY.

Caffeine, a psychoactive, plant-based alkaloid is found in a variety of food, which include coffee and tea leaves. Caffeine acts as a stimulant that has the potential to cause dependency if a large amount is ingested, and is anxiogenic (anxiety causing). Zebrafish (*Danio rerio*) is an ideal model organism for pharmacological studies and neurobehavioral studies, due to the homology of their nervous system with that of the human nervous system. This experiment was performed to gain a better understanding of the behavior of zebrafish when exposed to caffeine. This study tested the behavior of adult zebrafish with a concentration of 0.00625% caffeine. The behavior was quantified by counting the number of lines each zebrafish crossed on a grid in 30 seconds, using recorded videos. Out of all the fish that were tested, there was only one fish that was not mobile and did not cross a single line, and this fish was in the experimental group. The range of the number of lines crossed for the control fish was greater than the range for the experimental fish, but the mean number of lines crossed between the two groups did not significantly differ (control: 38.6; experimental: 36.0). This study, as well as other similar studies, can increase knowledge and understanding of how anxiogenic substances affect humans.

Signal Transduction and Activator of Transcription-3 Inhibits Osteoclast Differentiation. Stephanie Lochan and Andrew V. Nguyen, Queensborough Community College, Queens, NY.

Signal transduction and activator of transcription-3 (STAT3) is a transcription factor that is expressed in bone and joint cells which includes osteoclast and osteoblast cells. STAT3 is activated by different kinds of cytokines and growth factors. Osteoclast differentiation required two specific cytokines: colony stimulating factor-1 (CSF-1) to stimulate hematopoietic stem cells to become mononuclear phagocytic cell lineage and receptor activator of NF-kB ligand (RANKL) to become mature osteoclasts. The goal of this project was to analyze the role of STAT3 in osteoclast maturation of the pre-osteoclast RAW264.7 cell line and bone marrow derived osteoclasts. RANKL stimulation of RAW264.7 cells with knock down of STAT3 by siRNA and bone marrow derived osteoclasts from conditional knockout of Stat3 mouse showed an increase expression of differentiation-markers Cathepsin K, Nuclear factor of activated T-cells c1 (NFATc1) and c-Fos. These data suggest that normal function of STAT3 is to restrict osteoclast differentiation.

Variation in Reproductive Traits Among House Mice Adapted to Different Climates in the Americas. Tiffany Longo[1], Mallory Ballinger[2], Michael Nachman[2] and Megan Phifer-Rixey[1],[1]Monmouth University, Long Branch, NJ and [2]University of California, Berkeley, CA.

Although the house mouse, *Mus musculus domesticus*, is not native to the Americas, it has quickly adapted to many different climates and habitats. Mice are well known for their reproductive ability and reproductive traits are central to understanding adaptation, but little is known about differences in their reproductive traits among diverse climates of the Americas. To address this, we analyzed breeding data collected from wild-derived colonies of mice from Canada, New York, Brazil, Florida, and Arizona. We focused on the first and second generations of lab bred mice to control for environmental variation in wild-caught individuals and for the effects of inbreeding in later generations. We compared traits like age at first litter, average pups in each litter, sex ratio, etc. among the five colonies. Our results identified that litter sizes varied significantly between the colonies: litter size was larger for mice from the cooler regions (Canada and New York) compared to mice from the warmer regions (Brazil, Florida, and Arizona). Our findings support predictions from life history theory that animals in seasonal environments will concentrate their reproductive effort and suggest that differences in reproductive strategy may be part an important part of environmental adaptation in this system. Future work will focus on determining if there are also differences in pup weight among colonies, another important measure of reproductive allocation.

Regulation of the Class II Transactivator by 14-3-3β. Hagerah Malik and Drew Cressman, Sarah Lawrence College, Bronxville, NY.

The Class II Transactivator (CIITA) is an important transcription factor of Major Histocompatibility II (MHC II) genes. Defects in CIITA, as occur in Bare Lymphocyte Syndrome, lead to the loss of MHC II expression and subsequent inability to activate an immune response. Accordingly, CIITA has often been termed the master switch of the immune system. Its underactivation results in immunodeficiencies whereas its overactivation may lead to autoimmune disorders. Therefore, the activity of CIITA must be tightly regulated through multiple post translational modifications, including phosphorylation and ubiquitination, to ensure proper levels of activation. We identified a sequence within CIITA from amino acids 283 to 289 that matches a consensus 14-3-3 binding site motif: RxxxpTxP and decided to explore the effects of the 14-3-3β isoform on CIITA. We have shown through IPs that CIITA interacts with 14-3-3β and that this interaction leads to the proteasome mediated degradation of CIITA. Mutants of the binding site are more stable than wild type CIITA, indicating that they are less prone to degradation. Additionally, phosphorylation at the threonine residue in this site is necessary for the interaction and effects of 14-3-3β upon CIITA. We have shown that 14-3-3β leads to the degradation of CIITA by scaffolding it to a cellular factor and altering its stability. Much work remains to be done to determine what this cellular factor is and the changes in transactivation potential of CIITA as a result of 14-3-3β interaction.

Regulation of CaMKII at Inhibitory Synapses by Calcineurin. Mike Malkowski, Ayleen Pittar, Anna Yactayo and Reed Carroll, New Jersey City University, Jersey City, NJ.

Ca^{2+}/calmodulin-dependent protein kinase II (CaMKII) is known for its critical role in learning and memory. Activated CaMKII increases the strength of excitatory synapses, which is thought to be how memories are stored. CaMKII also regulates inhibitory synapses under different stimulus conditions. The question remains of how CaMKII can be differentially regulated at inhibitory versus excitatory synapses. Calcineurin is a calcium activated protein phosphatase, which dephosphorylates many CaMKII targets, and is also known to regulate the strength of both excitatory and inhibitory synapses. This investigation tested the hypothesis that dephosphorylation by calcineurin may regulate CaMKII trafficking to synapses. The activity of calcineurin was blocked using the inhibitor, cyclosporine A (CSA) and CaMKII localization at inhibitory or excitatory synapses were examined by immunocytochemistry. Results suggest that baseline activity in cortical neurons causes localization of CaMKII at inhibitory synapses, which was reduced by blocking CaMKII activation with KN-93. In the presence of CSA, there was an increase in colocalization of CaMKIIα at inhibitory synapses but no increase in colocalization at excitatory synapses. Additional experiments examined whether Protein Phosphatase 2A (PP2A), which can be activated buy caclineurin, affects CaMKII targeting to inhibitory synapses. In the presence of the PP2A inhibitor okadaic acid, there was no effect on the localization if CaMKII at inhibitory synapses. Overall, results support the possibility that calcineurin activity may reduce the localization of CaMKII at inhibitory synapses, possibly through regulating the autophosphorylation state of the CaMKII itself.

Detection and Characterization of Lysogenic Viruses in *Staphylococcus aureus* Isolated from a Suburban Human Population. Juan Marte, Sibora Peca, Joy Bochis, Jenifer Vasquez, Stephanie Zapata, Matt Gardner, Lisa Pincus and Luis Jimenez, Bergen Community College, Paramus, NJ.

Staphylococcus aureus isolates from suburban populations were analyzed by PCR analysis to determine the presence of lysogenic viruses. Lysogenic viruses are incorporated in *S. aureus* genomes as prophages. Prophages are associated to virulence factors such as Panton-Valentine leucocidin, exfoliative toxins, staphylokinase, and enterotoxins. DNA was extracted from 56 human isolates of *S. aureus.* PCR analysis was performed using SGA and SGF DNA primers. The DNA primers amplified 744bp and 155bp fragments of bacterial viruses belonging to serogroups A and F, respectively. The presence of the group F specific 155bp DNA fragment was found in 91% of isolates. However, bacterial viruses of group A were only present in 16% of *S. aureus* isolates. Prophages of group F were more abundant in *S. aureus* isolated from suburban populations. The percentage of *S. aureus* isolates infected by both viruses was 14%. Methicillin resistant (MRSA) isolates showed 87% infection rate with group F phages and 7% with group A. Infection by prophages can drive the evolution of *S. aureus* by providing additional genetic material to adapt to different environmental conditions and increase the pathogenicity of human isolates.

Engineering a Drug To Counteract Neurodegenerative Diseases. Christopher Mason and Najma Bibi, CUNY New York College Of Technology, Brooklyn, NY.

The basis of this research is the use of a computational approach to design drugs based on the tertiary structure of the protein VEGF-D. Vascular Endothelial Growth Factor-D has been discovered to have a profound role in neuronal growth in which it demonstrates its ability to repair memory and improve cognitive functions. This discovery of VEGF-D's new function has fascinated researchers as it shows promising results of being a possible cure against neurodegenerative diseases such as Alzheimer's however, its inability to bypass the blood brain barrier has

intrigued our collaborators to develop a set of peptides that may induce the same reaction as VEGF-D. The purpose of this research is to analyze the structural and functional details of VEGF-D complexed to its receptor VEGFR-3 at atomic level, design smaller drugs that have the potential to act as VEGF-D, and identify the best modeled peptide that interacts most favorably with the receptor to present to our collaborators for experimental testing. This work involves the designing of 14 small peptides for which molecular dynamic simulations were performed to investigate the behavior of the peptides along the trajectory. Information obtained from dynamics simulation denote peptide 56 as the most suitable candidate to induce the same reaction as VEGF-D.

Discovery of New Sphingosine Kinase 1 Inhibitors. Edison Mera and Michael Pulkoski-Gross, Queensborough Community College, Bayside, NY.

Sphingolipids are cell membrane constituents which can serve as signaling molecules that can determine cell fate. Ceramide (Cer) and Sphingosine (Sph) are two sphingolipids that have been established as pro-apoptotic lipids. Conversely, Sphingosine-1-phosphate (S1P), another sphingolipid, can provide pro-survival signaling through their specific G-protein coupled receptors. One of the enzymes responsible for maintaining the balance between Cer/Sph and S1P is Sphingosine Kinase 1 (SK1). SK1 phosphorylates Sph into S1P. In many different cancer types, including colon, lung, breast and renal cancers SK1 mRNA and protein levels have been shown to be increased relative to normal tissue. Furthermore, it has been shown that overexpression of SK1 in cells can enhance resistance to cell death. Due to the increase in SK1 in cancer and the pro-proliferative effects of S1P, SK1 has become an interesting target for drug development. In collaboration with Dr. Rizzo's group from the Department of Applied Mathematics and Statistics at Stony Brook University, we were able to take the structure of SK1 and dock over one million compounds to determine which compounds had the most favorable binding. For the first round of testing, 100 compounds were chosen which bound to the Sph binding pocket. From these compounds, 6 were found to inhibit ≥50%. We conducted a second round of docking with families of similar compounds from the top 6 in the first round. From the second round of docking, 106 compounds (about 18 from each of the 6 families) were chosen to be tested further. In this work we have started testing the the 106 compounds for their ability to inhibit SK1 activity.

Newest Kid on the Block: Characterization of the Novel Multidrug-resistant Pathogen, *Candida auris.*
Susanna Mirabelli[1], Lindsey Masone[1], Hiu Ham Lee[2], Luis R. Martinez[2] and Tejas Bouklas[1], [1]Long Island University-Post, Brookville, NY and [2]New York Institute of Technology College of Osteopathic Medicine, Old Westbury, NY.

Candida auris is a novel and emerging fungal pathogen capable of causing invasive, and often fatal, bloodstream and wound infections in immuno-compromised patients. Several outbreaks have been reported in hospitals across the world, including the United States, and predominantly in New York. exhibits extensive multidrug resistance that has never been seen in any species, and is often misdiagnosed for other species, thus limiting treatment options for patients. Our laboratory obtained 10 *C. auris* isolates in order to perform antifungal susceptibility testing and determine the Minimum Inhibitory Concentration (MIC) under Clinical and Laboratory Standards Institute guidelines. An alarming percentage (70%) of isolates exhibited a strong resistance to the commonly prescribed drug, fluconazole (MICs of 128 ug/mL or above). Many of these strains are projected to have an elevated resistance to other classes of drugs, such as polyenes and echinocandins. An model using the waxworm, was used to further study the highly-resistant *C. auris* strains, which demonstrated significantly different virulence in this host. Outbreaks of continue to increase on a worldwide scale, posing an immediate global health risk. and studies to characterize *C. auris* pathogenesis are imperative and fundamental to the proper diagnosis and treatment of this emerging threat.

Mesenchymal Progenitor Cells Influence Macrophage Phagocytosis Through Secreted Factors and Direct Contact But With Opposing Regulation. Anthony Morante, Anthony Ricigliano, Rachel Rex, Jillian Weiss and Jodi Evans, Molloy College, Rockville Centre, NY.

Mesenchymal progenitor cells have traditionally been studied for their regenerative properties, but more recently their immunoregulatory characteristics have been at the forefront. When interacting with immune cells they can be either suppressive or supportive and, therefore, represent an exciting new way to treat inflammatory diseases. In this study, we examined mesenchymal progenitor cell regulation of macrophage phagocytosis. Macrophage phagocytosis is an important part of the innate immune system response to infection and the mechanisms through which mesenchymal progenitors modulate this response are under active investigation. We hypothesized that mesenchymal progenitors regulate macrophage phagocytosis through both secreted factors and direct cell -cell contact and that direct contact regulation is dependent on mesenchymal progenitor cell expression of the vascular cell adhesion molecule 1 (Vcam1). To test

this hypothesis, a mouse spleen-derived macrophage cell line (SpMΦ) was exposed to conditioned medium from mouse aorta-derived mesenchymal progenitors (mAo) and their phagocytosis of yeast zymosan particles was subsequently measured. SpMΦ were also cultured directly with aorta-derived progenitors with and without Vcam1 knockdown via siRNA. SpMΦ phagocytosis of zymosan was suppressed after exposure to mAo cell conditioned medium. In contrast, SpMΦ phagocytosis of zymosan was increased after direct contact with mouse mAo; alternately, deficiency of Vcam1 in mAo cells reverses this increase. Our study illuminates tools to amplify or suppress the innate immunity in infectious disease. Future studies are needed to identify the specific mediators of these responses to condition cells to have a predictable and effective clinical use in the treatment of inflammatory diseases.

Antimicrobial Characteristics May Lead to Antibiotic Resistance in Soil Bacteria. Kimberly Garcia, Salina Nawaz and Mangala Tawde, Queensborough Community College, Bayside, NY.

Since bacteria co-exist in the environment with many other bacteria, they must possess self-defense mechanisms. Streptomyces are filamentous soil bacteria that produce important antimicrobial compounds as secondary metabolites. These chemical compounds are widely used as antibiotics and other antimicrobials. Streptomyces strains isolated from soil exhibited antimicrobial properties against other non-streptomyces gram positive bacteria. When grown together, Streptomyces caused significant growth inhibition of gram positive bacteria but had little effect on gram negative bacteria. Streptomyces strains also showed resistance to select antibiotics which could result from their inherent antimicrobial characteristics.

Synthesis of a Mini-Reporter to Test RNA Therapeutic Strategies to Block VEGFR2 and Angiogenesis in Human GBM. Koushik Muralidharan, Kerianne Fuoco, Arbaz M. Khan, Hemangi Patel and Martin J Hicks, Monmouth University, West Long Branch, NJ.

Glioblastoma multiforme (GBM), a grade IV tumor of the central nervous system, is the most common malignant primary brain tumor, and has a median survival of only 14 months. Poor survival is due to a lack of efficacy in current therapies, including radiation and chemotherapy, which is limited by the blood-brain barrier (BBB). GBM survival depends on the formation of new blood vessels, which is essential for the exchange of wastes and nutrients. Endothelial cells connect with each other and form the walls of new blood vessels, bridging the gap between the growing tumor mass and the established vasculature of the circulatory system. The membrane receptor that activates tumors to recruit endothelial cells to create new blood vessels is vascular endothelial growth factor receptor 2 (VEGFR2). In our lab, we are developing a novel therapy to alter the expression of the VEGFR2 receptor. Changes in VEGFR2 expression to block its activation would inhibit the development of new blood vessels. We are designing therapies to bypass the BBB and deliver the genetic sequences of anti-sense RNA molecules to alter the splicing pattern and expression of the VEGFR2 transcript, creating a soluble VEGFR2 decoy. We have designed and are cloning a mini-reporter-system that contains the regulatory elements of VEGFR2 splicing. This system measures the efficacy of RNA anti-sense therapeutics to alter the splicing of the VEGFR2 transcript. The visual marker, eukaryotic green fluorescent protein is used to mimic the natural splicing product, whereas the red fluorescent protein, mCherry detects changes in the efficacy of our RNA anti-sense therapy.

Eastern Oysters from Chincoteague Bay, VA, Contain a Polymorphism in the Cytochrome c Oxidase 1 Gene Found Predominately in Oysters Further South. Romain Nzebele, Gary Sarinsky and Craig S. Hinkley, Kingsborough Community College, Brooklyn, NY.

Eastern oysters (*Crassostrea virginica*) thrive on the east coast of the United States. This used to include Jamaica Bay, NY, but there are presently no large populations of eastern oysters in the bay. This absence is alarming considering their ecological roles, which includes filtering water and providing habitats for small organisms. The overall goal of our study is to reintroduce eastern oysters into Jamaica Bay but no one has a stock of the indigenous oysters from the bay. Therefore, we decided to determine whether all eastern oysters are the same population or if there might be subpopulations. To determine this, we compared genetic variation in the cytochrome c oxidase I (COXI) gene among eastern oysters from various locations along the U.S. coast. Previous studies showed there is an “A” polymorphism within the COXI gene in 70% of the oysters south of Cape Hatteras, NC, and only 3% of the oysters to the north. The oysters tested in this study were from Chincoteague Bay, VA. Our hypothesis was that eastern oysters from Chincoteague Bay would not contain an “A” polymorphism in the COXI gene. To test this hypothesis, we used the polymerase chain reaction to amplify a region of the COXI gene from DNA that was isolated from mantle or gill tissues. We then used agarose gel electrophoresis to verify that the amplified DNA was the correct size of approximately 700 base pairs. The amplified DNAs were sequenced by ELIM Biopharmaceuticals and BLAST searches were performed with each of the sequences confirming they were all from eastern oysters. A multiple sequence alignment showed that one of the ten oysters from Chincoteague Bay we tested had the “A” polymorphism. In conclusion, these results cause us to reject our hypothesis. Supported by grant 0537171091 of the CSTEP Program of NYSED.

TIM3 Expression on Natural Killer Cells in the Endocervix Is Not Associated with HPV Infection Status. Chenise O'Garro[1], Evelyn Gomez[1], Monika Lavi[1], Taryn Aulicino[2], Susan Holman[2], Deborah Gustafson[2], Howard Minkoff[2], Howard Strickler[3] and William Carr[1], [1] Medgar Evers College/ CUNY, Brooklyn, NY, [2]SUNY Downstate Medical Center, Brooklyn, NY and [3]Albert Einstein College of Medicine, Bronx, NY.

Women infected with Human immunodeficiency virus (HIV) and Human Papillomavirus (HPV) are at a greater risk for developing cervical cancer compared to women who are not infected with HPV and/or HIV. We hypothesized that immune exhaustion of Natural Killer (NK) cells, which are innate lymphoid cells that rapidly produce cytokines when activated and directly kill cancerous cells, would be greater among HPV infected woman compared to HPV uninfected women. To test this hypothesis, we measured expression of TIM3 on immune cells from blood and endocervix among 23 HIV-infected and 23 HIV uninfected adult women with and without HPV infection in an established cohort of women (WIHS) at SUNY Downstate Medical Center, Brooklyn, NY. Cervical lavage fluid (CVL) was collected for HPV strain determination by PCR analysis. Whole blood and endocervical cytobrush samples were also collected, surface stained with a panel of antibodies, and analyzed by flow cytometry with a 10-color Gallios flow cytometer. Specifically, we measured expression of markers of immune exhaustion (TIM3), acute activation (CD69), and chronic activation (HLA-DR) on NK cells, monocytes and CD8 positive T cells. Consistent with prior reports, immune cells in the endocervix were more exhausted than those in blood. We found thatTIM3 expression did not differ between HPV-infected and HPV-uninfected women; however,cervical NK cells tended to have less acute activation among women who acquired HPV strains associated with a high risk of developing cervical cancer. These pilot data imply acute activation may play a more important role than exhaustion in HPV pathogenesis.

Stimulation of Neurite Outgrowth of Rat Hippocampal Neurons by Extracellular Matrix Proteins. Ruth Opoku, Alani Antoine-Mitchell, Ijaz Ahmed, Mohsin U. Patwary and Alam Nur-E-Kamal, Medgar Evers College of the City University of New York, Brooklyn, NY.

Hypothesis: We have previously demonstrated that extracellular matrix (ECM) proteins facilitate neurite extension of rat cerebellar granule neurons (CGNs) in culture. We have also identified the functional domain(s) of these proteins involved in neurite outgrowth. Hippocampal neurons play an important role of storing memory of animals. We propose a hypothesis that "hippocampal neurons can be used to identify genes associated with storage of memory in animals". In this report we developed ECM-coated culture surface to growth primary rat hippocampal neurons and determined their neurite outgrowth. We have also compared the neurite outgrowth of CGN and hippocampal neurons. Method: Cerebellar granule neurons and hippocampal neurons were plated onto the cover slips coated with extracellular matrix proteins at a density of 60,000 neurons per ml. The neurons were allowed to extend neurites for 24hrs in NBM/ B27/KCl. The extent of neurite outgrowth was then determined using carboxyfluorescein diacetate (CFDA) labeling. CFDA (Sigma, St. Louis, MO) intensely stains the soma and all processes of cultured, living neurons. Images of the cultures were captured and analyzed with the NIH Image software. Samples of 100 neurons with well-defined processes were studied for each condition. Results: Laminin and fibronectin-coated surfaces induced neurite outgrowth of Cerebellar granule neurons and hippocampal. By immunostaining, immunoblot, and RT-PCR analysis we found alteration of expression of some important genes key genes involved in neurite outgrowth, Results of these studies with be presented in this report. Conclusion: We developed a condition to grow hippocampal neurons on ECM-coated surfaces. These hippocampal neurons will be used to apply different types of stimuli and expression of genes will be studied to find their role in saving memory in neurons. Identification of genes associated with saving memory might be useful in developing a therapy for neurological disorders including Alzheimer's, Parkinson's diseases.

Astrocytic Nrf2: Distinct Modes of Neuroprotection from Oxidative Stress. Natalia Ortiz, James Tatum, Christopher Simoes, Jonathan Dean, Steena Samuel, Shehreen Kheiri and Renée E. Haskew-Layton, Mercy College, Dobbs Ferry, NY.

Oxidative stress contributes to neuronal death in nearly all neurodegenerative diseases (e.g. Parkinson's disease, Alzheimer's disease, Huntington's disease), stroke and traumatic brain injury. Oxidative stress occurs via two mechanisms: 1) accumulation of reactive oxygen species (ROS - e.g. superoxide, hydrogen peroxide, and the hydroxyl radical) beyond a homeostatic set point, or 2) depletion of antioxidants (e.g. glutathione). Because neurons are highly susceptible to oxidative stress, they rely heavily on their metabolic coupling with astrocytes (a specialized glial cell type) for antioxidant support. Astrocytes provide antioxidant support in part by supplying neurons with precursors for the antioxidant molecule glutathione. The transcription of genes involved in the synthesis, degradation, and shuttling of glutathione precursors is regulated by the transcription factor Nrf2. While previous work from the Haskew-Layton group shows that astrocytic Nrf2 activation robustly protects neurons from glutathione depletion, our recent results show that astrocytic Nrf2 is less effective at protecting neurons from ROS accumulation. We therefore hypothesize that while glutathione-depletion induced cell death is prevented by Nrf2 activation, Nrf2-dependent genes do not ubiquitously protect against all forms of oxidative stress, as once

thought. To test this hypothesis, neurons were cultured from E6 chick embryos and astrocytes from E8 chick embryos. Neurons were exposed to hydrogen peroxide (to mimic ROS accumulation) or homocysteic acid (to induce glutathione depletion) in the presence or absence of astrocytes along with the Nrf2 activator sulforaphane. Our preliminary results suggest that sulforaphane is not effective at protecting neurons from hydrogen peroxide-induced oxidative stress. Although the Nrf2-dependent protection of neurons from glutathione has been established in rodent models, current experiments are underway to verify that this same mechanism exists in chick cells. Determining Nrf2's effectiveness in protecting neurons from distinct modes of oxidative stress will inform future therapeutic strategies aimed at leveraging Nrf2's antioxidant response.

Pesticides Exposure and Microglial's Dysfunction Causes Alzheimer's Disease. Gabriel Palencia and Mohammad Javdan, Queensborough Community College, Bayside, NY.

The etiology of most neurodegenerative disorders, such as as Alzheimer (AD) diseases attributes to genetic predispositions and exposure to harmful environmental factors. Limited studies have been documenting the low dose exposure to pesticides as one of the risk factors in developing of AD. However, the molecular mechanisms are not fully understood. The common features of AD is inflammation and protein aggregation. Microglia within the central nervous system playing a central role in response to chronic injury or inflammation. Microglia should constantly clear protein aggregations which are highly toxic to nerve cells. Over-activation of microglia have been well studied in developing AD. Therefore, we hypothesized that dysfunction of microglial cells could link the development of AD to the pesticide exposure. To test our hypothesis, we treated BV2 microglial cells with 1 and 5µg/ml of Permethrin for 24 hours. Permethrin as a pecticide which is used widely in and around households, including on pets, in mosquito control, and in agriculture. We assessed the effect of Permethrin on the cell viability, morphology and phagicytotic function of BV2 cells by performing the MTT assay, and the phagocytosis assay respectively. Our results showed Permrthrin significantly reduced cell viability of microglia and drastic changes in their morphology compared to the control group. These data help us to clarify the role of pesticides as environmental risk factors in the genesis of neurodegenerative diseases and understand the particular molecular mechanisms that are involved in neurodegeneration and pesticide exposure.and with western blot assay we got proof of HMGB1 pathway in effects of Pesticides on microglia, HMGB1 can interacts TLR ligand and activate cells by surface receptors such as TLR2 and TLR4,there was no exchanging in level of TLR4 in control and experimental samples.TLR2 will be our new target for future experiment.

Frequency and Characterization of Pathogenicity Genes in *Staphylococcus aureus* Isolated from a Suburban Human Population. Sibora Peca, Rozan Ramadan, Joy Bochis, Jenifer Vasquez, Stephanie Zapata, Matt Gardner, Mahtab Tazehabadi, Juan Marte and Luis Jimenez. Bergen Community College, Paramus, NJ.

DNA was extracted from 56 *Staphylococcus aureus* strains isolated from the nostrils of suburban populations. The DNA samples were analyzed by PCR analysis to determine the presence of pathogenic genes encoding for methicillin resistant (*mec*A), Panton Valentine Leukocidin (PVL), arginine catabolic element (ACME) *arc*A, and toxic shock syndrome (TSST-1). The *mec*A and PVL primers amplified 162bp and 83bp fragments, respectively. The ACME and TSST-1 detected 624bp and 325bp fragments on the chromosomal DNA of *S. aureus*. Positive reactions were confirmed by DNA sequencing of the different DNA fragments. The ACME gene showed the highest gene frequency with 64% of isolates showing the presence of the 624bp DNA fragment. The *mec*A gene was found in 29% of isolates. However, percentages for TSST-1 and PVL genes were 23% and 20%, respectively. Only 1 isolate was found to have all 4 pathogenic genes. However, 25% of the isolates did not show a positive reaction for any of the genes. Of the 16 *mec*A positive *S. aureus* strains, 94% carried the ACME gene, 31% the TSST-1 and PVL genes. Isolates with negative *mec*A reaction showed 53%, 20%, and 15% frequencies of ACME, TSST-1, and PLV genes, respectively. MRSA isolates showed higher frequencies of pathogenic genes than other *S. aureus* strains. Healthy individuals in suburbia carried *S. aureus* with *mec*A, PVL, ACME, and TSST-1 genes in the nasal cavities representing an unrecognized and understudy human reservoir of pathogenic genes.

Flow Cytometric and Microscopic Analyses of Zinc-Stressed Cyanobacteria *Microcystis aeruginosa* and *Synechococcus* sp. IU 625. Jose L. Perez and Tinchun Chu. Seton Hall University, South Orange, NJ.

Cyanobacterial harmful algal blooms have been implicated with the increasing occurrence of water system eutrophication, environmental contamination, and the indirect effects of climate change. Studies have shown that cyanobacteria outcompete eukaryotic algal species and produce harmful conditions to resident populations of aquatic organisms, as well as potentially leading to toxigenic effects within water systems, affecting human populations. In this study, we evaluated the effects of zinc chloride ($ZnCl_2$), on the morphology and phycobilin production in *Microcystis aeruginosa* and *Synechococcus* sp. IU 625 species. Zinc chloride ($ZnCl_2$) concentrations: 0 mg/L, 10 mg/L, and 25 mg/L were inoculated into *M. aeruginosa* and *S.* IU 625 cultures. The results showed that the *M. aeruginosa* culture showed growth inhibition at

10 mg/L and 25 mg/L $ZnCl_2$ compared to the control (0 mg/L), which was more sensitive than *S.* IU 625. This result contrasted with a past observation of a different, toxigenic (*mcy* gene containing) *M. aeruginosa* species - which showed more growth at 10 mg/L $ZnCl_2$ than the control. Flow cytometric and Microscopic analyses suggested morphological defect, growth inhibition, and phycobilin alteration for both cyanobacteria, possibly indicating zinc stress response mechanisms within these cyanobacteria species.

***Toxoplasma gondii* Was Not Found in Eastern Oysters (*Crassostrea virginica*) from Delaware Bay. Dominique Perez, Craig Hinkley and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.**

Toxoplasmosis is a disease caused by an infection with the parasite *Toxoplasma gondii*. Felids, such as domestic cats are the only known definitive hosts. They transmit the parasite in their feces which then transfers to warm blooded animals. Feces deposited on land can be transported to the oceans where *T. gondii* will become concentrated in bivalves such as oysters. Marine mammals and humans eating contaminated shellfish can then become infected with toxoplasmosis. Most people affected never develop signs and symptoms. For infants born to infected mothers, it may be responsible for brain damage. This study attempts to determine if *T. gondii* can be found in the Eastern Oyster (*Crassostrea virginica*) in Delaware Bay. Since *T gondii* has been observed in marine mammals and bivalves along the Pacific and East coasts, we hypothesize that it is present in Delaware Bay and will be found in the oysters. Twelve Eastern Oysters were collected from Delaware Bay. Gill and mantle tissues were excised from each and DNA was extracted. PCR reactions were used to amplify the mitochondrial cytochrome c oxidase 1 (CO1) gene using Folmers Primers. The correct size (702bp) of the PCR amplified DNA was verified using 2% agarose gel electrophoresis. The amplified products were sequenced and subjected to a NCBI Blast search which confirmed that the DNA was the CO1 gene from *Crassostrea virginica*. Extracted DNA plus a *T. gondii* positive control were amplified using the GRA6 Forward and GRA6 Reverse specific primers. We then ran gel electrophoresis to see if T. gondii DNA was present. *T. gondii* DNA was not found in any of oysters tested. However, the positive control was amplified. Sequencing the positive control confirmed that it was the *Toxoplasma gondii* GRA6 gene. Since *T. gondii* was not detected in the oysters tested our hypothesis was not supported.

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Identification of an Ideal Housekeeping Gene to Use in Quantitative RT-PCR for Inflammatory Studies Using the LADMAC Cell Line. Oumlissa Persaud, Jaclyn Kirshbaum and Mary Kusenda, Molloy College, Rockville Centre, NY.

It is necessary to have a reliable housekeeping gene in quantitative PCR experiments. Housekeeping genes, are genes which are always expressed in the cell and should not vary based on physiological conditions. We grew up LADMAC cells, a macrophage cell line, and use Lipopolysaccaride (LPS) to induce inflammation, as well as cells exposed to Phosphate-buffered saline (PBS) as a control. We chose 5 common housekeeping genes Beta-Actin (Actin) Glyceraldehyde 3-phosphate dehydrogenase (GAPDH), hydroxymethylbilane synthase (HMBS) beta-2-microglobulin (B2M), and beta- glucuronide (GUSB) and used qPCR using the SYBR green method to identify a gene which was reliable across replicates, did not vary between cells in which inflammation was induced and the control, and had high expression. We identified an ideal candidate to be GAPDH. Interestingly GAPDH was not shown to be an ideal candidate gene in other studies using macrophages, so our result may be cell line specific.

The Effects of Zinc Oxide Nanoparticles on Determinate Dwarf Cherry Tomato Plants. Ha Phan and Tetiana Delaney, St. Joseph's College, Brooklyn, NY.

Nanotechnology has cross over into many fields that affects all aspects of human lives. They are found in cosmetics, food, electronics, medical applications, and now even agricultural crop production. Therefore, it is imperative to understand the relationship between nanoparticles and plants, from the seed to the fruits the plants bear. Fertilizer has been considerably used in mass production. However, now that nanotechnology has been incorporated into so many products, it is only time before it makes its appearance in fertilizer. Zinc Oxide nanoparticles are currently being used in a diversity of products so there has been an increase in release of Zinc into the environment. This could be beneficial to plants as they need certain essential nutrients for normal functioning and growth. The effects of Zinc Oxide nanoparticles will be observed on the overall growth of a determinate dwarf cherry tomato plant. Since all plants need a certain amount of nutrients, it is expected that the growth of the plant will be stimulated at low concentrations and be inhibited at higher concentrations. There are four groups, the control being 0 ppm with no nanoparticles. The other groups are of varying concentrations of 10, 30, and 50 ppm. The seeds were placed into seed starting pots and watered daily and with the corresponding concentrations once a week for 3 weeks. It was then transplanted into a 6” planting pot where it is watered daily with the corresponding concentration of fertilizer. This study is conducted to give an insight on how effective nanofertilizers could be and if nanoparticles will have an adverse effect on the fruits.

Establishing a Method of MicroRNA (miRNA) Profiling Simultaneously with Comprehensive Chromosome Screening (CCS) in the Same Trophectoderm Biopsy. Jessica Rajchel, Xin Tao and Tinchun Chu, Seton Hall University, South Orange, NJ.

The application of CCS has increased implantation rates in Assisted Reproductive Technologies. However, not every transferred euploid embryo results in a successful pregnancy. More reproductive markers are needed to further improve success rates. MicroRNAs are single-stranded RNA molecules, which are emerging as important regulators of cellular differentiation and may be involved in establishing and serving as a biomarker of embryonic reproductive potential. This study aims to develop and validate a new methodology in which both miRNA and CCS can be evaluated from the same trophectoderm biopsy. Anueploid and euploid 7-cell human fibroblast samples were lysed using PowerSYBR green lysis solution and SUPERase (Thermo Fisher Scientific). In parallel, bulk total RNA was purified from the same cultures using the RNeasy Mini Kit (QIAGEN) to serve as a gold standard. Complimentary DNA (cDNA) was constructed using the Advanced miRNA cDNA Synthesis kit. The synthesized cDNA was pre-amplified with miRNA primers (hsa-let-7b-5p, hsa-let-574-3p, and hsa-miR-222-3p) and 96 previously validated CCS primers. The expression of miRNA by quantitative PCR (qPCR) was compared for consistency between a portion of the 7-cell pre-amplification product and bulk total RNA. qPCR CCS was performed on the preamplification products from the cDNA synthesis. CCS results from qPCR showed 100% consistency with expected karyotypes for both euploid and aneuploid cell lines. qPCR results of three miRNA assays from 7-cell samples showed consistent expression levels with bulk total RNA by using hsa-miR-16-5p as the endogenous control. This study established the validity of profiling of microRNAs in addition to CCS from 7-cell samples, which may be applied to trophectoderm biopsy and provide a foundation for the development of miRNA biomarkers of reproductive competence.

Is Eating Behavior Affected When *Uca pugnax's* Competitior *Sesarma reticulatum* is Introduced? Margaret Ramirez, Raysa Dominguez, Marily Ruiz, Julianna Jacobson and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

The fiddler crabs studied in this experiment, *Uca pugnax,* are found in marshes. Their distinguishing feature is one very large claw. We hypothesized that fiddler crabs in areas with less pollution would have a bigger claw than fiddler crabs in areas that are heavily polluted. The two different field sites were the Mullica River, a clean salt marsh with little to no pollution, and the Hackensack River, which is in an area with a very high level of pollution. The Hackensack River was also heavily invested with *Phragmites*. At least 30 crabs from each site were measured for claw size and the average claw size was found. It was found that regardless of where the crabs were found, in a clean area or heavily polluted area, there was not a significant difference in the claw size.

Development of a Model System for Zika Vrus Vector-borne Transmission. Margarita Rangel, Maria Noval, Elfie De Jesus, Juan Rivera-Correa, Ana Rodriguez, Ken Cadwell and Kenneth Stapleford, NYU School of Medicine, New York, NY.

Zika virus (ZIKV) is a member of the Flaviviridae family and is transmitted by the Aedes species of mosquito. Recent outbreaks of ZIKV in the Americas pose major threats to the region, especially due to its association with neurological disorders, including Guillan Barré syndrome and microcephaly. Despite the great public health and economic burden posed by this pathogen, basic aspects of ZIKV biology, including the underlying mechanisms of ZIKV vector-borne transmission, remain unknown, hampering the development of tools to fight infection. Importantly, mosquitoes are not passive carriers that transfer virus from one individual to another. It has been extensively shown that salivary gland components enhance arboviral pathogenesis by triggering host inflammatory response, viral factors in mosquito saliva, such as soluble NS1 protein influence the course of the infection and disease, and the viral minority variants that emerge in saliva during natural infections may differ from those generated in vitro. Thus, these observations highlight the need to establish an in vivo model system to study ZIKV mosquito transmission and disease under physiological conditions. To do this, we infected Ae. aegypti mosquitoes with the Ugandan strain of ZIKV and allowed them to feed on mice lacking the type I interferon receptor (Ifnar -/-). We found that ZIKV was efficiently transmitted to these mice and that infected mice developed disease, showed significant viral burdens in all organs, and mounted a unique immune response compared to needle inoculation. Taken together, in these preliminary studies we have established a vector-borne transmission model for ZIKV infection and highlighted potential differences between ZIKV vector-borne transmission and needle infections. This model will be an essential tool to not only elucidate the natural dynamics of ZIKV infection, immune responses, viral evolution, and transmission but also for the development of novel therapies against this devastating pathogen.

Mislabeled Herbal Supplements. Amandeep Rataul and Nidhi Gadura, Queensborough Community College, Bayside, NY.

Recent studies on herbal supplements suggest that four agencies were accused of selling supplements that do not contain the herbs listed on the container. Authorities had tested herbal supplements from different retailers and found out that only one out of five actually consisted of the supplement listed on the container. The authorities, on testing the herbal supplements, found out that rice flour, asparagus and other house plants were used as fillers. These fillers can be very dangerous for people who have allergies from a specific type of food. DNA barcoding is a very efficient method for identifying plant species from their genomic DNA. We hypothesized that upon DNA barcoding we will find some samples that are used as fillers. We did genomic DNA extraction from the supplements. We then proceeded to do PCR using rbcL primers which are designed to identify the plant species. We did gel electrophoresis to verify the PCR results. Bioinformatics is used to analyze the sequences. Results will be discussed.

Optimizing DNA Extraction for Historic Samples of Atlantic Sturgeon. Brian Reiss, Keith Dunton and Megan Phifer-Rixey, Monmouth University, Monmouth, NJ.

The Atlantic Sturgeon, *Acipenser oxyrhinchus oxyrhinchus,* is an anadromous fish listed under the US Endangered Species Act. Along the East Coast, it spawns predominately in the Hudson, Delaware, and James rivers. It is estimated that there been a 99.5% loss of population in the Hudson River area since 1890. This population crash has been primarily attributed to anthropogenic activities that endanger both the fresh-water juveniles and the salt-water adults. Smaller populations are vulnerable to the effects of inbreeding and genetic drift that can lead to decreased genetic diversity impacting future generations. The goal of this project was to determine if standard methods for the extraction of DNA from tissues could be easily amended with a liquid nitrogen grinding step to extract DNA from bony spine samples. We found that while high quality, high concentration DNA could easily be extracted from fin clips stored in ethanol, only low quality, low concentration DNA could be extracted from spines. While this DNA may be adequate for some genetic screens, future work will focus on testing more sophisticated methods for extracting DNA from archaic bone samples. The ongoing goal of this project is to assess genetic change in Atlantic Sturgeon populations and aid the conservation efforts.

A Study of Soils from Ellis Island's Abandoned Hospital Complex. Jena Richards, Cindy Arrigo, Nurdan S Duzgoren-Aydin and Deborah Freile, New Jersy City University, Jersey City, NJ.

The emergence of superbugs, or bacteria resistant to antibiotics, has grown while the discovery of new antibiotic strains has waned. With 80% of present day antibiotics originating from soil organisms, researchers have turned their attention back to topsoil, especially impacted by anthropogenic activities. We reasoned that soils from Ellis Island's abandoned hospital complex would present a unique opportunity to screen for organisms that synthesize antibiotics. We collected soil samples (top 20 cm) from Ellis Island's abandoned hospital complex due to the area's interesting soil provenance (a mixture of fill mainly from excavations in NYC), and its medical history as one of the largest public health hospitals in US history. The samples were collected from different areas of the hospital complex, evaluated for particle size fraction, analyzed for their heavy metal compositions (Cu, Pb, Hg, and As) using both pXRF and ICPMS, and screened for antibiotic producing bacteria. Results showed that areas of the complex with lower heavy metal content, specifically Cu, yielded higher numbers of diverse bacteria. These areas were also home to coal burning furnaces which could have added to the uniqueness of the bacterial growth area. The furnace areas also yielded the most antibiotic producing bacteria. These data suggest that further soil sampling in coal bearing soil, low in Cu and in areas of similar anthropomorphic land-use could yield high numbers of antibiotic producing bacteria. Profiling areas based on these criteria would provide a less time consuming, more focused effort in the search for new antibiotics.

Monitoring and Identification of Harmful Algal Bloom Causing Cyanobacteria in Drinking and Recreational Water. Christian J. Rios-Ruiz, Joshua Steier and Tinchun Chu. Seton Hall University, South Orange NJ.

Over the past decade, we have faced the increasingly growing occurrence of Cyanobacterial Harmful Algal Blooms (CHABs). Cyanobacteria are photosynthetic microorganisms and their blooms have been reported in various bodies of freshwater, such as reservoirs and recreational bodies. It has been recognized that cyanobacterial blooms are a serious threat to aquatic life and some species, such as Microcystis, Cylindrospermum and Anabaena, have the ability to produce harmful toxins. This study focused on using three approaches to detect and analyze cyanobacteria and the potential presence of cyanotoxin in various water sources. Freshwater samples were weekly collected from April through November from eutrophied water sources in New Jersey and their water chemistry such as pH, temperature, and level of dissolved oxygen (DO) was recorded. Flow cytometry serves as a rapid method to detect cyanobacteria and other related species in the water sample. Microscopic observation and polymerase-chain reaction (PCR)-based assays help

further confirm the genus and species. In South Orange Duck Pond (SODP), DO ranged from 0.42 to 6.54 mg/L; pH ranged from 6.5 to 9.21 and water temperature ranged from 12.5 to 24.9 °C. For Branch Brook Lake, DO ranged from 0.27 to 3.1 mg/L; pH ranged from 5.89 to 9.8 and water temperature ranged from 19.7 to 30.7 °C. Results of water chemistry showed that, in general, as the temperature of the water increased, the lower the level of dissolved oxygen was measured. Flow cytometric results showed the presence of Cylindrospermum and Microcystis -like species in both Duck Pond and Branch Brook Lake. PCR assays confirmed cyanobacterial presence, with over 85% of the samples processed showing the presence of photosynthetic species.

Physiological Study of the Neurotoxic Actions of Manganese on Dopamine Cell Signaling in *Crassostrea virginica*, Downstream of D2-Like Receptor Activation. Cheyanne Robertson, Edward J. Catapane and Margaret A. Carroll, Medgar Evers College, Brooklyn, NY.

Dopamine, a neurotransmitter in invertebrates, is well studied in bivalve gill and heart. Lateral gill cell cilia (LGC) of *Crassostrea virginica* are controlled by dopaminergic-serotonergic innervation. Dopamine slows beating of GLC cilia. We found dopamine postsynaptic receptors of GLC cilia are D2-like (D2DR). The D2DR signaling pathway involves inhibition of adenylyl cyclase and activation of phospholipase C (PLC). The effects of dopamine on cAMP in oyster gill is well known. Activation of PLC has not been well studied. PLC activation increases cellular (IP3) diacylglycerol. IP3 and DAG are second messengers. IP3 binds to IP3 receptors, increasing cytoplasmic calcium. High cytoplasmic calcium slow down GLC cilia. DAG activates protein kinase C. Manganese causes Manganism in people, a Parkinson's-like syndrome, and disrupts dopamine induced cilio-inhibition of GLC cilia in *C. virginica*. Our lab showed the site of action of manganese is the D2DR receptor. We hypothesize IP3 and DAG is cilio-inhibitory but not effected by manganese. We studied this by testing IP3, a DAG analog, a DAG kinase inhibitor, and manganese on GLC cilia. Cilia activity (beats/sec ± sem) was measured by stroboscopic microscopy. Results showed IP3, the DAG analog and DAG kinase inhibitor each produced a dose dependent (10^{-6} – 10^{-4}M) decrease in GLC cilia beating. Acute treatments with 500 μM of manganese did not reduce the effectiveness of IP3 and the DAG analog to reduce cilia beating. This study provides new knowledge of the physiological actions of the PLC, IP3 and DAG components of the D2DR pathway on GLC cilia of *C. virginica* and demonstrates manganese did not affect those aspects. The study provides a foundation to further study physiological roles of PLC in bivalve gill as well as neurotoxic actions of manganese on the D2-like receptors in gill. This work was supported by the Carnegie Foundation.

Altered Microglia Morphology and AGE Accumulation in the RAGE- and DIAPH1-null Aged Murine Somatosensory Cortex. Moises Rodriguez, Julia Derk, Michael MacLean, Paul Mathewsand Ann Marie Schmidt, Medgar Evers College, Brooklyn, NY.

In the Central Nervous System (CNS), aging is linked to functional impairments in microglia, as well as glucose homeostasis in both mice and humans. The production of Advanced Glycation End Products (AGEs), accumulate in aging mice and humans. These AGEs bind their chief cell surface receptor RAGE, (Receptor for Advanced Glycation Endproducts) with pathological consequences. AGE-RAGE ligand binding induces intracellular signaling cascades, in part via diaphanous-1 (DIAPH1), which leads to increased RAGE expression, and the ignition of a positive feedback loop driving chronic inflammation. Over time, this may contribute to inflammatory changes in microglia, which may be quantified by assessing morphological changes through surface area to volume ratio (SA:V). As well as studying processes and branches of microglia This study aims to examine the changes in microglia morphology and AGE accumulation in the murine somatosensory cortex in the presence and absence of RAGE or DIAPH1. This experimental design will be accomplished through studying aged (24-36 mo) and young (2 mo) global -null (referred to as RAGE KO) and -null (referred to as DIAPH1 KO) as compared to WT (C57BL/6 mice) young and old mice (N=3). We hypothesize that in aged mice, the absence of RAGE and DIAPH1 will partially rescue cortical microglia from the progression into amoeboid morphology, with decreased SA:V, decreased peak brachiness and soma distance as measured by sholl analysis. In addition, we hypothesize that RAGE KO and DIAPH1 KO mice will display a decreased production of AGEs during old age as compared to WT aged From our results, we conclude that the somatosensory cortex in RAGE KO mice undergo altered age-dependent shifts in microglia morphology and AGE accumulation, as observed through significantly improved SA:V ratio and peak branchiness of RAGE KO aged cortical microglia, as well as diminished AGE accumulation in the RAGE KO cortex during aging.

Phosphorylation of Hexim1 is Critical for Prostate Cancer DU145 Xenograft Growth in Nude Mice. Sarah Sadik, Kristelle Pierre and Manya Mascareno, SUNY at Old Westbury, Old Westbury, NY.

Prostate cancer (PCa) affects 1 in 6 males in their lifetime, and is the second leading cause of cancer death in men in the US. The identification of novel markers and therapeutic targets in advanced prostate cancer and androgen-independent disease is critical for improving diagnosis and therapy. Ideal targets for prostate cancer therapy would include proteins that are exclusively expressed in advanced disease and not present in normal tissue. Previous work in our laboratory has identified Hexim1 as a molecule that is expressed in high Gleason grade PCa. We have also identified conserved YXXL

motifs in the Hexim1 that are phosphorylated by JAK2 kinase. The phosphorylated YXXL Hexim1 expression is increased in androgen independent DU145 human PCa cell line and in high Gleason grade human prostate biopsies. We investigated the role of phosphorylation of these residues during tumor growth and progression. To this end, we generated stable cell lines of DU145 cells that overexpressed substitution mutation in the YXXL motifs sites. The growth of these cell lines was investigated in vivo by conducting xenograft implantation in nude mice. The results indicated that the growth of tumors was completely attenuated in the DU145 expressing loss of both tyrosine phosphorylation residues. We further analyzed the growth of cell lines carrying Hexim1 substitution mutations in in 3D model using Matrigel. The results showed that YXXL mutant DU145 cells ability to grow in the 3D culture is impaired.

Interrelationship Between C-SRC and SIT in the Regulation of Osteoblast Activity. Samuel Sanchez, Sydney Kauffman, Candace Morales-Wilde, David Cifelli, Joseph Tarr, Stephen Popoff, Nicole Rodstrom and Thomas Owen, Ramapo College, Mahwah, NJ.

Deletion of the c-src gene results in decreased osteoclast and increased osteoblast activity. Inhibition of c -src family kinases in calvarial osteoblasts or MC3T3 cells by the c-src inhibitor compound PP2 increases their differentiation. In Ros 17/2.8 osteosarcoma cells and in primary bone marrow cells though, PP2 results in a diminution of osteoblast phenotype markers, suggesting a differential role for the src family kinases in osteoblast function depending on the developmental origin. More recently, SIT (SHP2-interacting transmembrane adaptor) was described as a potential target for phosphorylation by src-family kinases in osteoblasts. When the SIT gene is deleted in mice, they show increased trabecular number, bone volume fraction, and connectivity density, as well as decreased trabecular thickness and spacing. The intracellular portion of the SIT protein has three tyrosines in motifs which are known to mediate phosphorylation-dependent interaction with the SH2 domains of c-src family kinases. In T-cells, these tyrosines are phosphorylated following activation of the T-cell receptor and mediate binding to proteins including Grb2, SHP2, and Csk. Since the deletion of both c-src and SIT in mice results in increased osteoblast activity and they are known to interact in the immune system, it is reasonable to hypothesize that in osteoblasts, they interact to influence signaling pathways and ultimately regulate bone mass. We used the crispr-Cas9 system to independently target c -src and SIT in Ros 17/2.8 cells. Preliminary analysis of osteoblast phenotype marker expression in the antibiotic resistant pools following transfection of either c-src or SIT crispr-Cas9 shows that the levels of gene expression for OC, OP, DMP, and AP decrease as does AP enzyme activity. These data are consistent with our previous observations using PP2 in Ros 17/2.8 cells but also demonstrate that it is c-src itself and not a family member that is responsible for this activity.

The Effects of Taurine on Manganese Accumulations in Gill of the Eastern Oyster, *Crassostrea virginica.* Rafael Santos[1], Emmanuel Agyei[2], Elvin Griffith, Jr.[3], Margaret A. Carroll[2] and Edward J. Catapane[2], [1]Kingsborough Community College, Brooklyn, NY, [2]Medgar Evers College, Brooklyn, NY and [3]Notre Dame High School, West Haven, CT.

Taurine is neuroprotective against some neurodegenerative diseases including Alzheimer's, Parkinson's and Huntington's. Manganese is a neurotoxin causing Manganism, which often is confused with Parkinson's disease. Manganism has is no effective treatment. The oyster *Crassostrea. virginica*, has a serotonergic-dopaminergic innervation of gill lateral cells (GLC). We showed manganese disrupts dopaminergic innervation of GLC and taurine protects against manganese toxicity on dopamine innervation. We hypothesize taurine actions is by reducing manganese accumulations in gill or by enhancing manganese removal from gill. We treated gills 2 days with 500 μM TAU, 500 μM manganese, or taurine and manganese (500 μM each), rinsed, dried, weighed and digested in HNO_3 in a CEM Microwave Digester. Aliquots were analyzed by Atomic Absorption Spectroscopy. We found manganese treatments caused higher manganese accumulations compared to controls or TAU treatments. Co-treated with taurine and manganese had no significant difference in manganese accumulations compared to treatments of manganese alone suggesting taurine does not block manganese accumulation into gill. To determine if taurine removes manganese from gill, gills were treated 2 days with manganese (500 μM), rinsed, then treated 2 days with taurine (0.5 to 2.5 mM), or EDTA (0.5 to 2.5 mM). We found EDTA (2.5 mM) was the most effective at removing manganese from gill (80% compared to controls). Taurine treatments were effective to a lesser degree, removing about 25%. The study shows while taurine did not prevent manganese accumulations, it did remove manganese, similar to how chelating agents are used in treatment of metal toxicity. Considering taurine is a natural biological component of cells and metabolism and shows success as a protective agent in other neurodegenerative diseases, more studies are needed to determine if taurine would be an effective and safer therapeutic agent for clinical treatment of Manganism. Supported by NIH grant 2R25GM06003 and the Carnegie Foundation.

A Comparison of NY/NJ Harbor Estuary Water Quality Data Between 2016 and 2017: A New York Water Trails Association Initiative. Maria Shapiro, Zanna Shapiro, Rob Buchanan, Nina Hitchings, Alison Dell and Kathleen A. Nolan, St. Francis College, Brooklyn, NY.

The New York Water Trails Association has been testing the water quality of the New York Harbor Estuary since 2012. This summer there were a total of 66 sites that collected water quality data for twenty weeks. (We personally collected water from the Brooklyn Bridge Park Dumbo site) In this project we are comparing water

quality results from 2016 to 2017 for twelve weeks from sites from Randall's Island, Queens, Brooklyn, Manhattan, New Jersey, Yonkers, and Staten Island (we only have 2017 data from Staten Island). Through pie graphs, we show a comparison of the two years (except for Staten Island) of what was considered acceptable, unacceptable if the conditions persisted, and highly unacceptable water quality conditions based on the Enterolert test. This test was developed by the company IDEXX and it examines the number of enterococci present in the water sample. Enterococci are gram-positive bacteria, and are an indicator of pollution. For each day of testing, the Most Probable Number (MPN) of colonies per 100 ml was recorded. The following are the New York City Department of Health (NYDOH) Standards in color tags (for swimming).Green: <35 MPN—acceptable. Yellow: 35-104 MPN--unacceptable if levels persist and Red: >104 MPN—unacceptable. There were significantly more "red days" in 2017 compared to 2016 for the following locations: Randall's Island, Yonkers, Queens; and slightly more in Manhattan, New Jersey, and Brooklyn. The "green days" decreased for Queens and Randall's Island in 2017, compared to their levels in 2016. Temperature is also compared to bacteria counts, in some cases.

Screening and Identification of Inhibitors for Activated Cdc42-associated Kinase (ACK) to Reverse v-Ras-induced Cancerous Phenotype of Mammalian Cells. Jaleel Shepherd, Ijaz Ahmed, Raj Rajnarayanan and Alam Nur-E-Kamal, Department of Biology, Medgar Evers College of the City University of New York.

Hypothesis: The superfamily of Ras GTPase has been reported to control different aspects of mammalian cell growth. Our lab demonstrated a possible role of Ras-Cdc42-ACK signaling in the survival of v-Ras-transformed cells. We also found that ACK-deficient v-Ras transformed NIH 3T3 cells undergo apoptosis while the parental NIH 3T3 cells grow normally. We proposed a hypothesis that "ACK-induced phosphorylation plays a critical role in the survival of Ras-induced transformed cells". Based on three-dimensional structure of ACK, our lab in collaboration with other group screens chemicals to identify potential specific inhibitors for ACK. In this report, I will present computer aided screening protocol and the effect of these inhibitors on growth of v-Ras-induced transformed and parental NIH 3T3 cells.Method: I have used software to screen and identify potential inhibitors for ACK. These inhibitors were then used to treat v-Ras transformed and parental NIH 3T3 cells. The cell growth was monitored by MTT assay. I have further studied the effect of these inhibitors on gene expression using immunostaining, immunoblotting, and polymerase chain reaction. Results: I have identified some compounds that have strong affinity for ACK and inhibit growth of v-Ras transformed cells. Treatment of v-Ras cells with these inhibitors was found to activate apoptosis. I have used several markers of apoptosis. These results will be described in this report. Conclusion: I have found that ACK inhibitors inhibited the growth of v-Ras transformed cell. I am designing novel compounds with more specific binding to ACK. Development of specific ACK inhibitors will be useful in better understanding the role of ACK in the growth of normal and cancer cells.

Low-level Copper Exposure Causes Developmental Defects in the Embryonic Zebrafish. K. Michalak, A. Shields, K. Figueroa, J. Pagnotta, M. Islam, K. Nolan and A.L. Dell, St. Francis College, Brooklyn. NY.

Neuronal and cardiac birth defects are correlated with pesticide application and water quality. Human exposure to these pollutants may occur through drinking water, or during contact with surface water, but the molecular pathways that cause these defects are not well defined. GPCR signaling pathways constitute one primary mechanism for cells to respond to their environment. Using the zebrafish retinotectal projection as a model system, we previously showed that GPCR signaling is required for axon guidance during normal development. Retinal ganglion cell (RGC) axons that express a dominant negative G-protein subunit GalphaS fail to cross the midline and misproject. Our aim was to use this system to dissect cell signaling events that translate exposure to environmental pollutants into neuronal developmental defects. We measured elevated copper levels at sites along Newtown Creek, one of the most polluted waterways in New York City and designated Superfund Site validating our findings with EPA data. We report generalized developmental as well as cardiac and behavioral deficits in zebrafish embryos transiently exposed to low levels of copper ions during development. To discover the molecular and cellular basis of copper toxicity we identified potential gene targets of copper by analyzing GEO2R datasets, and refined our candidate list to targets expressed in the right time and place to direct growing retinal axons. Using Isl2b transgenic embryos, as well as lipophilic dye tracings of retinal axons, we will asses the affect of copper on axonal trajectory correlating these developmental changes with alterations in expression of canonical GPCR signaling components.

Acrylamide Gel Stain to Quantify DNA Fragments. Shenin Siddiqui, James Tilton and Jonathan Ouellet, Monmouth University, Monmouth, NJ.

To understand the structure/function relationship of many nucleic acids, kinetics of the DNA is monitored over time and separated on acrylamide gels using radioisotope phosphorus-32. Currently, nucleic acid kinetics is observed mainly through the use of radioactivity. However, using radioactivity raises safety concerns and heavy regulations. Therefore, this project will be focused on determining which dye is best fitted to quantify small quantity of short DNA fragments on urea-denaturing polyacrylamide gels. To observe the DNA fragments, DNA (70 nucleotides) are separated by a polyacrylamide gel. Next, the DNA in the gel is fixated and saturated with

different dyes. Afterwards, the gel is de-stained in a manner that allows only the DNA to be stained and the rest of the gel to remain clear. This method allows the DNA to be detected under white light or ultra violet light as well as under light and dark background. With the help of the dye, DNA at different concentrations can be observed and quantified using the software image (ImageJ) to do densitometry analysis on a picture of the gel. As of now, DNAs (70 nucleotides) have been observed with Methylene blue, SybrGold, and Gelred dyes. Many different dyes will be used to find the ultimate dye that would give the best result to observe DNA and the function and structure of nucleic acids. Once set with DNA, this technique could be used to monitor kinetics of DNA cleavage. More importantly, it could be used in the field of RNA kinetics to monitor the RNA cleavage of ribozymes. In the future, more dyes with DNAs (70 nucleotides) as well as other different lengths of DNAs will be used for observation.

Genetic Delivery of RNA Molecules to Alter Expression of EGFR in Glioblastoma Multiforme. Nicole Sivetz, Sarah C. Falotico and Peter Nekrasov, Monmouth University, West Long Branch, NJ.

Glioblastoma multiforme (GBM), the most common central nervous system (CNS) malignancy, is characterized by overexpression of the membrane bound epidermal growth factor receptor (EGFR). Activated EGFR promotes GBM tumor proliferation and growth. Current prognosis for patients receiving standard care is approximately fourteen months due to the aggressive nature of this cancer and the isolating abilities of the blood brain barrier. Our novel approach to deliver DNA encoding anti-sense RNA molecules to alter pre-mRNA splicing of the EGFR mRNA transcript in GBM cells has the potential to bypass this barrier. In the strategy presented, we have designed a pre-trans-splicing RNA molecule (PTRM) to deliver a polyadenylation signal (PAS) into the EGFR pre-mRNA transcript upstream of the exon corresponding to the transmembrane domain, altering the mature EGFR transcript. In our design, optimization of the EGFR antisense binding domain and a U7 snRNA-SmOpt localization signal will enable the PTRM to compete against the downstream 3' splice sites of the EGFR transcript, generating a shortened mRNA transcript. This shortened transcript would translate into a non-membrane bound soluble peptide decoy and inhibit activation of the EGFR pathway. The PTRM therapy construct was cloned into an adeno-associated viral plasmid vector and delivered to GBM cell lines. Total RNA was isolated from cells and reverse transcribed using a random primer mix and target-specific primers to generate cDNA. PCR with specifically pre-designed primer sets was used to detect therapy expression and alternative splicing of EGFR transcripts. Our novel approach to harness the cellular pre-mRNA splicing machinery and gene therapy to generate a targeted therapy may be an effective strategy in the treatment of GBM.

Protein Quantification in Reproductive Tissues of *Petunia hybrida*. Angel Jizzelle Smith, Ivan Shun Ho and Farshad Tamari, Kingsborough Community College, Brooklyn, NY.

Reproductive organ proteins have not be quantified in. Our goal is to determine tissue-specific protein concentrations ([protein]) at different developmental stages (i.e. bud stages at four (-4), three (-3), two (-2) and one (-1) days before anthesis, as well as anthesis) for both female and male reproductive organs and for one non-reproductive tissue. We hypothesize that 1. The changes in protein quantities throughout development differ for reproductive tissues compared to non-reproductive tissues. 2. Proteins quantities in the reproductive tissues are temporally controlled and increase steadily throughout development; but reach their peak when the organ is reproductively active. To achieve our goal, flowers were dissected and reproductive and non-reproductive organs were extracted in PBS. Samples taken from each flower included the sepals, styles/stigmas, ovaries, and anthers. A conventional Bradford protein assay was used to determine the total amount of protein in each sample. Basic data analyses were performed using Microsoft Excel 2013. All statistical analyses were performed using SigmaPlot 12. There is considerable variation in [protein] due to tissue and developmental stage specificity. The highest [protein] was obtained in styles/stigmas (4.54 ±0.088 to 7.96±0.22 µg/µL), but varied considerably. Other [protein] measurements were as follow: Anthers (4.14 ±0.30 to 5.88±0.46 µg/µL), ovaries (2.40 ±0.025 to 6.20±0.35 µg/µL), and sepals (0.45 ±0.14 to 2.05±0.24 µg/µL). In most cases, there appears to be a build-up of proteins throughout development. Data provided in this research will shed light into the overall protein expression throughout development for this commercially important .

Inhibition Of Pathogenic Bacterial Biofilm Formation Using Cell-Free Extracts of *Neisseria sicca* and *Erwinia carotovora.* Alexandria Stanley, Jenique Klinkerth, Sonam Dosanjh and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

Biofilm forms when bacteria attach to a surface and to each other creating an extracellular polymer that enhances attachment and matrix formation. By forming a biofilm, pathogenic bacteria create a type of protective barrier that makes them resistant to not only antibiotics and antimicrobial agents but also to our immune system. Biofilms play an important role in public health. Most infectious diseases and device related infections, such as catheters at hospitals are caused by biofilm forming pathogenic bacteria. The focus of our research is the identification and characterization of new anti-biofilm substances. Cell free extracts of and were made, tested, and show strong antibiofilm properties against pathogenic biofilm forming bacteria such as *Pseudomonas aeruginosa*, *Staphylococcus epidermis*, *Staphylococcus aureus*, *Escherichia coli*, and *Enterococcus faecalis.* Further characterization will be conducted to identify the unknown bacteria and the secreted compounds.

Native Free Radical Mediated Crosslinking of Functionalized PEGs as a Targeted Delivery Mechanism. Victor Manuel Suarez[1], David I. Shreiber[2] and Christopher Lowe[2], [1]Kean University NJ and Rutgers, The State University of New Jersey.

A localized, elevated concentration of free radicals (FRs) is a shared trait among many different injuries and disease states. Low levels of FRs are regulated through native mechanisms, but in injury or disease these mechanisms are overcome, and indiscriminately oxidize nucleic acids, proteins, and lipid membranes. However, in polymer chemistry, FRs act as effective initiators of polymerization and crosslinking. We hypothesize that native FRs that arise due to injury or disease can be leveraged to specifically target and distribute therapeutics to afflicted tissues, by means of coupling therapeutics to a FR reactive polymer. The reactive polymers will crosslink via the elevated concentrations of FRs, immobilizing therapeutics to the damaged tissue. In this study, polyethylene glycol (PEG) functionalized with different FR sensitive functional groups were evaluated to assess their ability to react with biologically relevant species such as reactive oxygen species (ROS) and reactive nitrogen species (RNS). Using hydroxide and nitric oxide generated radicals along with DPPH, a known stable radical, characterization of reactivity was obtained indicating that thiolated and acrylated PEGs react strongly to detoxify the elevated FRs. In addition to reactivity, the cellular metabolic activity of rat dermal fibroblasts (RDFs) was examined to test for potential cytotoxicity of functionalized PEGs to confirm viability of the compounds *in vitro*. Preliminary data indicate that thiolated and acrylated PEGs react strongly with ROS. Further studies will seek to characterize the coupling of the compounds via rheometry, NMR, and gel permeation chromatography.

Ionic Liquid Mixtures with Single-Walled Carbon Nanotubes as Electrolytes for Dye-Sensitized Solar Cells. Rawlric A. Sumner[1], Tirandai Hemraj-Benny[1], Sharon Lall-Ramnarine[1] and James F. Wishart[2], [1]Queensborough Community College, CUNY, Bayside, NY and [2]Brookhaven National Laboratory, Upton, NY.

The use of dye-sensitized solar cells to replace silicon-based solar cells is attracting increased attention. However, it is necessary for more efficient electrolytes to be developed in order to facilitate their increased commercialization. In this study, the properties of mixtures containing single-walled carbon nanotubes (SWNTs) in 1-(alkyl or ether)-3-methylimidazolium bis (trifluoromethylsulfonyl)amide ionic liquids (ILs) were determined as the addition of SWNTs was believed to advance the rate of ion diffusion in ILs. The ionic liquids were prepared by reaction of 1-methylimidazole with the alkyl halide or alkoxyalkyl halide to yield an imidazolium halide salt. The halide salt was then converted to a bis (trifluoromethylsulfonyl)amide (NTf_2) IL. Nuclear Magnetic Resonance (NMR) spectroscopy was used to confirm the structures of the prepared ILs. Subsequently, SWNT-IL mixtures were prepared by grinding with a mortar and pestle. The conductivity of ILs and SWNT-IL mixtures were measured in a low-moisture environment. Preliminarily, conductivity values greater than 5.0 mS/cm at 25 °C were obtained for SWNT-IL mixtures, showing that SWNTs have the ability to raise conductivity via an increased rate of ion diffusion therefore making them promising electrolytes for use in electrochemical devices.

Identification and Genetic Characterization of Vancomycin Resistant Bacteria in a Community Setting. Hakim Thomas, Elizabeth A. Mulligan and Grace L. Axler-DiPerte, CUNY: Kingsborough Community College, Brooklyn, NY.

Vancomycin resistant bacteria are an increasing threat in hospital settings, causing many serious illnesses and infections. While the human microbiome is diverse, inhabitants such as *Enterococcus faecalis* can cause disease in immunocompromised hosts. Additionally, antibiotic resistant bacteria have been well documented in hospital settings. We hypothesized that genetically resistant bacteria, previously observed in healthcare facilities, can be found in a community setting. Kingsborough Community College, Brooklyn, NY was examined for the presence of vancomycin resistant bacteria. We attempted to distinguish natural from genetically acquired resistance to low levels (16 μg/ml) of vancomycin. Over an 8-week period; we visited 10 sites twice, gathering bacteria from frequently touched surfaces with 4 sterile cotton swabs wet with 0.5% sterile saline solution for each site. One swab was inoculated onto one each of Tryptic Soy Agar (TSA; general growth medium) or Bile Esculin Azide Agar (BEA; selective and differential for staphylococci and enterococci) plates both with and without vancomycin. The plates were incubated at 37°C for approximately 48 hours. Growth ranging from 2 to greater than 300 colony forming units (cfu), (52.1 average cfu, σ = 42.4) was found on each TSA plate without antibiotics. Vancomycin resistant bacteria were observed on 3 TSA plates with vancomycin ranging from 1 to 45 cfu 1 of 20 BEA plates with vancomycin resulted in 2 cfu. Several vancomycin resistant colonies were tested via Polymerase Chain Reaction (PCR) for the vanB gene, which indicated the presence of corresponding products. This data supports our hypothesis indicating that genetically acquired resistance to vancomycin may be present in a community setting. Further work will focus on more detailed characterization of vancomycin resistant bacteria found in the community.

Serial Isolates of *Cryptococcus neoformans* Demonstrates Altered Resilience to Nutritional Stress. Rupali Ugile[1], Zachary Cain[1], Bettina C. Fries[2] and Tejas Bouklas[1], [1]Long Island University-Post, Brookville, NY and [2]Stony Brook University, Stony Brook, NY.

Cryptococcus neoformans is an opportunistic fungal pathogen that causes fatal meningitis in immunocompromised individuals, especially HIV+/AIDS patients. It has a high propensity to persist and relapse despite antifungal therapy. Cerebrospinal fluid from recurrent infections is routinely drawn, and raises the question of whether later isolates survive host stresses better than earlier isolates. Previous studies have shown that the two aging models of chronological and replicative lifespan are altered by nutrition deficiency, and advanced age cells show phenotypic variations during chronic infections. Therefore, both mitotic and post-mitotic aging of cells may play an important role in maintaining their fitness in the host. We hypothesized that later isolates respond differently to nutritional stresses, such as glucose availability, which is significantly reduced in cerebrospinal fluid. We investigated the fitness of serial isolates from several patients in New York City, USA, by measuring their growth rates and viability in media with severely restricted glucose comparable to spinal fluid. Further in vitro and in vivo characterization of the isolates was performed. The fitness of later isolates was comparably improved compared to earlier isolates depending on the patient, and the length of time between the isolates. This study stresses the importance of studying multiple isolates, rather than only the first isolate, in the case of recurrent infections. We propose that in patients where later isolates show improved fitness, the strains be investigated for differences to help understand why the infection persisted as this may lead to improved therapy against recurrent infections.

A Preliminary Study of Pharmacological Perturbation of STAT6 on the Growth of Malignant B Lymphoma, *In Vitro.* Luis Valerio[1], Stephen Redenti[2] and Rajendra Gharbaran[1], [1]Bronx Community College and [2]Lehman College/CUNY, Bronx, NY.

A subset of aggressive malignant B cell lymphomas harbor activating mutation for Signal Transducer and Activator of Transcription 6 (STAT6), a member of the JAK/STAT signaling pathway. STAT6 activating mutation is associated with poor prognosis. In this study, we showed that AS1517499 (AS), a potent and selective STAT6 inhibitor, disrupts growth of malignant B lymphoma, in vitro. WST-1 cell viability assay showed that AS reduced cell viability in a dose (0,1, 2.5, 5, 10 uM)-dependent manner, in the STAT6+ malignant B cell lines, HDLM2, KMH2 and L428. Acridine orange(AO)/ethidium bromide (EtBr) – AO/EtBr – staining showed significant cell death resulting from AS treatment. In this assay, live cells stain green with AO and nuclei of dead cells stain red with EtBr. Immunofluorescence analyses revealed that AS -induced cell death occurs via caspase 3 (CASP3) activation. Quantitative real-time polymerase chain reaction (qPCR) showed that AS treatment of L428 resulted in downregulation of Bcl-xL, a gene that codes for the anti-apoptotic protein BCL-xL. These preliminary results suggest AS reduces growth of malignant B lymphoma by inducing apoptosis.

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

The objective of this experiment was to observe the effect of semi-precocial development on the movement of juvenile common terns (*Sterna hirundo*) as the chicks aged. Semi-precocial species begin to wander away from the nest at around two to three days old. Over the course of two months, two sites in Barnegat Bay, off Long Beach Island, New Jersey were observed to examine common tern chick movement from the nest. Once the chicks hatched, data was collected on the chicks: band numbers, the chicks' distance from the nest, as well as the distance between neighboring nests. The results that were collected were expected to reflect semi-precocial development, meaning that as the chicks aged, they would be found farther from the nest. Observations of o chicks from seven different age groups supported the hypothesis that chicks moved from the nest as they matured. In the first age group of 1 to 3 days, it was found that the median distance from the nest was only 0.10 m away from the nest. In the next age group of 4-6 days, the median distance away from the nest was 0.45 m away. In the age group of over three weeks old, the median distance away from the nest was 6.45 meters; no chicks were found at their nest, and the chicks were about to fledge. Although complications did arise such as storms, predation by gulls, and the chicks moving into dense vegetation, enough chicks were recorded to demonstrate that chicks move away from the nest after only days of hatching. Ultimately, the data show that common tern chicks are not attached to the nest site, despite continuing to rely on their parents for care.

Permethrin and High-mobility Group Box1 Protein Pathway on Microglial Dysfunction. Miguel Vera and Mohammad Javdan Queensborough Community College, Bayside, NY.

Microglia within the central nervous system playing a central role in response to chronic injury or inflammation. Microglia constantly clear protein aggregationswhich arehighly toxic to nerve cells. Over-activation of microglia have been well studied in developing AD . We hypothesized that dysfunction of microglial cells could link the development of AD by pesticide exposure. To test our hypothesis, we treated BV2 microglial cells with 1 and 5µg/ml of Permethrin for 24 hours, Permethrin as a pecticide is used widely in and around households, including on pets, in mosquito control, and in agriculture.

We assessed the effect of Permethrin on the cell viability and morphology of BV2 cells by performing the MTT assay, Our results showed Permethrin significantly reduced cell viability of microglia and drastic changes in their morphology compared to the control group. After collection of supernatant of our samples by using centrifuge centricone filters we concentrate proteins and did westurn blot assay also remaining cells at the bottom of plate were lysed and did westurn bolt assay, we fund that permethrin causes HMGB1 to move from neucleus to the cytoplasem of microglial cells in experimental group and not in control group so we got proof of HMGB1 pathway in effects of Pesticide on microglia cells.

Molecular Analysis of Ground Spiders (Gnaphosidae) of Asia and Australia. A. Vindas-Cruz[1], V.I Suarez[1], B. Zakharov[2,4], V. Ovtcharenko[3,4] and M. Shusmkaya[1], [1]Kean University, Union, NJ, [2]LaGuardia Community College CUNY, New York, NY, [3]Hostos Community College CUNY, New York, NY and [4]American Museum of Natural History, New York, NY.

Gnaphosidae is one of the largest families of spiders currently placed sixth in the number of described species from all Araneae. The molecular data available is extremely limited for the described species, with only 46 out of 125 genera having any molecular data (212 species from 2,195 of known species, or roughly 9.7%) (BOLD SYSTEM, 2017). Due to unequal geographical distribution of Gnaphosidae, most described species are from Holarctic region, with only minor amounts of species (only 8) being described from Australasian region (Australia, New Zealand). The aim of this study is to perform a DNA analysis of several genes used for barcoding of Araneae (18S, 28S, co1, wnt, H3) from six genera collected in Australia, New Zealand and Asia. Two close genera, with species *Zelanda erebus* (L. Koch, 1873), *Zelanda* sp., *Zelanda* sp. 1, *Zelanda* sp. 6 and *Encoptarthria echemophthalma* (Simon, 1908) are currently analyzed, in addition to two species from Eurasian genus *Haplodrassus* (*H. signifer* (C. L. Koch, 1839) and *H. hiemalis* (Emerton, 1909)) whose genes are missing from the NCBI Database, such as 18S, 28S, wnt, and H3. The DNA-based molecular phylogeny of the studied spiders is being developed.

Biomedical Implications of Herring Gull Data Obtained at Kingsborough Community College. Rosanne Wallach and Mary T. Ortiz, Kingsborough Community College, CUNY, Brooklyn, NY.

In 2013 research began at Kingsborough Community College (KCC) to identify/catalog birds at three campus locations (Sheepshead Bay-SB, Jamaica Bay-JB, Rockaway Inlet-RI) to determine biomedical implications these aves may indicate. Twenty-nine bird species have been identified; the most populous the Herring Gull-HG. Previously, descriptive statistical analysis of HG data was completed. Here, inferential statistical analysis of these data commenced. The hypothesis is inferential statistical analysis of HG data obtained at KCC will support descriptive findings about bird trends at the campus and shed light on biomedical implications. Inferential statistical analysis of HG data from Comparative Anatomy classes at KCC, was conducted using ANOVA and Kruskal-Wallis tests (α=0.05) to determine differences across three locations 2013-2016. HG data were analyzed because this is the most populous KCC bird. Results across 2013-2016 for HG populations include: no significant difference in SB, a decline in JB, a significant increase in RI. Results across the three campus locations for HG populations include: no significant difference in 2013, a significant difference using ANOVA 2014-2015, but no significant difference using the Kruskal-Wallis test, and a significant increase in RI compared to SB/JB for 2016. Results suggest HGs are most populous in RI, possibly due to presence of the cafeteria, beach, and people in this campus area. RI is protected by two jetties, food is plentiful with a sizable KCC Beach for habitation. Recently, the KCC Beach closed due to high bacterial counts. With increases in HG populations 2013-2016, beach closings may increase because of public health risks. The hypothesis is accepted. Large HG population at RI may harm humans using the beach. Future studies will further investigate campus birds to determine biomedical implications these populations may indicate. Supported by grants 2R25GM062003 of the Bridge Program of NIGMS and 0537171091 of the CSTEP Program of NYSED.

Molecular Analysis of Deadwood-Inhabiting Fungi Biodiversity at Stephens State Park, Hackettstown, NJ. Jenelle Yearwood, Marut Wojciech, Blue Shazneka, Vindas-Cruz Alessa and Shumskaya Maria, Kean University, Union, NJ.

Deadwood has been shown to protect against erosion, provide sources of crucial forest elements (carbon, nitrogen, calcium, etc.) and energy, facilitate and condition the regeneration of trees, improve water retention in the ecosystem, increase the species richness of fungi, plants, and animals, and create a variety of diverse ecological niches that support saproxylic taxa (Gutowski, Zub, Pawlaczyk, & Laudenslayer, 2005). Deadwood-inhabiting fungi belong to one of the main groups of saproxylic taxa which are an essential component of the forest ecosystem; they produce enzymes to decompose wood cell walls and make it available for other groups of organisms to consume and survive. This research is a part of a large project on the assessment of biodiversity of deadwood-inhabiting fungi in areas with varying degrees of human modification such as removal of foliage, snags and coarse woody debris. Our goal is to compare areas with different forest management practices in order to assess the human impact on the biodiversity of the fungal species. Presented here are the preliminary results of the biodiversity of deadwood fungal species collected in one of the research locations for the project, Stephens State Park in Hackettstown, NJ, which is a park that is not heavily

managed. Substantial amount of dead-wood inhabiting fungal specimens were collected and GPS coordinates were recorded using the iNaturalist application. The nuclear ribosomal Internal Transcribed Spacer (ITS) region was used as a DNA barcoding marker, with the ITS1 and ITS2 regions being targeted to allow the identification of the fungal species via DNA sequencing and bioinformatics methods. The diversity of the fungal community and its relation to park management practice is discussed.

Potential Antiviral Mechanism of Theaflavin-3,3'-digallate (TF3) on Herpes Simplex Virus Type 1 (HSV-1). Ayuni Yussof, Aline de Oliveira and Tinchun Chu. Seton Hall University, South Orange, NJ.

Herpes Simplex Virus Type 1 (HSV-1) infection is known to be a prevalent program worldwide. With more studies reported that HSV-1 is an increase cause for genital herpes, finding an alternative therapeutic agent for HSV-1 infection is vital. Theaflavin-3,3' digallate (TF3), a black tea polyphenol extracted from the leaves of *Camellia sinensis*, has been shown to be a promising candidate compound due to its antiviral properties. This study focuses on evaluating the potential antiviral mechanism of TF3 on HSV-1. Glycoprotein B (gB) of HSV -1 was studied as it is directly involved in the attachment of the virus to heparan sulfate, which is part of the viral entry step. Software Biovia Draw, Vega ZZ, Autodock Tools, Autodock Vina and Pymol are included in this study. Binding and penetration assay results suggested the antiviral activity of TF3 is based on its ability to prevent the virus from binding or penetrating the host cell. For the binding assay, at 50 μM and 75 μM of TF3 shows 0% of infection in both Vero and A549 cells compare to the controls while for the penetration assay, at 75 μM of TF3 shows 0% penetration in Vero cells and 15% penetration in A549 cells compare to the controls. The results from Autodock indicated that the range of binding affinity of TF3 to gB is between -8.1 kcal/mol to -7.4 kcal/ mol.

Species Identification From A Mixed Insect Sample Using DNA Barcoding. Stephanie Zapata, Jenifer Vasquez, Herbert Miller, Mariah Curet, Michael De La Fuente and John V. Smalley, Bergen Community College, Paramus, NJ.

Biodiversity studies have characteristically required the expertise of taxonomists familiar with the groups of organisms under investigation to make accurate species identifications. Such expertise is esoteric and can be hard to come by. The use of short, agreed-upon, phylogenetically diagnostic DNA sequences (DNA Barcodes) circumvents these potential problems by utilizing reliable and available molecular signatures to identify the species present in a given habitat. In this study, we employed DNA barcoding, using a standard marker, cytochrome c oxidase subunit I (COI) to identify species of insects collected in standard bowl traps. To date, using genomic DNA recovered non-destructively from the preservative fluid surrounding the specimens, we have been able to PCR amplify and sequence a section of the COI genes present in the preservative. Comparison of the sequences obtained with those residing in the Barcode Of Life Data System (BOLD), as well as morphological examination both converged on the following organism: Coenosia tigrina. Future work will employ similar methodology to identify the remainder of the species present in these mixed samples.

Doc, My Head Hurts, I'm Moody and I Keep Dropping Things...What's Wrong With Me? " Diagnosis of a Nervous System Disorder.

Diana Colgan, Catharine Potok and Patrick Field,
Kean University, Union, NJ.

This case study is an interrupted case study that proceeds through the stages of determining a diagnosis for a neural condition/disease in a 62 year old female that includes the medical history, presenting signs/symptoms, pre-diagnoses, evaluation/observations, testing, analysis of the results from testing, narrowing the differential diagnosis, and the final diagnosis. In order to be successful during this case, readers will have to be familiar with the epidemiology, signs/symptoms, pathophysiology, diagnostic testing, and results of testing of several neural conditions/diseases: Creutzfeldt-Jakob Disease, Guillian-Barre Syndrome, Huntington's Disease, Hydrocephalus, Multiple Sclerosis, Parkinson's Disease, Primary Amebic Meningoencephalitis and Subacute Sclerosing Panencephalitis. Students will create a table encompassing the characteristics of those diseases, completing it with the information provided in each stage to narrow down the diagnostic possibilities until the final diagnosis. By the end of the case study, students will understand that overlapping characteristics among these neural conditions/diseases increases the difficulty with reaching the final diagnosis. This case will be beneficial for upper level undergraduate and graduate students who pursue a future career in the allied health professions.

Academic Boot-camps for Undergraduate Science Courses.

Irina Ellison[1] and Alison Dell[2],
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During the first semester of freshmen year, biology and prehealth professional students are often enrolled in anatomy and physiology or general biology. These rigorous and fast-paced courses require students to build upon fundamental knowledge of chemistry and biology, as well as to have exceptional study science skills in order to succeed. This poses a challenge, as many students are underprepared, lacking firm foundations in science, as well as overwhelmed by the pacing and demands of college-level coursework and owernship of their own learning. As a result, these courses often result in low levels of student success with high D, F and withdraw (DFW) rates. To address these challenges and the associated impacts on student success, academic boot-camps were developed for Anatomy and Physiology and General Biology courses for students at two New York undergraduate institutions that focus on educational access to traditional and nontraditional students, including many who are racially/ethnically diverse, low income and first-generation: Mercy College and St. Francis College. The boot-camps were offered free of charge to the students and introduced course pacing, effective study and testing strategies, course and college resources, peer instruction, teambuilding and metacognitive exercises through intensive programming. The boot-camps resulted in improved student success.

Implementation of a Semester-long Research Project in an Introductory Biology Laboratory Course to Promote Students' Basic Skills in Scientific Inquiry and Civic Engagement.

Maria Entezari and A. Lucia Fuentes,
LaGuardia Community College, Long Island City, NY.

Educational assessments show that providing lifelong learning and civic engagement are important in preventing high attrition in STEM majors. Lifelong learning can be promoted by incorporating research projects as part of students' undergraduate experience. These interventions improve students' critical thinking, problem solving, writing and communication skills. In most schools, opportunities for involvement in research usually occur outside the classroom or in upper level and capstone courses, and are limited to a small number of already high achieving students. However, statistical data show that 65% of students drop out from STEM majors before their second year, and most students who continue and move to the higher-level courses are not properly prepared. Therefore, there is an urgent need to transform the first-year science courses to improve student's retention and make required alignments with needs identified in upper level courses as well as existing learning objectives in STEM programs. In this study we present our approach and development of a novel, semester-long, inquiry-based series of laboratory modules that incorporate the course learning objectives and required core competencies in an introductory biology course at LaGuardia Community College. Here we will go over our objectives, pedagogical design strategy and examples of the laboratories and assignments that allow students to formulate questions, hypotheses, conduct experiments and analyze and present original data. We also discuss how choosing water quality as the topic of the research project, allowed us to promote students understanding of the social dimensions of scientific practice and insight into possibilities for civic engagement.

Analysis of the Genome of Mycobacterium Phage CharlieB.
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The bioinformatics research provides a better understanding of the genetic organization, function and evolution of the bacteriophage genomes. In this project we analyzed the genome of Mycobacterium phage CharlieB. We received the sequence of CharlieB through the adopt-a-phage of Howard Hughes Medical Institute Phage Hunters program. To study and analyze the genome of CharlieB we used several bioinformatics programs: DNA Master, Basic Local Alignment Search Tool, HHpred, Gene Mark, Glimmer, Aragorn and tRNAscan-se. CharlieB was found by Brigham Wright, a student from Brigham Young University in Provo UT. It belongs to the cluster C, sub-cluster C1. CharlieB's genome has a length of 155527 base pairs and has 264 predicted genes. This genome contains gaps ranging from 50 to 80 base pairs and multiple instance of a 3 base pairs overlap. Blast of the full nucleotide sequence of CharlieB shows that it is most similar to the genomes of Mycobacterium phage Cali and Mycobacterium phage Bxz1. Blast of individual genes showed that majority of predicted proteins match genes from Mycobacterium phage Cali and Mycobacterium phage Bxz1 and additional matches to the genes from Mycobacterium phage ET08, Mycobacterium phage Catera, and Mycobacterium phage Gizmo. One interesting feature of the Mycobacterium phage CharlieB is that it carries 30 genes for tRNA genes and majority of these tRNA genes are located in one segment from 91100 base pair to 97544 base pair. BLAST of this sequence showed that it is most similar to tRNA-rich segment of Mycobacterium phage Cali, LRRHood, Lukilu, ScottMcG and Spud. The genome contains many genes with well predicted functions such as structural proteins: Major capsid, Tail assembly chaperone, Minor tail, tail tube, tape measure, baseplate J and head decoration; and enzymatic proteins such as: lysins A, Lysin B, lysin M, holin, endonuclease, terminase, helicase, recombinase, and DNA polymerase III.

Statistical Analysis of Specimens of *Duchesneodus uintensis* (Mammalia, Perissodactyla, Brontotheriidae) from the Duchesneodus Quarry, West of Vernal, Utah.
Bryn J. Mader,
Queensborough Community College, Bayside, NY.

Brontotheres (= Titanotheres) are extinct relatives of the horse and rhino. In 1931, several brontothere skulls, jaws, and postcranial elements were collected from a single quarry in the Duchesne River Formation, approximately 11 miles (18 km) west of Vernal, Utah. It is believed that all of these specimens represent a single species: *Duchesneodus uintensis*. Therefore, the quarry sample affords an excellent opportunity to assess the effectiveness of various statistical techniques that have been employed in the past to distinguish between fossil taxa. This study indicates that use of the Coefficient of Variation (V) and cluster analysis (using Euclidean Distance and Nearest Neighbor) can be useful in identifying specimens of a single taxon and distinguishing them from specimens belonging to similar taxa (species, or perhaps, subspecies) differing from them only in size. However, there is also evidence that these statistical techniques should be applied with caution and it is better to consider an overall statistical picture rather than focus on individual statistical results. Individual results (such as individual values of V) can suggest taxonomic differences when, in fact, the statistics are reflecting intraspecific variation (such as sexual dimorphism) or even random factors. Brontotheres lived during the Eocene Epoch, about 56 - 34 million years ago, in both North America and Central Asia. They belong to the family Brontotheriidae of the Order Perissodactyla (horse/rhino group). Duchesneodus lived during the Duchesnean Land Mammal Age of North America, approximately 42 - 38 million years ago.

Research in Class, From Wish List to Reality.
Catarina Mata,
Borough of Manhattan Community College, New York, NY.

Experiential learning science at BMCC has meant student research with faculty. This works well, but limits student participation opportunity. Research as part of a class is a solution to this problem. I have been doing it in Plant Biology, an elective class. The students have so far not been too many, 12 to 14. They work in groups of 4 or 5. We chose a test plant, the bean (Phaseolus vulgaris) and the students get to research and choose what kind of environmental stress factor or chemical they want to study, within logistical limits. Each group gets to have one treatment and we keep one set on control plants for the whole class, keeping numbers manageable. Students start with a library class on how to do a proper literature research, propose the work they plan to do, and define their own methods, searching literature. Once the experimental treatment is defined it is tested on germination and students share introductions and material and methods proposals on Blackboard on a discussion board. We have laptops in lab. The experiments are followed weekly during our three hour lab, and all data must be entered in the format previously agreed on Blackboard (based on previous mistakes). Students take turns measuring the controls. Simple parameters such as total length, number of leaves, size of the second leaf and color and followed, and then total pigments and biomass are measured in the end, and whatever else is needed for the treatment. Students graph their results in class, with support from one another and the instructor. They prepare and present a group poster to class. Edited posters are presented at the Research poster day at BMCC, and often other venues. I learned what are reasonable expectations, where to increase support and where to foster independence. How to go from stressful and frustrating with data gaps, to complete (or almost complete results) with proud happy students and posters that win them competitions.

A How-to Guide on Developing Open Educational Resources: Our Experiences Creating a Microbiology Laboratory Manual.
Joan Petersen and Susan McLaughlin,
Queensborough Community College, Bayside, NY.

The use of Open Educational Resources (OER's) is becoming more common throughout academic institutions, including community colleges. A recent initiative in New York State seeks to increase the number of CUNY and SUNY students that have access to OER's to make college education more affordable. OER's offer a cost-effective, easy access alternative to expensive textbooks, and also allow the instructor to customize materials for their own courses. We will outline the preparation of an OER Microbiology Laboratory Manual that we developed over the course of several semesters. Our approach was to use student and faculty feedback to guide the revisions of the manual. Our two student readers offered a unique perspective and made several helpful suggestions about improving the structure and readability of the exercises. We also used survey data from students who were taking the class to assess their satisfaction with the OER manual. The laboratory exercises were revised based on this feedback as well as suggestions from other faculty teaching the course. To minimize printing costs, we used only black and white images in the manual-supplemental color materials are available on the course Blackboard site. Our survey results showed that the vast majority of students preferred the OER format over a general laboratory manual and have a positive impression of the manual. Our presentation will focus on the successful methods that we employed to prepare the manual and offer helpful suggestions to others who want to prepare their own OER materials. The preparation of the manual was funded by an OER grant from QCC Library.

Effect of Microbial Restoration After Early-life Antibiotic Treatment on Intestinal Microbial Communities and on Host Gene Expression and Function.

Victoria E. Ruiz[1,2], Thomas Battaglia[2], Ceren Ozkul[2] and Martin J. Blaser[2],
[1]St. Francis College, Brooklyn, NY and [2]NYULMC, New York, NY.

Broad-spectrum antibiotics are frequently prescribed for children and in cases of viral infection, provide no clinical benefit. Antibiotic courses administered early-in-life, a dynamic period of microbial community succession, have durable effects on microbial community structure and host immunity. Using a murine model to mimic early-life antibiotic exposure, we have previously shown that macrolide-induced intestinal microbial perturbations were both necessary and sufficient to lead to long-term immunologic deficiencies and to accelerate the colitis induced by the intestinal irritant dextran sodium sulfate (DSS). We hypothesized that the introduction of a healthy (control) microbiota after an antibiotic course can protect the host from accelerated DSS-induced colitis induced by the macrolide treatment. To test this hypothesis, 5-day old C57BL/6 mice were given a single 5-day antibiotic course or not (control). At day 24 of life, mice were gavaged with microbial contents from control (healthy) donors, sham (diluent alone), or not gavaged. Surveying intestinal communities via 16S rRNA sequencing showed that a single gavage increased community diversity and altered microbial composition compared to the no gavage controls. Two weeks after gavage, control groups that received microbial gavage demonstrated altered intestinal (ileal) gene expression profiles. In a subsequent DSS challenge, microbial gavage prevented the accelerated weight loss seen in the unrestored antibiotic-exposed pups. These results provide evidence that microbial communities can be restored after antibiotic treatment and can have durable effects on host functions.

Leveraging Civic Engagement in Upper Level Courses.

Davida Smyth,
Mercy College, Dobbs Ferry, NY.

The incorporation of civic engagement into the science and mathematics curriculum is something that faculty do well for introductory and non-major science courses. While this can be helpful in attracting students to the sciences, can we also vertically integrate civic engagement into upper level coursework, and support student success, engagement, and retention in these more content and skill driven courses? This session will provide an example of such a strategy in an upper-level biology class. Davida Smyth, Associate Professor of Biology at Mercy College (Dobbs Ferry, NY) will present her research-based course "Microbiology of Urban Spaces" as a model for promoting civic and scientific literacy while integrating civic engagement into the microbiology curriculum. She will describe the potential impact of her efforts on student retention, engagement, and success. She will also demonstrate how she is leveraging the course to pursue her authentic research, with her undergraduate students, into antibiotic resistant Staphylococci. Following Dr. Smyth's presentation and Q & A, participants will have the opportunity to share related strategies they use, and brainstorm new ideas for incorporating meaningful engagement activities into their major STEM courses.

Changes in Vascular Plant Diversity of Cuttyhunk Island, Massachusetts.

Richard Stalter and Navida Rukhsha,
St. Johns University, Queens, NY.

Cuttyhunk Island, Dukes County, Massachusetts USA, comprising 235 ha, 41 25' N, 70 56 W, was formed during the retreat of the Wisconsin Glacier approximately 14,000 years ago. We performed a complete inventory of the vascular flora of Cuttyhunk Island confirming the taxa collected by previous investigators with 26 additional vascular plant species identified in the present study. Of the 364 species, 107 are invasive taxa and 257 are native species. In numbers of species the largest families in the flora are the Asteraceae (52) Poaceae (37) and Cyperaceae (31). The largest genera are *Carex* (21) *Juncus* (14), Cyperus (7) and *Eleocharis*(7).. There has been a decline in ferns, orchids, rushes and sedges since Fogg's floristic inventory in 1923. Invasive taxa have increased: 25% of the flora in 1923, 34% in 1974, and 38% in 2017. Across the past 93 years of botanical study, the island's flora has changed in response to a dynamic landscape impacted by human activity and coastal storms.

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