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In This Issue:

The Effects of Bisphenol A and Alternatives, Individually and in Combination, on Larval Development of *Xenopus laevis* (Clawed Frog)*

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ABSTRACT

Bisphenol A (BPA) is an industrial chemical used in the production of polycarbonate plastics and epoxy resins which are used in food and drink packaging. The purpose of this study is to compare the effects of BPA, a known environmental endocrine disruptor (EED), to those of its replacements, bisphenol S (BPS) and bisphenol F (BPF), individually, and in combination, on the development of *Xenopus laevis* (clawed frog). BPA is known to stimulate cellular responses by binding to estrogen receptors and via other mechanisms. The effects of BPS and BPF are not yet fully understood, however they have been detected in urine samples. The development of *X. laevis* has been used as a model system due to the transparent larvae and the complete categorization of its development. *X. laevis* embryos were incubated at the blastula and neurula stages in concentrations of BPA, BPS, and BPF individually and in combination to observe early and larval development. Malformations were observed in BPA, BPS and BPF, especially in combinations. There was also an increased mortality rate in 10 μg/mL BPA. The results of this study provide evidence that BPS and BPF are not safe alternatives to BPA.

Key Words: Bisphenol A, Bisphenol F, Bisphenol S, endocrine disruptors, amphibian development

Introduction

Human exposure to bisphenol A (BPA), a known environmental endocrine disruptor (EED), is widespread. The 2003-2004 National Health and Nutrition Examination Survey (NHANES), conducted by the Centers for Disease Control and Prevention (CDC), found that BPA was detected in 95% of the urine samples examined, at concentrations over 0.1 μg/L urine[1]. Recent studies have shown a downward trend in BPA intake in the USA from 52.82 to 27.62 ng/kg bw/day during the period of 2003-2014[2]. As the use of BPA has decreased, alternative bisphenols, BPS and BPF, have been utilized in its place in many products. Therefore, it is important to determine the effects of BPA and its commonly used substitutes, individually and in combination, on human health.

*Part of this work was presented at the annual meetings of the Society for Developmental Biology (Boston, August 2016) and the American Society for Cell Biology (Philadelphia, December 2017).

Bisphenol A (BPA) is the common name for 2,2-(4,4-dihydroxydiphenol) propane. It is an organic molecule made up of two phenol rings connected by a methyl bridge with two methyl groups attached to the central methyl bridge. There are several ways that BPA can be introduced into the environment; for example, factories can discharge BPA directly into the atmosphere and it can also leach from plastic containers into water[3]. Around 99.9% of domestically produced BPA is used by manufacturers as an intermediate in the production of polycarbonate and epoxy resins, flame retardants, and other specialty products[4]. It can be found in adhesives, protective coatings, powder paints, and paper coatings as well[5]. Extensive studies have been done on exposure to BPA and on its mechanism of action, leading to the conclusion that BPA is an EED. Studies initially showed that BPA binds to ERα and ERβ, two nuclear estrogen receptors, but it still had a lower affinity for the estrogen receptors than estradiol, a primary female sex hormone[3]. However, recent studies show that BPA can stimulate cellular responses at low concentrations through other pathways and by binding membrane-associated forms of the estrogen receptors. BPA has also been found to disrupt thyroid hormone (T_3) action by acting as an antagonist[6]. It was found that BPA disrupted transcriptional activity that is stimulated by T_3 in physiological concentrations. BPA displaces T_3 from the thyroid receptor and recruits a transcriptional repressor. In addition, Guo *et al.*[7], showed that detrimental effects on early porcine development might be due to DNA and mitochondrial damage.

There have been numerous studies conducted on the effects of BPA, including human studies on prenatal BPA exposure and early childhood behavior. A study conducted by Braun *et al.*[5], found an association between mean prenatal BPA concentrations at 16 weeks of gestation and hyperactivity and aggressive behavior among the female children. Additionally, other studies have examined the increased incidence of infertility, genital tract abnormalities, and breast cancer and their putative causation due to BPA exposure during early development[3]. In rhesus macaques, exposure to BPA during pregnancy can alter the airway cells of the fetus by increasing the expression of secretory proteins in the fetal airway tissue[8]. Other studies describing the effect of low concentration exposure of BPA on animals show outcomes such as prostate cancer, mammary gland cancer, decrease of tyrosine hydroxylase neurons in sexually dimorphic circuits in the hypothalamus[9], onset of estrus cyclicity and earlier puberty, increased body weight, genital malformations, and many others[3]. Some of the studies on *Xenopus laevis* larvae have also shown that exposure to BPA can cause head malformations such as shortened distance between the eyes[10], scoliosis[11], feminization[12], hyperactivity[13], anti-metamorphic effects[14], and several other teratogenic effects.

These many studies on BPA's adverse effects on animals, including humans, caused a public outcry for the banning of BPA in plastic production. Due to this societal pressure, the FDA banned the use of BPA in baby bottles and "sippy cups[15]." The FDA since then has been reluctant to implement further legislation banning BPA in the production of plastic materials. As public pressure mounted, manufacturers began looking for alternatives to BPA in the production

of plastic products. Some of the most common replacements for BPA have been other bisphenols.

BPA Substitutes

Bisphenol S (BPS), also called sulfonyldiphenol, and Bisphenol F (BPF), alternatively called bis(4-hydroxyphenyl) methane, are both similar in structure to BPA and two of the most frequent replacements for BPA. All three are symmetrical and have two phenol groups, but whereas BPA has a carbon with two methyl groups joining the phenol groups, BPS has a modified sulfonyl that lacks chlorine and BPF is linked by a methylene group. BPS is used primarily for industrial applications, such as an electroplating solvent and as a constituent of phenolic resin. It is also used as a developer in thermal paper (receipt paper)[16]. BPF is used especially for systems that require increased thickness and durability, such as tank and pipe linings, industrial floors, road, and bridge deck toppings, and structural adhesives. BPF epoxy resins are also used in lacquers, varnishes, liners, plastics, water pipes, dental sealants, and food packaging[16]. Urine samples were collected from 100 American adults without occupational exposure; BPS was found in 78% of these urine samples at concentrations up to 12.3 ng/mL (0.0491μM), while BPF was found in 55% of urine samples at concentrations up to 212 ng/mL (0.605 μM)[17].

Bisphenol S (BPS)

There have been studies conducted on the possible effects of BPS *in vivo* and *in vitro*. For example, a study was conducted by Viñas and Watson[18] to determine if BPS had similar effects to BPA, as an endocrine disruptor. The study examined signaling pathways in rat pituitary cells. They found that BPS disrupts membrane-initiated E_2-induced cell signaling, leading to altered cell proliferation, cell death, and inhibition of prolactin release.

Another study[19] attempted to understand the potential toxic effects of BPS on rat hearts and the underlying mechanism. They found that female rat hearts that were exposed to 10^{-9} M BPS showed an increased heart rate. BPS-exposed hearts showed an increase of arrhythmogenic-triggered activities in female ventricular myocytes and altered Ca^{2+} concentrations. These effects are very similar to those reported for BPA, suggesting that BPS might not be a safer alternative for BPA.

Embryonic zebrafish were exposed to BPS at a concentration of 0.0068 μM, which is 1,000 fold lower than the expected concentration of daily human exposure. Results showed that there was a 240% increase in neurogenesis in the rostral hypothalamus, which is involved in hyperactivity, and a 160% increase in locomotor bursting activity[13]. These results are astounding because the concentration used was very small and it still caused a large disruption in neuronal development. This shows that even a small concentration of BPS found in the environment could affect early development. A recent study on zebrafish larvae[20], demonstrated that exposure to BPS upregulated genes related to thyroid development, such as the PAX8 gene.

Bisphenol F (BPF)

There are fewer studies examining the effect of BPF, as compared to BPS. An *in vivo* and *in vitro* combination of assays examined the estrogenic activity of BPF in

zebrafish-specific assays[21]. The *in vitro* study found that BPF transactivated ß-subtype zebrafish estrogen receptors in zebrafish hepatic reporter cell lines. They further studied the *in vivo* effect of BPF and found that BPF strongly induced vitellogenin synthesis in adult male zebrafish. The authors concluded that BPF shows a similar estrogenic activity to BPA[21].

A study conducted by Higashara *et al.*[22], exposed female rats to 20 mg/kg BPF and results showed decreased body weight accompanied by decreased serum total cholesterol, glucose, and albumin. Another study using pregnant and non-pregnant Sprague-Dawley female rats exposed to BPF found that BPF was excreted mainly in urine and that detectable quantities were found in all tissues, with the largest amount in the liver[23]. Pregnant rats dosed at day 17 of gestation also had BPF residues in the uterus, placenta, amniotic fluid, and fetus. Yamasaki *et al*.[24] performed an immature rat uterotrophic assay with many chemicals, including BPF, and found that BPF did induce uterine growth. BPF was also positive for the estrogen receptor-binding assay, meaning that it could have possible estrogenic activity. Ohtani *et. al*.[25] conducted a study to observe the possible effect BPF could have on the behavior of mice exposed to BPF in the gestational period. The results showed that BPF increased anxiety and depressive states in both male and female mice when compared to the control.

In an ideal situation the replacement for a toxic chemical would be less harmful than the original chemical. However, when these replacements have not been tested properly there is a possibility that the replacement can be more harmful than the original. In addition, as far as our literature search determined, there have been no previous studies on the effects of BPA, BPS, and BPF in combination. Kolatorova *et al.*[26] reviews interactions between bisphenols and paraben, another environmental disruptor. They emphasize the importance of studying the effects of the combinations of endocrine disruptors, of which there is very limited research. In nature, no organism is exposed exclusively to one pollutant or factor, and it is very likely that humans have been exposed to BPA, BPS, and BPF at the same time and to their possible additive or synergistic interactions. Therefore, the purpose of this study is to determine the effects of BPA and alternatives, individually and in combination, on metamorphosis of *Xenopus laevis.*

Materials and Methods

Model System

The model system used was developing *Xenopus laevis* (clawed frog). Amphibians are an excellent model organism that can be used to detect if there is an imbalance in the environment, such as the accumulation of chemicals in an ecosystem, because they live in water as larvae and are vulnerable to chemicals in the water[27]. They have a relatively rapid rate of development and the large number of offspring produced make them an ideal model system. *X. laevis* was chosen because their larvae are transparent, so any internal malformations during development can be observed through the microscope. The development of embryos/tadpoles has been extensively categorized in the Nieuwkoop and Faber stages[28], so that development of the tadpoles in the experiment can be compared to what is

standard. The influence of thyroid hormone (TH) on the metamorphic transformation in *X. laevis* has also been well documented so it is an excellent species to test environmental endocrine disruptors, such as BPS and BPF[29-31].

Animal Care and Maintenance

Fertilized eggs were ordered from *Xenopus1*. The embryos were incubated in glass finger bowls. Twenty-four hour aged tap water was changed three times per week. A 1 mL yeast and aged-water suspension was added to each bowl once every two days. All animals were maintained and experiments were conducted at room temperature.

Preparation of Solutions

Two liters of each solution were prepared prior to obtaining the embryos by dissolving the BPA, BPS, and BPF in aged tap water. All solutions were made in concentrations of µg/mL. After preparation, solutions were stored in glass containers with lids, labeled, dated, and set aside to await the arrival of the specimens. BPA, BPS, and BPF were purchased from Sigma-Aldrich chemical company.

Incubation in Solutions

All specimens were staged according to the Normal Table of Development[28] so they could be incubated at the same stage in all control and experimental groups per trial. Each group contained the same number of specimens. Four trials (see below) were completed over the course of two years.

Trial 1

Trail 1 consisted of 10 specimens per group and lasted 31 days. The specimens were incubated at tailbud stage 26. The experimental groups are 5 µg/mL BPA, 10 µg/mL BPA, 5 µg/mL BPS, 10 µg/mL BPS, 3 µg/mL BPA: 6 µg/mL BPS; 6 µg/mL BPA: 3 µg/mL BPS; 5 µg/mL BPA: 5 µg/mL BPS.

Trial 2

Trial 2 consisted of 20 specimens per group and lasted 27 days. The specimens were incubated at stage 26. The experimental groups are the same as in Trial 1 (above).

Trial 3

Trial 3 consisted of 15 specimens per group and lasted 46 days. The specimens were incubated at a blastula stage (stage 8). In addition to the experimental groups from trial 1 and 2 (above), 10µg/mL BPF, 5µg/mL BPF, and 5µg/mL BPA:5µg/mL BPF were also included.

Trial 4

Trial 4 consisted of 10 specimens per group and lasted 23 days. The specimens were incubated at neurula stage 16. The experimental groups were 10 µg/mL BPS, 5 µg/mL BPS, 10 µg/mL BPF, 5 µg/mL BPF, 5 µg/mL BPA: 5 µg/mL BPS, 5 µg/mL BPS: 5 µg/mL BPF, 5 µg/mL BPA: 5 µg/mL BPF, and 5 µg/mL BPA: 5 µg/mL BPS: 5 µg/mL BPF.

Collection and Analysis of Data

As the experiment progressed, photographs and measurements were taken daily to compare the groups. The

specimens were examined specifically for mortality and any visible malformations. The total body length and tail length were measured for the extent of metamorphosis and the tadpoles were also staged according to Nieuwkoop and Faber[28]. Any notable differences in overall developmental rate were also noted by comparing the stages of experimental groups to the control. The survival rate was illustrated by constructing a survivorship curve.

Most of the photos of the specimens were taken using the EOS utility with a mounted Canon camera model Rebel TS6. In addition, the LEICA EZ4 dissecting microscope was used to view the specimens for staging purposes. Microsoft Excel was used to graph all the data collected. In the Results and Discussion sections, assume "μg/mL" follows the numbers describing the groups.

Results

Trial 1

In Trial 1, a higher incidence of the 'bubble head' malformation was observed, wherein the tadpole's head swelled up in a clear bubble and its spine curled (Figure 1). Bubbles were also seen around the eyes and in some, there was visible deformation of the intestines. These specimens all died prior to the end of the trial. Malformations were observed in groups 3BPS: 6BPA and 5BPS. The only groups that had survivors at the end of the trial were the control, 10BPA, 10BPS, and 6BPA: 3BPS groups. Groups 10BPA and 6BPA: 3BPS had only 1 test specimen by the end of the trial with 10BPA having the steepest mortality rate (Figure 2). Another interesting observation was that the 10BPS group had survivors to the end of the experiment, whereas 5BPS did not. There were no differences in Nieuwkoop and Faber stages (Figure 3) and lengths (Figure 4) among the groups in trial 1.

Trial 2

In trial 2, the 10BPA group was the only group to exhibit 100% mortality in this trial; all other groups survived to the end of the trial. Groups 5BPA and 5BPA: 5BPS had only 1 surviving test specimen while groups 5BPS and 6BPA: 3BPS had 8-9 surviving test specimens. Groups 10BPS and 3BPA: 6BPS had 19-20 surviving test specimens, which were the highest survival rates in the trial (Figure 5). There were no observable differences in the Nieuwkoop and Faber stages (Figure 6). There was a difference in lengths between the control and the other groups. The control group had an average length of 1.65 cm by the end of the trial while the other surviving groups had an average length above 2 cm. Group 6BPA: 3BPS had the longest average length with 2.55 cm while group 5BPA had the shortest average length among the experimental groups with 2.1 cm (Figure 7). Bubble malformations were also observed in this trial: groups 5BPA and 5BPA: 5BPS (Figure 8).

Trial 3

On Day 2 of the third trial, bubble malformations (Figure 9) were observed in certain groups. The test specimens were in the early tailbud stage (stages 26-27) when this malformation was observed. The bubble malformations were usually located on the body of the tailbud where it swelled up in a clear bubble and its spine curled. Specimens that showed this malformation died by the

Table 1: Incubation in Solutions by Trial

Trial	Control	5 BPA	10 BPA	5 BPS	10 BPS	5 BPF	10 BPF	3BPA: 6BPS	6BPA: 3BPS	5BPA: 5BPS	5BPS: 5BPF	5BPA: 5BPF	5BPA: 5BPS: 5BPF
1	X	X	X	X	X			X	X	X			
2	X	X	X	X	X			X	X	X			
3	X	X	X	X	X	X	X	X	X	X		X	
4	X				X	X	X			X	X	X	X

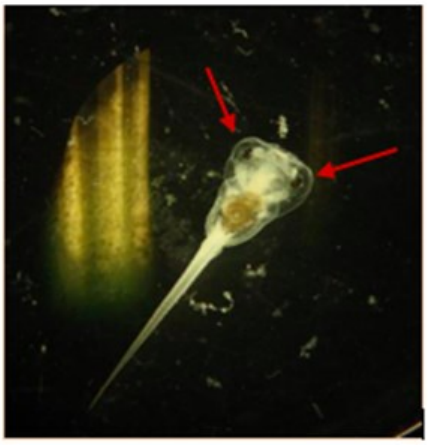

Figure 1: Malformed tadpole in 3 BPS: 6BPA

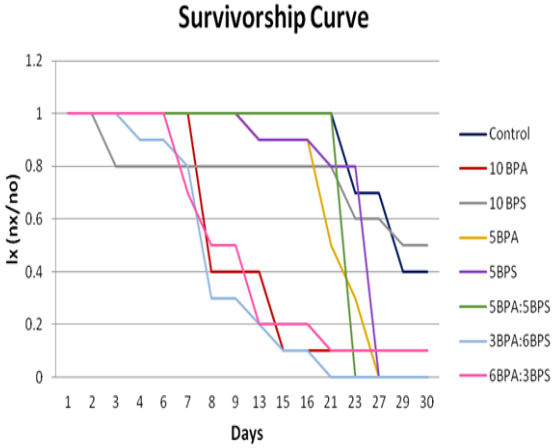

Figure 2: Survivorship Curve (l_x vs. Days)

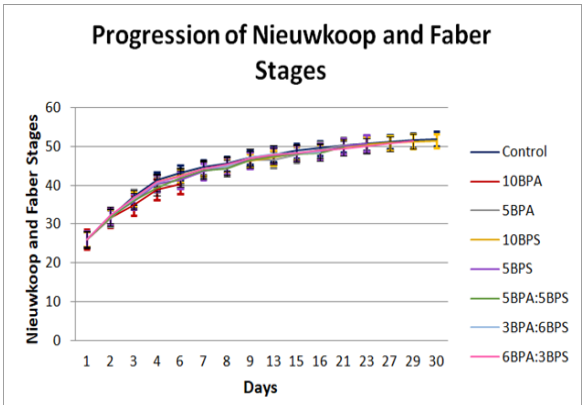

Figure 3: Progression of Nieuwkoop and Faber Stages of *X. laevis.* Error bars indicate ±1 SE.

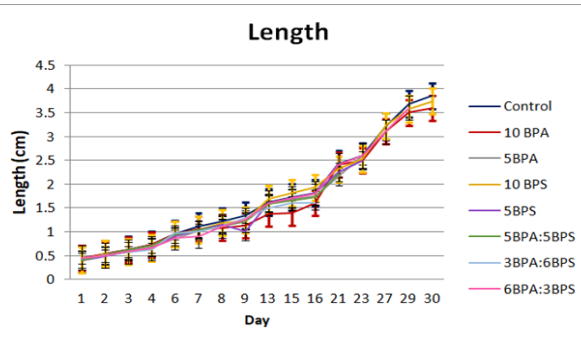

Figure 4: Average Lengths (cm vs. Days) of *X. laevis.* Error bars indicate ±1 SE.

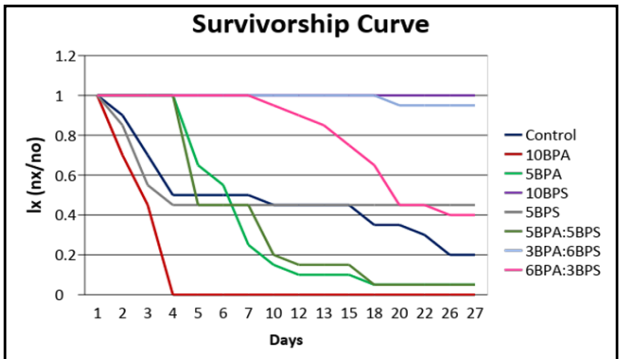

Figure 5: Survivorship Curve (l_x vs. Days)

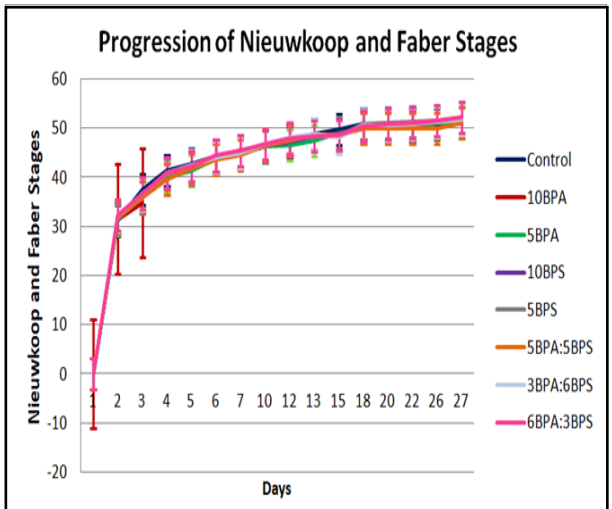

Figure 6: Progression of Nieuwkoop and Faber Stages of *X. laevis.* Error bars indicate ±1 SE.

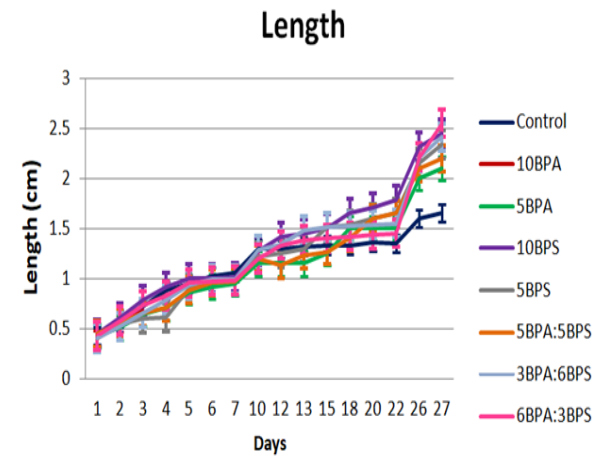

Figure 7: Average Lengths (cm vs. Days) of *X. laevis.* Error bars indicate ±1 SE.

next day. Test groups that showed this malformation were 5BPA, 10BPS, 10BPF, and 6BPA: 3BPS. None in the control group showed these malformations.

The survivorship curve (Figure 10) shows that the only remaining groups to survive until the last day of the experiment were 10BPS, 3BPA: 6BPS, 6BPA: 3BPS, and the control group; there were only 1-2 survivors in each group, however. The 10BPA, 10BPF, and 5BPF groups had died by day 4 of trial 1. The 5BPA and 5BPA: 5BPS groups died by day 9 of the trial. The staging of the tadpoles (Figure 11) showed that the surviving four test groups developed at a comparable rate. All groups were between stages 53-55 on the last day of the trial. The standard error bars showed that there was no difference among the groups. The average lengths (Figure 12) show a slight difference among the surviving four groups. Standard error bars of ± 1 were added to the graph to confirm the differences among the groups. There was a difference among the 3BPA: 6BPS,

6BPA: 3BPS and the control and 10BPS groups, with the control and 10BPS groups being ~1 cm smaller than the 3BPA: 6BPS and 6BPA: 3BPS groups.

Trial 4

In trial 4, the bubble malformations were observed again, however the bubbles were not located on the body of the tadpole but in the head region (Figure 13). The tadpoles that exhibited this malformation were also at a later stage, stages 39-41. The malformations were seen in 5BPF and 5BPA: 5BPF. Other malformations were also observed. In the 10BPS group, a tadpole, at stage 46, had a bent tail. Another tail malformation was seen in 5BPA: 5BPS, where the tail was shaped differently. The control group did not show these malformations.

Figure 14 shows information on mortality in trial 4. Groups 5BPF: 5BPA, 10BPF, and 5BPF died within the first ten days, with 5BPF: 5BPA and 10BPF having the fastest mortality rate. Within the next 10 days, groups 10BPS, 5BPS, and 5BPA: 5BPS: 5BPF died as well. The only remaining groups were the control, 5BPS: 5BPF, and 5BPA: 5BPS groups. The 5BPA: 5BPS group had the largest surviving number of tadpoles. The staging of the tadpoles (Figure 15) showed no observable differences. All tadpoles were at stages 48-51 by the end of the trial. The average lengths of the tadpoles did show a difference however. The groups 5BPA: 5BPS and the control were ~2 cm larger than 5BPS; 5BPF.

Discussion

The results of our study indicate that BPS and BPF do have potentially adverse effects on *X. laevis*. In comparing the survivorship curves the control groups had a lower mortality rate than the 10BPF and 10BPA groups did. Based on the results of this study, BPF may have a similar level of toxicity as BPA since 10BPA and 10BPF killed the specimens within the first 2 days.

The combination groups showed interesting results as well. In trial 3, the combinations of 3BPA: 6BPS and 6BPA: 3BPS were larger in size when compared to the control group. In trial 4, the combination of 5BPF: 5BPS was smaller in size when compared to the control. This could mean that different combinations of BPA, BPS, and BPF have different effects on the tadpoles than they do separately. This is an important finding, as there has not been a study on the effects of the combinations of bisphenols. In addition, this model system could be used to gain information on whether BPS and BPF are obesogens.

One of the most significant results of this study is the observation of the malformations in the experimental groups. These malformations were seen in BPA, BPF, and BPS individually and in combination. The bubble malformation is an especially unique malformation that was observed in all four trials. In trial 3, these malformations only appeared on the body of the tadpoles, while in trials 1, 2 and 4 the malformations were isolated to the head region. This difference in the location of the malformation could be due to the earlier- stage incubation of the test specimens in trial 3.

A study done by Imaoka *et al.*[11] also showed head malformations, although they were of a different kind than the malformations seen in our study. Imaoka *et al*.[11] treated *X. laevis* embryos with BPA at stage 10.5 (early gastrula). They exhibited a shortened distance between the eyes at stage 35. The embryos in our study, specifically trial 4, were incubated at stage 16 and developed a bubble in the head region at stage 39-41. These malformations, although both in the head region, are different; this could perhaps be due to the different incubation times. Likewise, the study done by Imaoka *et. al*.[11] had only exposed the embryos to BPA, while our study exposed the embryos to BPA, BPS, and BPF. The groups showing the head malformations in our experiment were not the individual BPA groups, but the BPA and BPS combination group and the BPF group.

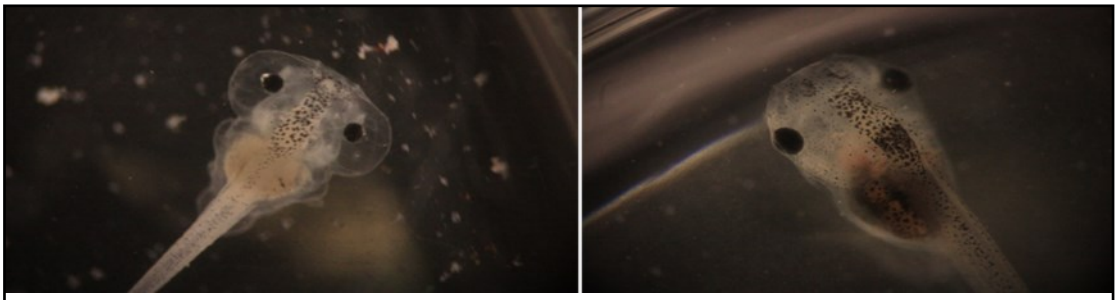

Figure 8: Malformed head of tadpole in 5BPA (left) compared to normal tadpole (right)

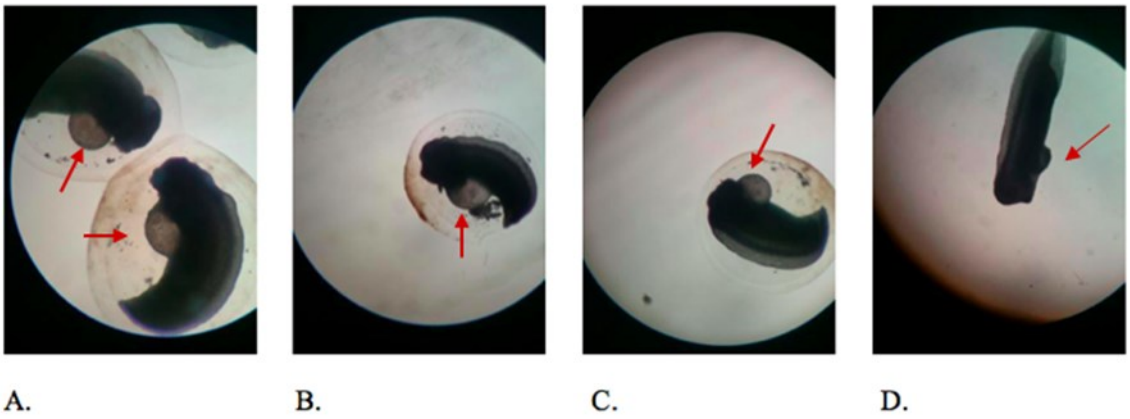

Figure 9: A. Malformed tailbud in 5BPA; B. Malformed tailbud in 6BPA: 3BPS; C. Malformed tailbud in 10BPF; D. Malformed tailbud in 10BPS.

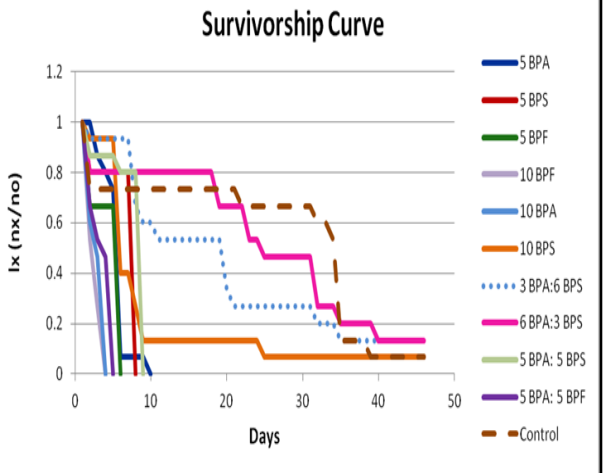

Figure 10: Survivorship Curve (l_x vs. Days)

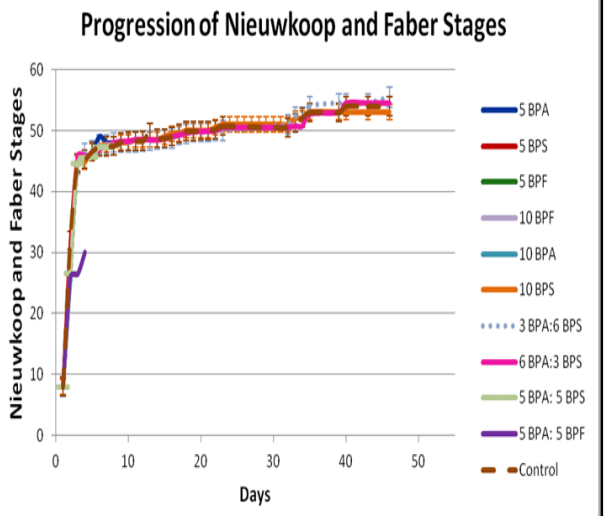

Figure 11: Progression of Nieuwkoop and Faber Stages of *X. laevis.* Error bars indicate ±1 SE.

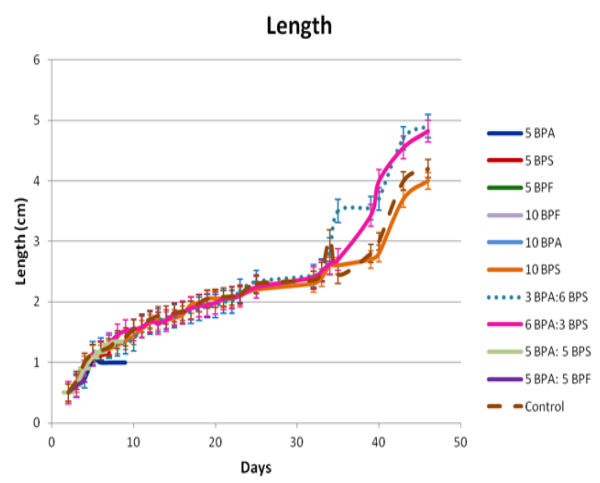

Figure 12: Average Lengths (cm vs. Days) of *X. laevis.* Error bars indicate ±1 SE.

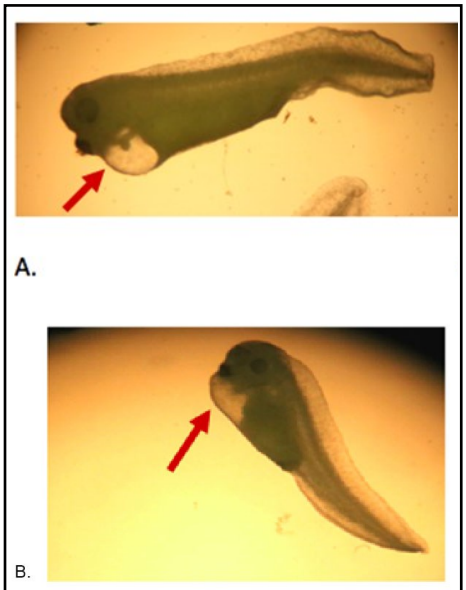

Figure 13: A. Bubble malformation in 5BPF; B. Bubble malformation in 5BPA: 5BPF.

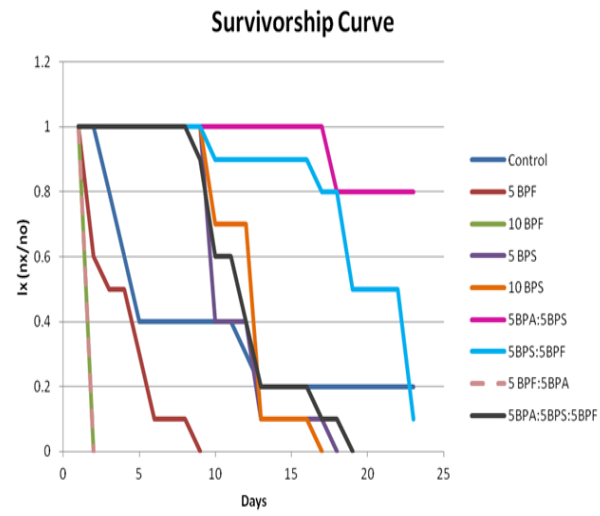

Figure 14: Survivorship Curve (l_x vs. Days).

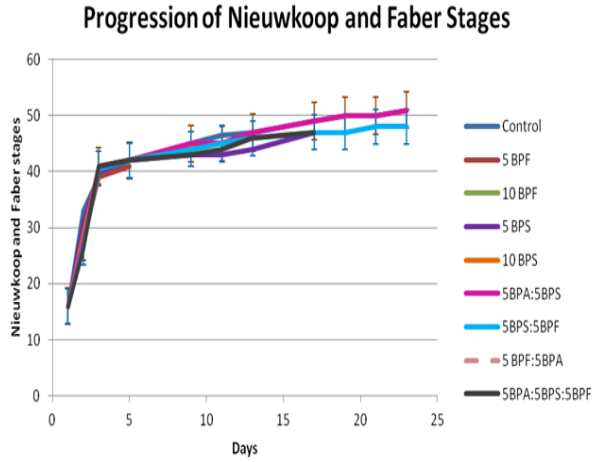

Figure 15: Progression of Nieuwkoop and Faber Stages of *X. laevis*. Error bars indicate ±1 SE.

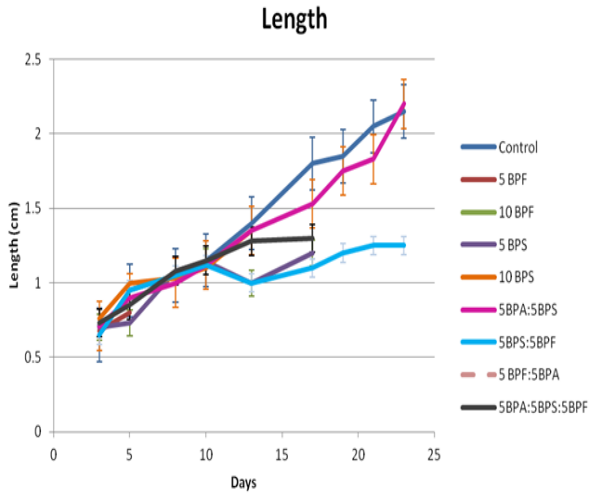

Figure 16: Average Lengths (cm vs. Days) of *X. laevis*. Error bars indicate ±1 SE.

This perhaps means that although the exact mechanism is not known, the effects of BPF could be similar to BPA. The study by Imaoka[11] found that BPA had decreased the expression of the Pax-6 gene, a gene that regulates the morphogenesis of the eyes. Similarly, BPF might interfere with the expression of a gene that regulates the formation of the head region.

In trials 1 and 2, the specimens incubated in lower concentrations of BPA and BPS exhibited more malformations than high-dosed specimens. Therefore, this indicates a need to review regulations to look more carefully at low- dose effects.

Future areas of study could focus on the practical applications. Yamamoto and Yasuhara[32] studied the leaching of BPA from plastic wastes in water. It would be interesting to test the effect of water from leaching of bisphenols of plastics on organisms. The water with leached bisphenols could be incubated with later-stage tadpoles to see if the plastic-containing water affects the metamorphosis of the tadpole.

While it is already known that BPA is detrimental to humans, BPS and BPF in combination and individually do have harmful effects on *X. laevis*. It is not certain, but it seems likely that they would affect humans, and they are not safe alternatives to BPA. Additionally, future studies are needed to investigate the effects of the combinations, or mixtures, of the bisphenols as environmental endocrine disruptors.

Acknowledgments

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MACUB 2018 Conference

Poster Presentation Award Winners

COMMUNITY COLLEGE

Biochemistry, Biophysics and Biotechnology

First Place

Imidazole as a Novel and Robust Gold Binding Group at STM-BJ Method
**Shanelle Smith, Xiaofang Megan Yu, Tianren Fu, Jiayi Xue,
Latha Venkataraman and Sujun Wei
Queensborough Community College and Columbia University**

Second Place

Effect of Single Walled Carbon Nanotubes on Breast Cancer Cell Migration
**Yingxian Tan, Tobore Edema, Sunil Dehipawala,
Tirandai Hemraj-Benny and Regina Sullivan
Queensborough Community College**

Third Place

Osteoclastic Signal transduction and activator of transcription-3 Enhances the Migration of Osteoblastic cell line MC3T3
**Miguel Fernandez, Stephanie Lochan and Andrew V. Nguyen
Queensborough Community College**

Developmental Biology and Genetics

First Place

American Horseshoe Crabs (*Limulus polyphemus*) Juvenile Population Growth on Plumb Beach, Jamaica Bay, NY
**Kera Mansfield and Christina Colon
Kingsborough Community College**

Environmental Biology and Ecology

First Place

Comparison of the Response of Microglia and Primary Murine Macrophages Upon Exposure to Pesticides
Amirabbas Maghsoudi, Mohammad Javdan and Zahra Zakeri
Queensborough Community College and Queens College

Second Place

Direct PCR Detection, Cloning, and Characterization of 16S rRNA from Archaea Species in New Jersey Soils
Stephanie Perez, Arianna Pinto, Sibora Peca and Luis Jimenez
Bergen Community College

Third Place

Investigating the Population Density and Developmental Biology of Juvenile American Horseshoe Crabs (Limulus polyphemus) at Plumb Beach, Brooklyn, New York
Akankaye Waul and Christina P. Colon
Kingsborough Community College

Microbiology and Immunology

First Place

Efficacy of Infraslow Fluctuation Training (ISF) in the Attenuation of Anxiety, Utilizing Brainmaster Discovery Quantitative Electroencephalogram (qEEG) and Self-Report
Adelejda Turku, Jacqui Gonzalez, Alexander Thomas, Hynbin Kang, Sadik Erisen and Coleen DiLauro
Bergen Community College

Second Place

Beta-barrel Assembly Pathway and Quality Control in Gram-negative Bacteria
Lindsey Njanja, Matthew Doyle and Harris Bernstein
Bergen Community College

Third Place

Folk Remedies As Antibacterial Agents
Claudia Melo and Catarina Mata
Borough of Manhattan Community College

Physiology, Neuroscience and Clinical

First Place

The Role of Dectin-1 Receptor in LPS-Induced Phagocytosis Stimulation in Microglial Cells

Darlene Urena, A. Lucia Fuentes and Maria Entezari
LaGuardia Community College

Second Place

Scavenger and C-type Lectin Receptors Mediate Phagocytosis of Zymosan in LPS and HMGB1 Stimulated Microglia

Gian Izquierdo, Maria Entezari and A. Lucia Fuentes
LaGuardia Community College

Third Place

Pharmacological Inhibition of STAT6 Suppresses Viability and Induces Cell Death of Hodgkin's Lymphoma, *In Vitro*

Jessica Perng[1], Bo Zhang[2], Stephen Redenti[2] and [1]Rajendra Gharbaran
[1]Bronx Community College/CUNY and [2]Lehman College/CUNY

MACUB 2018 Conference

Poster Presentation Award Winners

SENIOR COLLEGE

Biochemistry, Biophysics and Biotechnology

First Place

Inhibitor of CBP Histone Acetyltransferase Downregulates p53 Activation- Potential to Prevent Toxicity from Chemotherapy
Loveth Igbineweka, Vimal Arora, Mihaly Mezei , Michael Ohlmeyer and Shiraz Mujtaba,
Medgar Evers College and Icahn School of Medicine at Mount Sinai

Second Place

TFIIIB Alterations in Gliomas.
Paul Espiritu, Keyla Payano and Laura Schramm
St. John's University

Third Place

Effect of K197E Mutation of Protein Tyrosine Phosphatase 1B in Epidermal Growth Factor Receptor Signaling
Melody Young and Youngjoo Kim
SUNY College at Old Westbury

Developmental Biology and Genetics

First Place

Functional Validation of *Drosophila* Blood Cell Development Genes
Brian Tang, Henry Wu, Harmeet Kaur Rebecca Spokony
Baruch College, CUNY

Second Place

Spatial Genomic Analysis of the Axolotl Wound Epithelium via HCR FISH
Breanna Chandler, Kofi Acheampong, Alex Lovely and James Monaghan
St. Francis College

Third Place
IFN-γ Regulation of Canonical TLR Pathways
Gabriele D'Orsi and Emily Calderon
Molloy College

Environmental Biology and Ecology

First Place

Detection of Microcystins in the Tissues of Freshwater Shrimp Bought From a Fish Market Near Lake Tai
Ronojoy P. Hem[1], Kristen N. Slodysko[2] and Gregory L. Boyer[2]
[1]St. Joseph's College - New York and [2]State University of New York College of Environmental Science And Forestry

Second Place

Optimization Methods for Cyanobacterial Detection, Identification and Seasonal Monitoring in Recreational Water
Christian J. Rios-Ruiz and Tinchun Chu
Seton Hall University

Third Place

Identifying Cyanobacterial Communities in Barnegat Bay
Roksana Rahman, Christian J. Rios-Ruiz, Yan Wang, Paul (Jyung) Yoon and Tinchun Chu
Seton Hall University

Microbiology and Immunology

First Place

There are Bacteriophages in Your Sponge
Linesha Davis, Lovejit Kaur, Brianna Weiss and Bryan Gibb
New York Institute of Technology

Second Place

Isolating Hydrocarbonoclastic Microorganisms from Newtown Creek
Valeria Cevallos and Joby Jacob
Queens College

Third Place

Bioinformatic Analysis of Heavy Metal Stress Response in Cyanobacteria.
Jose L. Perez and Tinchun Chu
Seton Hall University

MACUB 2018 Conference

Poster Presentation Award Winners

Physiology, Neuroscience and Clinical

First Place

The Role of Fatty Acid Oxidation in Astroglial Xenobiotic Detoxification
Logan Brown[1], Moises Rodriguez[2], Jordan Rose[3] and Rodrigo Franco[3]
[1]Spelman College, [2]Medgar Evers College and [3]University of Nebraska-Lincoln

Second Place

Immunohistofluorescence Study of the Actions of Manganese on the β-Arrestin and Gβγ Mechanisms of Dopamine D2 Signal Transduction Pathway in *Crassostrea virginica*
Mohamed Eid[1], Rafael Santos[2], Margaret A. Carroll[1] and Edward J. Catapane[1]
[1]Medgar Evers College and [2]Kingsbrough Community College

Third Place

Is Ironman Invincible?; Risk of Stress During Strenuous Exercise
Frank Cristallo III, Emily Cruz, Rachel Julian and Kristen Lacey
Molloy College

Third Place
Going Green in the Lab: Extent of green practices in academic labs in NYC
Marcus Banks, Davida Smyth, Katayoun Chamany
The New School

MACUB 2018 Conference

Poster Presentation Award Winners

GRADUATE SCHOOL

First Place

Assessment of Dead Wood Fungi Biodiversity in Urban Parks and Natural Reserves Across New Jersey
Shazneka Blue, Abdurrahim Vardar, Christopher Zambell and Maria Shumskaya
Nathan Weiss Graduate School, Kean University

Second Place

Characterizing HPV16 Induced Cytoskeleton Rearrangement Events Mediated by Downstream Signaling Remodeling As a Mode of Viral Entry
Alyssa Biondo, Snezana Stankovic and , Patricio I. Meneses
Fordham University

Third Place

Going Green in the Lab: Extent of Green Practices in Academic Labs in NYC
Marcus Banks, Davida Smyth and Katayoun Chamany
The New School


Conference Highlights

Microbial Diversity in Urban Environments: Concern for Antibiotic Resistance. Ality Aghedo and Mangala Tawde, York College, Jamaica, NY and Queensborough Community College, Bayside, NY.

Antibiotic resistance is a serious concern in the field of medicine as recent increase in antibiotic-resistant microbes can threaten infectious disease treatments. Overuse of antibiotics may lead to microbial resistance as bacteria exposed to various chemicals mutate enabling them to reduce or negate the effectiveness of antimicrobial drugs that are designed to kill them. Overuse of antimicrobial drugs in animal feed, crops and plants lead to increased concentration of antibiotics in our waters and soil. As bacteria mutate, they acquire new genetic elements contributing to antibiotic resistance. Soil being a large reservoir of environmental microbes, these elements find their way in soil bacteria. Therefore, we decided to identify the bacteria found in New York City's various soil environments and to determine their sensitivity (or resistance) to commonly used antibiotics. We identified bacterial isolates by Biolog system and tested their susceptibility to various antibiotics using Kirby-Baur method. Fortunately most of the bacteria isolated from different soil samples exhibited sensitivity to most of the antibiotics; however high percentage of isolates were found to be resistant to Penicillin. Resistance to Penicillin is plausible since Penicillin is one of the most widely used antibiotic. Awareness about microbial antibiotic resistance amongst general public is warranted.

Nervous System Defects Result From Transient Low Level Copper Exposure In The Embryonic Zebrafish. Amy Alfy, Gwendolyn Roberts, Joeseph Pagnotta and Alison L. Dell, St. Francis College, Brooklyn, NY.

To understand the cell signaling events that translate exposure to environmental pollutants into birth defects – we have examined the effect of transient exposure to copper ions on neuronal development. We previously reported cardiac and behavioral deficits in zebrafish embryos exposed to low levels of copper. We hypothesized that the neuronal effects could stem from cell death, or could result from misrouting of axons. Using lipophilic dyes to trace the axons of the retinal ganglion cells revealed that these neurons sometimes misroute on their way across the midline –never seen in controls. To test the hypothesis that copper might be toxic to retinal and sensory axons, cell survival assays were performed. Propidium iodide staining was used to assess numbers of neurons in the retina. Isl2b:GFP+ cells in the spinal cord were counted to assess the survival of sensory neurons in spinal cord. These results test the hypothesis that the behavioral deficits we observe are related to axonal guidance, not cell survival.

Isolation of Actinomycetes from Plumb Beach Sediment Samples. Nikita Alim, Saraf Nabiha and Joan Petersen, Queensborough Community College, Bayside, NY.

Actinomycetes are prokaryotes which are known for their useful secondary metabolites that may have antibacterial, antifungal, antiparasitic, and antitumor properties. Although most actinomycetes have been isolated from soils, a few recent studies have focused on culturing actinomycetes from marine sediments. The purpose of our research is to isolate actinomycetes from sediment samples collected at Plumb Beach, NY and to determine whether or not these isolates are adapted to saltwater environments. We diluted marine sediment samples onto actinomycete isolation agar prepared with saltwater and freshwater. The number of unique colonies that grew on each type of media was quantified. Colonies were then transferred and grown in pure culture. Freshwater isolates were tested for their ability to grow in saltwater agar and vice versa. To date, we have isolated a total of 43 unique actinomycetes-32 of these were isolated on freshwater agar and 11 were isolated from saltwater agar. From these 43 isolates, 36 grew on both saltwater and freshwater media. Out of these 36 isolates, 7 of them have different phenotypes. Of the 7 isolates, 4 of the isolates only grew on freshwater media while 3 of the isolates only grew on saltwater media. We also inoculated plates with plugs from the unique phenotypic isolates and tested them for their ability to inhibit the growth of *Escherichia coli* and *Staphylococcus aureus.* Six isolates created biochemical compounds that inhibit the growth of *S. aureus*: two of these six isolates also inhibited the growth of *E. coli.* We will continue testing the two actinomycete isolates that inhibited both types of bacteria against additional bacterial species, and further characterize them using metabolic tests and 16s rDNA sequencing.

IFN-γ Differentially Regulates Expression of Genes for Components of Opsonized and Non-opsonized Phagocytic Pathways in Macrophage Cells. James Almodovar, I'Nyaah Burrell, Diego Guaman, Saad Mian and Jodi F. Evans, Molloy College, Rockville Centre, NY.

Often while fighting a viral infection a person's susceptibility to a bacterial infection increases. During a viral infection interferon-γ (IFNγ), an inflammatory cytokine, is released by activated lymphocytes of the adaptive immunity. IFNγ is an activating signal that triggers macrophage cell destruction of opsonized pathogenic microbes already present in the phagolysosome. However IFNγ can also suppress macrophage phagocytosis of non-opsonized particles compromising the innate immunity and its ability to fight a

concomitant bacterial infection. Based on previous work, we hypothesized that IFNγ will suppress macrophage phagocytosis of several non-opsonized microbial particles and that it does so through regulating expression of genes that code for proteins involved in phagocytic activity. Spleen-derived murine macrophage cells (SpMΦ) were treated with IFNγ and then exposed to pH-rhodo conjugated *E. Coli, S. Aureus* or zymosan particles. Fluorescent intensity was measured over a 1 hr period and used as a reflection of phagocytic activity. IFNγ significantly suppressed phagocytosis of all three microbial particles. To begin to understand the mechanism behind the suppression, IFNγ regulation of genes coding for proteins involved in phagocytosis were then explored using gene array panels. Our results demonstrate that genes involved Rac1 and Rho regulation of cytoskeletal changes during phagocytosis were not affected. However, genes for components of opsonized pathways were upregulated such as C-reactive protein (4.27 fold). While genes for key components of non-opsonized pathways were down-regulated such as macrophage receptor with collagenous structure (-1.54 fold). These data contribute to our current understanding of the interface between the cells of the innate and adaptive immunity and have the potential to lead to prophylactic treatments designed to prevent secondary bacterial infections during a primary viral infection. This work was supported by Department of Biology Chemistry and Environmental Studies.

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

Bacteria are prevalent in the environment and can have an effect on human health, as they contribute to disease. Over time, there has been high antibiotic overuse, which contributes to antibiotic resistance. In order to attack bacteria that may now be resistant to antibiotics, new targets need to be considered. One potential new target includes the bacterial cytoskeleton; one system unique to bacteria are the bactofilins. BacM is one of the four paralogs of bactofilins encoded in *Myxococcus xanthus*, a bacteria used as a model organism for studying social interactions, biofilm formation, and motility. BacM contributes to the proper rod-shaped morphology of *M. xanthus*. BacM has been observed as a large form (BacM-L) and a small form (BacM-S). They differ at the N-termini, where BacM-S lacks ~27 amino acids. Two hypotheses regarding the generation of these isoforms of BacM were considered. The first hypothesis suggested BacM-L is synthesized as a precursor protein that is cleaved by a protease at the sites of cytoskeleton elongation. The second hypothesis suggested that BacM-L and BacM-S are generated through alternative start site selection by the ribosome. These hypotheses were tested by engineering a plasmid containing bacM with its 5' untranslated sequence; point mutations were introduced using PCR-directed mutagenesis. Mutants were made to abolish the start codon (M1L), introduce a frameshift after the start codon (K8 frameshift), abolish the putative second start codon (V24L), and abolish a putative internal ribosome binding sequence using silent mutations (?RBS2). When observed by immunoblot, mutants M1L and K8 frameshift expressed only BacM-S, whereas mutants V24L and ?RBS2 expressed only BacM-L. These results are consistent with the second hypothesis, that BacM-L and BacM-S are generated through alternative start site selection, and falsify the first hypothesis of proteolysis.

Isolation of Marine Bacteria with Broad Range Antimicrobial Activity. Daniel Antunes, Charlie Encalada, Rameen Shah and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

Scientists around the world are in search of new antibacterial and antibiofilm treatments to combat the steady rise of nosocomial infections caused by antibiotic resistant pathogenic bacteria. The purpose of our research is to screen and characterize unknown bacteria isolated from the surrounding waters of the Jersey City area for potential production of natural antimicrobial compounds. Streaks and Cell free extracts from the unknown bacteria were tested for antibacterial property against different strains of *Staphylococcus aureus*, *S. epidermidis*, *Enterococcus faecalis*, *Pseudomonas aeruginosa*, and *Escherichia coli*. Ten out of more than a hundred unknown extracts tested have a strong antibacterial effect on gram-positive bacteria. Unknown bacteria with active extract were tested with gram staining, anaerobic growth, catalase, and hemolysis. Further studies will be conducted to better characterize the bacteria and the active compound in the cell free extract.

Nitroxide's Protective Effect on Myoglobin Catalytic Cycle in Oxidative Environment. Ike Ariza, Naomi Shohet, Liron Fedida, Dylan Xue, Jonathan Shadan, Jay Woo, Jorge Ramos and Uri Samuni, Queens College, Flushing NY.

Myoglobin (Mb), one of the main heme proteins present in the body, is crucial for oxygen storage and supply to the tissue. Surprisingly under conditions of oxidative stress, such as during inflammation, Mb is capable of acting as a catalyst of redox reactions with important implications for the mechanism and propagation of oxidative damage. However, overtime, the protein itself can undergo structural degradation and the catalytic cycle is broken. We studied the catalytic cycle of Mb in the disproportionation reaction of hydrogen peroxide under different experimental conditions, varying [Mb], [H2O2] and pH. We used UV/vis spectroscopy to follow the oxidation state and concentration of Mb as it shuttles between the met and ferryl forms and to determine the rate of the protein's degradation. We employed colorimetric assay and oximetry to follow the concomitant rates of hydrogen peroxide depletion and oxygen evolution. Further insight

into the protein's degradation mechanism and a possible approach for preventing the protein's degradation was explored by investigating the effects of Nitroxides, a class of potent antioxidants. Our data yielded the corresponding rates of Mb degradation and hydrogen peroxide depletion and allowed to determine the number of catalytic cycles a Mb molecule can go through until it undergoes degradation. Furthermore our results show a clear protective effect of the nitroxide (TEMPOL), essentially eliminating Mb's degradation. This work was supported by the PSC-CUNY Research Award Program.

Going Green in the Lab: Extent of Green Practices in Academic Labs. Marcus Banks, Katayoun Chamany and Davida Smyth, The New School, New York, NY.

Each year, approximately 300 million tons of petroleum-based plastics are manufactured. Their production and disposal damage ecosystems and contribute to climate change. There is limited data on the contribution of academic research and teaching labs for this problem. Precisely because of the following reasons, research in this area is needed: 1) many different types of plastics are used 2) many cannot be recycled due to biosafety regulations 3) most often disposal occurs after a single use. Data from the University of Exeter in the UK revealed that 280 of their bench scientists generated about 267 tonnes of plastic waste in 2014. At the New School, the University Labs are housed in a LEED-certified building dedicated to being as sustainable as possible. In our teaching labs, we reuse pipette tips in some of our workshops (that do not involve pathogens), we use glassware when possible instead of plastic, we use Millipore drainage water for soaking and cleaning glassware, we use microfiber towels instead of paper towels for cleaning and drying hands, and we ensure equipment like ice machines, incubators, when not in use are switched off. In Fall 2018, we established our new BSL2 laboratory. BSL2 laboratories pose unique challenges for sustainability due to biohazardous waste generation. Our project is focused on determining what we can do to improve sustainability in our labs and, in particular, in the BSL2 space. To this end, we present data on the recycling and sustainability habits of academic and research science labs. This data will be used to develop and distribute easy-to-follow, downloadable sustainability guides. So far, the reporting institutions account for over 350 biology and chemistry lab sections annually. 71% of institutions (n=7) reported being aware of packaging material ship-back programs, while only 43% of the institutions reported they participate in these ship-back programs. Eighty six% of universities or colleges were either unsure or do not have decontamination protocols for non-toxic, uncontaminated, recyclable glass and plastic. Zero institutions reported recycling any gloves used in academic or research settings.

Project Feeder Watch at Saint Peter's: How Four Years Have Flown By. Alaa Barbour, Sara Gonzalez, Busayo Adewale, Gabriela Mosqueda, Brittanie Fils, Sherane Raymond, Alexis O'Callahan, Vasilios Orologas, Brandy Garrett Kluthe and Katherine Wydner, Saint Peter's University, Jersey City, NJ.

We report results for four years of Project FeederWatch (PFW) at Saint Peter's University, with an emphasis on our most recent season. For 22 weeks between November and April, suet and birdseed were provided within a defined area on the Saint Peter's campus (Jersey City, NJ). Following a protocol established by the Cornell Lab of Ornithology, data were collected on species of birds, highest number of each species, and environmental factors such as weather conditions and snow cover. Fourteen species were identified this season 2017-18, bringing total species observed over four years to eighteen. Five species have been present every winter. Gregarious house sparrows (*Passer domesticus*) dominate the feeder, while mourning doves (*Zanaida macroura*) are second in making the most use of supplemental feeding. Due to a fungal rust last summer, hawthorn trees within our site failed to produce berries; as a result, robins (*Turdus migratorius*) were scarce and mockingbirds (*Mimus polyglottos*) less common in the winter of 2017-18. Starlings (*Sturnus vulgaris*) remain a consistent presence every winter. New species reported in 2017-18 include brown-headed cowbird (*Molothrus ater*), yellow-bellied sapsucker (*Sphyrapicus varius*), and American kestrel (*Falco sparverius*). A kestrel was observed eating a small bird on the roof of a building.

Role of Gßγ G Protein Subunit in the Dopamine D2 Signaling Pathway on Ciliary Activity of Gill Lateral Cells in *Crassostrea virginica*. Kameca Baxter[1], Margaret A. Carroll[2] and Edward J. Catapane[2], [1]Kingsbrough Community College and [2] Medgar Evers College, Brooklyn, NY.

Gill lateral cell (GLC) cilia of *Crassostrea virginica* are controlled by serotonin-dopamine innervations. Dopamine slow down, serotonin increases GLC cilia beating. GLC post-synaptic dopamine receptors are D2 type (D2R). D2R signaling pathway inhibits adenylyl cyclase and splits G protein into Gßγ and Gai/o. Gßγ activates PLC (phospholipase C). Gßγ has not been well studied in bivalves. We hypothesize Gßγ is involved in slowing down GLC cilia beating rates. We conducted acute experiments testing Gßγ activators and inhibitors, on excised gill. GLC cilia beating was measured by stroboscopic microscopy. Dopamine (10^{-6} - 10^{-3}M) caused a dose-dependent decrease of beating. Applying guanosine 5'-O-(3-thiotriphosphate) (GTP), a Gßγ activator, was slightly inhibitory over the range of 10^{-7} - 10^{-3}M. Adding dopamine before GTP did not alter GTP effects. The Gßγ inhibitor gallein increased GLC cilia beating. The study shows Gßγ play a role in GLC cilia beating. Activating Gßγ activates PLC, causing cilio-inhibition. Inhibiting Gßγ increased cilia beating. It appears the PLC path contributes to cilio-

inhibition. This study provides new knowledge of the actions of Gßγ in the D2R pathway in bivalve gill. Because the D2R pathway is involved in actions of antidepressants, neuroleptics, drugs of abuse and implicated in neuropsychiatric and neurodegenerative disorders, further investigations of the physiological role of D2R using this gill system should be helpful to understand the D2R signaling pathway. This work was supported grants NIGMS-2R25GM06003, NIH-K12GM093854-07A1 and PSC-CUNY -604060048.

Examining Environmental isolates of *Staphylococcus aureus* using loop mediated (LAMP) amplification. Oscar Bermudes, Diana Mata, Gaozhen Li, Miguel Fernandez and Andrew Nguyen, Queensborough Community College, Bayside, NY.

Antibiotic resistant bacteria are becoming a major health concern for treatment in hospitals. Detection of pathogens that cause infections and food poisoning using traditional methods for amplification are time consuming and require expensive machines. We seek to develop a cheaper and a less expensive method for detection of *Staphylococcus aureus* and/or methicillin resistant *S. aureus* (MRSA). Recent studies have shown that loop mediated isothermal amplification can be used to amplify DNA using a single water bath and a specialized enzyme without the need for the expensive PCR machine. We have employed this strategy to target the amplification of three specific genes of *S. aureus*, 16S rRNA (for the genus of *Staphylococcus*), femA (for the species of *S. aureus*) and mecA (for methicillin resistance). This method requires six primers specific for each gene which form loops per cycle and the Bst DNA polymerase that can add nucleotides and at the same time displace the newly made strands. As a proof of concept, we have tested the method to amplify *S. faecalis* and *S. aureus* and showed that the method is specific for *S. aureus*. We are in the process of analyzing its specificity using several different microorganisms and testing its specificity.

Characterizing HPV16 Induced Cytoskeleton Rearrangement Events Mediated by Downstream Signaling Remodeling As a Mode of Viral Entry. Alyssa Biondo, Snezana Stankovic and Patricio I. Meneses, Fordham University Bronx, NY.

Human Papillomavirus (HPV) is a non-enveloped, DNA virus that infects mitotically active human epithelial cells. A decade of research has identified important protein interactions involved with HPV16 binding events to the extracellular matrix and along the basolateral surfaces of keratinocytes. However, the internalization process of HPV remains heavily debated because the process does not utilize mechanisms commonly used by other viruses. Recent studies have indicated that HPV16 utilizes a macropinocytosis- derivative mechanism to enter the cell. Macropinocytosis is a mechanism of internalization facilitated by intracellular signaling which activates cytoskeleton rearrangements one of which is filopodia. Filopodia are thin protrusions at the membrane that act as endocytotic hubs for viruses. Our research aims to identify key effector molecules downstream of signaling events activated after initial HPV16-cell membrane binding. Our putative target is Crk II, an adaptor protein known to crosslink actin formation and induce filopodia formation. Due to the versatile roles of Crk II in actin rearrangement, we hypothesize that HPV16 induces Crk II mediated actin remodeling during initial binding. We upregulated Crk II protein by treating the cells with different concentrations of epidermal growth factor (EGF) at different time points. The Crk II bands were most intense when treated with 100 ng of EGF for ten minutes. We determined that this concentration will be used to treat the cells when investigating the role of Crk II in HPV16 infection. We modeled HPV16 infection using pseudovirion that mimics observed HPV16 viral membrane interactions. In order to visualize how HPV utilizes host actin-rearrangement mechanisms during infection, we used confocal imaging to observe co-localization of actin networks, our target Crk II, and capsid protein L1. Filopodia formation increased after virus binding and scratching of the monolayer of cells (wound modeling). Few studies have focused on the novel impact of cytoskeleton rearrangement used by viruses.

Assessment of Dead Wood Fungi Biodiversity in Urban Parks and Natural Reserves Across New Jersey. Shazneka Blue, Abdurrahim Vardar, Christopher Zambell and Maria Shumskaya, Kean University, Union, NJ.

Ecosystems with high species richness such as forests rely on biodiversity of decomposers to boost availability of forest elements. Dead wood is an important component of any forest. It is a decomposition site, it protects against erosion, improves water retention in the ecosystem, and creates ecological niches. Dead wood-inhabiting fungi are saproxylic taxa that decompose cellulose and/or lignin. Here, we assess biodiversity of deadwood-inhabiting fungi in areas with varying degrees of human modification (removal of foliage, snags, logs). We hypothesize that removal of dead wood from urban parks diminishes the diversity of dead wood fungi which may affect the stability of ecosystems. Our goal is to compose a comprehensive database of dead wood inhabiting fungi and compare areas with different forest management practices to assess human impact. We present preliminary results from assessment of different locations spanning across northern to southern NJ. Fungal fruit bodies were collected for two hours at each sampling site and photos and GPS coordinates were recorded and shared via iNaturalist.org. Online database is available for the global scientific community at https://www.inaturalist.org/projects/saproxylic-fungi-of-new-jersey. Collections were performed together with citizen scientists from the New Jersey Mycological Association and undergraduate students from Kean University. Fungi identification was performed using both morphology and DNA sequence analysis. The nuclear ribosomal Internal Transcribed Spacer (ITS1, ITS2) region was used as a DNA barcoding marker, allowing

identification of fungal species via DNA sequencing and bioinformatics methods. We currently have identified 75% of samples. Sample rarefaction shows that after 16 sites sampled and 242 species observed, we have not yet plateaued in analysis of wood decay fungi. The Chao 2 species estimator suggests a total species richness of 333 species. Cluster analysis and NMDS suggests that there are consistent differences between fungal communities of the sandy soiled pine forests of Southern NJ versus the mixed hardwood forests of northern NJ. Dead wood fungal communities align by similarity along a north-south axis. Most frequently encountered species: *Stereum ostrea* and *Trichaptum biforme*, at 94% of communities sampled. Rare species will be identified once sampling is complete, and biodiversity of dead wood fungi in sites with different human management approaches will be evaluated. The presented research contributes to the ongoing efforts of conservation mycologists across the world. We continue to map and analyze the saproxylic fungi species distribution across the state to provide data on the effect of park management practices on diversity of saproxylic fungi, which in future can support fungal conservation.

Factors Influencing Pulmonary Edema Associated with Acute Airway Obstruction. Tenise Bowman[1], Amanda Wildstein[2], Richard Kollmar[2], Mark Stewart[2] and Anna Rozenboym[1], [1]Kingsborough Community College and [2]SUNY Downstate Medical Center, Brooklyn, NY.

During seizure in epilepsy, laryngospasm can occur occluding airways, causing pulmonary edema, and contributing to death. Once fluid enters lungs, stretch receptors send messages to the vagus nerve, which decreases arterial pressure and constricts bronchi. We sought to study the development of pulmonary edema as an element of the total pathophysiological picture. We tested effects of cutting the vagus nerve, and if more pulmonary edema will develop during anesthesia with ketamine/xylazine than with urethane because urethane is hyper-osmotic. Sprague-Dawley rats were randomized into two experimental groups - urethane vs. ketamine/xylazine anesthesia, and subdivided based on vagus nerve treatments. Rats were monitored with EKG, tracheal pressure and pulse oximetry. Acute airway occlusion for 60 seconds was conducted to simulate laryngospasm. Pulmonary edema was quantified with the ratio of wet to dry lung weight. Results show the fractional lung fluid was greater in animals anesthetized with ketamine/xylazine than with urethane. In urethane anesthetized rats, the fractional lung fluid was greatest in animals with bilateral nerve transection. In ketamine/xylazine anesthetized rats all groups tended toward greater lung water than urethane anesthetized animals. There appear to be three major findings: (1) simulated laryngospasm, associated with intense inspiratory effort, can be associated with increased lung fluid; (2) the difference in fractional lung water between urethane and ketamine/xylazine anesthesia is likely due to two factors - the higher osmolarity of urethane compared with ketamine/xylazine and the greater inspiratory effort in animals in ketamine/xylazine condition; (3) the impact of vagus nerve transection was best seen in urethane anesthetized animals where bilateral nerve transection was associated with the greatest lung fluid accumulation. Overall, the results suggest this model may be highly valuable for exploring the development of pulmonary edema during laryngospasm. This work was supported grants NIGMS-2R25GM06003 of the Bridge Program.

The Role of Fatty Acid Oxidation in Astroglial Xenobiotic Detoxification. Logan Brown[1], Moises Rodriguez[2], Jordan Rose[3] and Rodrigo Franco[3], [1]Spelman College, [2]Medgar Evers College and [3]University of Nebraska-Lincoln.

Astrocytes are the first line of defense against xenobiotic compounds passing through the blood brain barrier, and provide metabolic and synaptic support for neurons, particularly in the uptake and conversion of the excitatory neurotransmitter glutamate to glutamine. The xenobiotic arsenic is water soluble and readily passes through the blood brain barrier. Arsenic exposure has been linked to the development of neurological degenerative disorders. Previous experiments in the Franco Lab have illustrated that in vitro exposure of astrocytes to arsenic causes a significant increase in glutamate efflux into the media, and that the entry of carbons from pyruvate and fatty acid oxidation (FAO), but not glutamine, into the mitochondria are vital for astrocyte survival during arsenic exposure. In this study, we seek to both corroborate these findings, and explore the role that fatty acids in particular play in xenobiotic detoxification. We pursue these finding by culturing primary cortical astrocytes from rats and dividing astrocytes into several experiments. Astrocytes were treated with varying concentrations of arsenic, and were then used for Inductively coupled plasma mass spectrometry, to analyze the intracellular levels of arsenic. An Elisa was conducted on astrocytes treated with arsenic and inhibitors to analyze the levels of extracellular glutamate present in different conditions. Mitochondrial respiration/oxygen consumption profiles were generated using the Seahorse Mito Stress Test and Seahorse Fatty Acid Oxidation Test. Lastly, the measure of glutathione was conducted using flow cytometry on astrocytes treated with arsenic and palmitate with/without the presence of carnitine. These experiments have assisted in corroborating previous studies done in the Franco lab and provides new insights on the necessity of fatty acids and its role of xenobiotic detoxification. This work was sponsored by the National Science Foundation grant DBI-1757951 and the Nebraska Redox Biology Center REU program.

Effects of Electroconvulsive Seizure on GABA Concentrations in Mouse Models of Autism. Nicholas S. Buhta, Alec Stepanian, Melissa M. Staley, Cindy W. Jiang, Mikhail V. Pletnikov and Irving M. Reti, Johns Hopkins University, Baltimore, MD.

Self-injurious behavior (SIB) is displayed in approximately one quarter of individuals with autism spectrum disorder (ASD). Electroconvulsive therapy (ECT) has proven to be an extremely effective treatment for self-injurious behavior in individuals with ASD. Previous research has shown that GABAergic dysfunctions are strongly associated with ASD and SIB phenotypes. Therefore, we hypothesize that the electroconvulsive stimulus (ECS) delivered in ECT may modulate GABAergic systems to suppress SIB in ASD patients. To better understand the effective mechanism in which ECT operates, this study analyzes GABA concentration variations and behavioral changes in response to ECS of two transgenic autistic mouse models, Shank3B-/- and Viaat-Mecp2-/y conditional knockout variants, which express behavior analogous to SIB. This study is not yet complete, however, the data show that Shank3B-/- mice display a significant increase in striatal GABA concentrations in response to ECS.

PEA-15 Expression in Acute Promyelocytic Leukemia in Presence of HIV-TAT. Andres Cabezas and Yufeng Wei, New Jersey City University, Jersey City, NJ.

Phosphoprotein Enriched in Astrocytes-15 kD (PEA-15), is a small protein with a N-terminal death effector domain (DED) and a unstructured C-terminal tail at residues 1-90 and 91-130 respectively. PEA-15 appeals to many biochemists for its ability to regulate apoptosis, proliferation, and other cellular pathways. It gains this ability to regulate these processes via protein-protein interactions with other proteins and it achieves binding affinity to numerous proteins by changing structural conformation depending on the phosphorylation state of its Ser104 and Ser 116 residues. Trans-activator of transcription (TAT), is one of the 15 proteins endoded by the human immuno deficiency virus (HIV) genome. It gained its name for its ability to enhance HIV genome transcription, however, it has also been shown to be toxic to central nervous system (CNS) cells even disruptiong blood brain barrier integrity. The mechanisms for this are an active area of research. Using immortalized acute promyelocytic leukemia cell line, HL60, we treated these cancerous immune system cells with HIV-TAT of lengths 86 and 101 amino acids to analyze PEA-15 expression under these conditions and further elucidate PEA-15 possible therapeutic potential.

Identification of LRRC8a Protein in Chick Brain Cells. Daejah Campbell, Jael Agbabiaka and Renee Haskew-Layton, Mercy College, Dobbs Ferry, NY.

Volume regulated anion channels (VRACs) are ubiquitously expressed proteins that protect cells from swelling through a process known as regulatory volume decrease. VRACs accomplish this through the release of organic osmolytes, including glutamate. The molecular identification of VRACs was only recently discovered. The leucine rich repeat containing 8a (LRRC8a) protein is thought to make up the major protein components of the VRAC pore. While this protein has been identified in rodent cells, it has not yet been identified in chick cells. Since this is a ubiquitous protein necessary for cell survival, we hypothesize that, as in rodent cells, chick VRAC is composed of LRRC8a protein. We therefore performed preliminary Western blots to determine if LRRC8a is present in chick primary neurons and astrocytes, cultured from E6 and E8 embryos respectively. Preliminary results are inconclusive and suggest that an antibody specific for chicken LRRC8a is needed to better monitor protein levels. Future work includes characterizing glutamate released from LRRC8a as a potential mechanism of neuronal death in a stroke model.

Immunohistofluorescence Study of the Actions of Manganese on the DARPP-32 Mechanisms of Dopamine D2 Signal Transduction Pathway in *Crassostrea virginica*. Naomi Campos[1], Rosanne Wallach2, Mohamed Eid[1], Margaret A. Carroll[1] and Edward J. Catapane[1], [1]Medgar Evers College and [2]Kingsbrough Community College, Brooklyn, NY.

Manganism, a human disease caused by inhalation of manganese fume, is serious in areas with high industrial air pollution. The neurotoxic mechanism is not fully understood. It involves disruption of dopamine function rather than degeneration. Gill lateral cell (GLC) cilia of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervation. Dopamine causes cilio-inhibition; serotonin cilio-excitation. Post-synaptic GLC dopamine receptors are D2 (D2R). Manganese disrupts the dopamine-induced cilio-inhibition. D2R signaling pathway inhibits DARPP-32, a protein phosphatase inhibitor. DARPP-32 influences dopamine-mediated behaviors, and neuropsychiatric and neurodegenerative disorders. D2R activation inhibits protein kinase A-mediated phosphorylation of DARPP-32. DARPP-32 is involved in regulating behavioral responses to physiological and pharmacological stimuli, including antidepressants, neuroleptics and drugs of abuse. DARPP-32 hasn't been well studied in bivalves, nor has the effects of manganese on it. We hypothesize DARPP-32 can be visualized in GLC by immunohistofluorescence. We will determine if manganese effects its visualization. Briefly, gills were cryostat sectioned and incubated with 1° DARPP -32 antibodies and FITC-labelled antibodies. Sections were viewed and photographed with the same camera setting. GLC showed bright green fluorescence indicating the presence of DARPP-32. Gills also were treated for 1 or 24

hours with 500μM manganese or zinc. Fluorescence intensity (FI) was quantified using ImageJ from NIH. FI in manganese-treated GLC was not different after 1 hour, but significantly increased (22%) after 24 hours. For zinc, the opposite, 18% increase after 1 hour, no change after 24 hours. The study shows DARPP-32 is present in GLC of C. virginica and manganese as well as Zn caused significant changes in FI. This study provides new knowledge of the actions of manganese on the D2R pathway in bivalve gill. Future experiments will test if manganese effects the physiological actions of DARPP-32 on GLC cilia activity. This work was supported by grants NIGMS-2R25GM06003 and K12GM093854-07A1 and PSC-CUNY-604060048.

Determining the Role of the GABRA2 Gene in the *Gallus gallus* Chick. Esra Celik, Samantha Perez, Nadine Khalil, Orli Weiss and Cathryn Kubera, Monmouth University, West Long Branch, NJ.

Fetal Alcohol Spectrum Disorder (FASD) is a condition that leads to learning disabilities, heart defects, and craniofacial abnormalities due to premature exposure to alcohol. This disorder affects 2-5% of infants in the United States. Studies show *Gallus gallus* to be an effective model organism for the study of Fetal Alcohol Syndrome. Structural and functional abnormalities arising in the cerebellum during FASD could be due to the impact of alcohol on developmentally regulated genes like those for the GABA receptor. This project hypothesizes that the GABRA2 gene plays an important role in embryonic cerebellar development and contributes to cerebellar defects when alcohol exposure occurs at critical time points. A model for FASD was developed through air sac injections of 20% ethanol in *G. gallus* eggs at embryonic day 7 (E7). Also, CRISPR vectors were constructed to target and knock down GABRA2 activity in vitro in avian DF-1 fibroblast cells. In this study, CRISPR vectors were successfully constructed to contain scrambled and target sequences for the GABRA2 gene. Avian DF-1 cells were successfully transfected *in vitro* using the CRISPR vectors. Tissues from control and FASD model chicks were collected during different embryonic stages (E9, E11, & E13), which will be used for future RNA expression or immunostaining analysis.

Isolating Hydrocarbonoclastic Microorganismsfrom Newtown Creek. Valeria Cevallos[1] and Joby Jacob[2], [1]Queens College, CUNY, Queens NY and [2]LaGuardia Community College, Long Island City, NY.

Newtown Creek is a heavily polluted waterway which forms part of the border between Brooklyn and Queens. It is known to be one of the most polluted waterways in the country and was designated a Superfund site in 2010. It has been subject to two kinds of pollution in particular, over 200 years of industrial pollution and combined sewage overflows. It is the site of two major oil spills - the Greenpoint Oil Spill which is the largest underground oil spill in the history of the United States and the Blissville Seep. These oil spills have resulted in a sediment heavily enriched in hydrocarbons. Metagenomics of microorganisms from Newtown Creek suggest the presence of petroleum-hydrocarbon-degrading bacteria species (unpublished Calderon, *et al*.). Such species of bacteria have been reported at other oil spill sites. We have already successfully isolated one such species from the creek. In this research we wish (1) to use sampling techniques to isolate more species to better get a handle on the community of organisms which break down hydrocarbons, both in the sediment and in the water column; and (2) to look at more types of hydrocarbons which the bacteria can break down. Petroleum hydrocarbons are a class of environmental pollutants that have accumulated in the environment due to a variety of anthropogenic activities. We isolated and characterized a bacterium from Newtown Creek Nature Walk. This species is capable of breaking down the petroleum hydrocarbons Octacosane, Octadecane, and Eicosame. The tests identified a gram-negative bacteria, which we identified by DNA sequence of 16S rRNA sequencing as *Pseudomonas putida*.

Spatial Genomic Analysis of the Axolotl Wound Epithelium via HCR FISH. Breanna Chandler, Kofi Acheampong, Alex Lovely and James Monaghan, St. Francis College, Haverford College and Northeastern University.

Urodele amphibians possess a unique capability to regenerate amputated limbs throughout adulthood. Understanding how signals generated during wound healing influence limb regeneration is crucial to one day being able to regenerate complex human body systems. To gain a greater understanding of how these animals initiate a regenerative response, a multiple round, multiplexed HCR FISH technique to examine the spatial mRNA expression of six genes highly expressed in the wound epithelium (WE) was used. The genes looked at were Keratin 5, Uromodulin, Methyltransferase-like, Sp9, Wnt5a, and Mmp3. Each hybridization consisted of three genes at a time. We were able to successfully use this technique to visualize the spatial mRNA expression of some genes highly expressed in the WE of a regenerating axolotl limb. This approach will help fill in the spatial information lost from more traditional methods such as qPCR and RNA seq used to examine gene expression in the field. We were able to show that these six genes are spatially expressed differently among cells in the WE of the regenerating axolotl limb. What we consistently saw was that Keratin 5, is highly expressed throughout the WE. UMOD, is highly expressed only in the outermost layer of the WE. Methyltransferase-like, an uncharacterized gene, is highly expressed throughout the WE. Sp9, is highly expressed only in the outermost layer of the WE. Wnt5a, is highly expressed in the innermost, basal layer of the WE. Mmp3, is highly expressed in the innermost, basal layer of the WE. The next step for this

study is to spatially visualize more genes relevant to the WE, including markers of specific cell identities and genes associated with limb development. This can be used to characterize the distinct cell populations present in the WE, which could give us insights into its signaling role in limb regeneration.

Pathophysiology of Obesity-Associated Metabolic Inflammation. Jemima Constanza, Sahebveer Miglani and Zulema Cabail, SUNY Old Westbury, Westbury, NY.

In 1948 the World Health Organization (WHO) recognized obesity as a disease. Since then obesity has become a global epidemic with a profound health burden and a significant impact on health care expenditures. In addition, obesity is associated with the incidence of multiple co-morbidities, including insulin resistance, which contributes to the development of diabetes mellitus type 2 (DM2) and metabolic syndrome. A significant underlying cause of insulin resistance induced by obesity is a chronic low-grade systemic inflammation. This systemic metabolic inflammation observed in obesity (also known as meta-inflammation) results from the infiltration of immune cells into the adipose tissue, driving a pro- inflammatory environment. The main goal of this study is to investigate the intracellular and molecular players that initiate this meta-inflammation, and why such condition is chronic. Our working hypothesis states that activation of the cellular pro-inflammatory pathway Nuclear Factor k B (NFkB) by free-fatty acids (FFA) in obesity results in inhibition of adipose tissue macrophage autophagy (a normal physiological process that maintains homeostasis), which in turn promotes the polarization of non-inflammatory macrophages to a pro-inflammatory state. We tested this hypothesis using a murine macrophage cell line, RAW264.7, and exposed them to a lipid-rich microenvironment to mimic the cellular metabolic inflammation observed in obese adipose tissue. Our results suggest that NFkB modulates autophagy in macrophages subjected to a hyper-caloric microenvironment. These preliminary data provide a foundation for the molecular underpinnings of the pathophysiology of obesity-induced adipose tissue inflammation. At a broader level, this investigation will provide a platform that could lead to improved strategies for the treatment of the chronic low-grade systemic inflammation observed in obesity.

M05D6.2, an Ortholog of Human T-complex Protein 11 (TCP11), Is Necessary For Sperm Function and Fertility in *Caenorhabditis elegans.* Danielle Cooley, Emily Lopes, Amber Jacob and Matthew Marcello Pace University, New York, NY.

Human t-complex protein 11 (TCP11) is a testis-specific gene product that is hypothesized to be necessary for proper sperm capacitation, acrosome reaction, and sperm morphology. TCP11 function is of clinical interest because human patients have identified with mutations in the gene encoding TCP11. Our goal is to investigate the function of the *C. elegans* ortholog of TCP11, M05D6.2, to understand the role of TCP11 in human reproduction. *C. elegans* sperm activation includes processes similar to sperm capacitation and acrosome reaction in mammals, and we hypothesize that M05D6.2 is necessary for proper sperm activation in *C. elegans*. We have used RNA interference (RNAi) to disrupt the gene function of M05D6.2 in *C. elegans*. Hermaphrodites subject to M05D6.2 RNAi-treatment show no reduction in fertility. However, when male *C. elegans* are subject to M05D6.2 RNAi-treatment our results indicate that they have a significant decrease in fertility, despite making a normal number of sperm. We have generated three transgenic *C. elegans* strains using CRISPR/Cas9 genome editing (a deletion mutant, a mutant mimicking mutations found in infertile male patients, and a GFP-tagged version of the protein) to further characterize M05D6.2 function and localization. We are also investigating *C. elegans* strains with single nucleotide polymorphisms (SNPs) in the gene to characterize the function of specific residues in the TCP11 domain.

PEA-15 Phosphorylation Homeostasis and Allosteric Regulation of Cell Proliferation and Apoptosis. Sergio Crespo, Sherouk Hassan, Andres Cabezas and Yufeng Wei, New Jersey City University, Jersey City, NJ.

PEA-15 (phosphoprotein enriched in astrocytes, 15 kD) is a small, non-catalytic, death-effector domain (DED) containing protein, that is widely expressed in different tissues and highly conserved among mammals. Although the overall expression level of PEA-15 is mostly constant in most tissues, its phosphorylation states of the two serine residues on the C-terminal tail vary significantly depending on cell and tissue types and/or cellular environment and conditions. The phosphorylation states control the interactions of PEA-15 with other protein targets in various pathways, including Fas-associated death domain (FADD) and procaspase-8 (apoptosis), extracellular signal-regulated kinase (ERK) 1 and 2 (cell cycle entry), and phospholipase D (PLD) 1 and 2 (diabetes). We have previously reported a surprising conformational change of PEA-15 DED upon interaction with ERK2 using nuclear magnetic resonance (NMR) dynamics and residual dipolar coupling (RDC) data. We recently demonstrated again that the DED conformation is also modulated by the phosphorylation states of the C-terminal serine residues. Upon phosphorylation, mimicked by serine to aspartic acid mutations (PEA-15DD), the DED conformation is very distinct from the wild type protein, and its binding specificity switches from ERK1/2 to FADD. Additionally, the PEA-15DD structure is not significantly different from the FADD complex. Based on our most recent results, we propose that the DED conformation is allosterically controlled by the phosphorylation states of the C-terminal tail, which in turn determines the binding specificity of the protein. We

further propose that the balance between phosphorylated and unphosphorylated PEA-15 is strictly regulated in different cell types and tissues to control the cellular outcomes, which we termed phosphorylation homeostasis, and any disruption of the delicate balance could lead to various diseases, such as cancers and neurodegenerative diseases.

Is Ironman Invincible?; Risk of Stress During Strenuous Exercise. Frank Cristallo III, Emily Cruz, Rachel Julian, Kristen Lacey and Noelle Cutter, Molloy College, Rockville Centre, NY.

Regular physical activity has been linked to greater overall health, and this notion has been widely accepted for many years. Recent studies support that extended increments of strenuous exercise can lead to oxidative stress. The Ironman Triathlon is a widely known grueling competition which can induce this oxidative stress response in its participants. Using smart watch data, athlete profiles were constructed for each participant. The profiles included information on age, height, weight, resting heart rate, heart rate MAX, exercise time, sleep time, and VO2 max. The selected participants for this study were also screened for common stress genetic markers, cortisol stress levels, and damage to DNA. Results of the study indicate that the athletes experienced an increase in the formation of ROS when compared to the control group. Additionally, the participants' cortisol levels remained elevated 24 hours post-race. In the future, this study can be further developed to examine the efficacy of antioxidant intake as well as DNA repair for for athletes undergoing strenuous exercise.

How Do Primary and Secondary Cells Respond to Zika Virus Infection? Bartosz Czuj[1], Sidra Jabeen[1], Joselyn Landazuri[1], Sounak Ghosh Roy[1], Panayiotis Koumas[1], Amirabbas Maghsoudi[2], Richard Lockshin[1], Zahra Zakeri[1], [1]Queens College and Graduate Center of CUNY, Flushing, NY and [2]Queensborough Community College, CUNY, Bayside, NY.

Zika virus (ZIKV) is an emerging global threat with recent severe disease-causing outbreaks. This arbovirus of the Flaviviridae family is transmitted by Aedes species. ZIKV attacks neurons, causing apoptosis, cell-cycle arrest, and inhibition of neural progenitor cell differentiation, resulting in cortical thinning and microcephaly. Apoptosis is an essential aspect of normal cell turnover, embryonic development, and function of the immune system. After 24 hours, ZIKV infected and killed 25% of vero cells (an aneuploid line from kidney epithelium of African green monkey, sex not specified) compared to only 5% in mock-infected cells. However, it did not kill either MDCK (canine kidney epithelium, sex not specified) or A549 cells (Adenocarcinoma human alveloar basal epithelial cells, sex not specified) 24 hpi. As most of these cells are not primary we asked if the effect of Zika would be different in the primary cells as they are the in vivo targets of the virus. Since male and female macrophages differ in their ability to carry out phagocytosis, we asked whether primary macrophages extracted from male and female mice respond differently to ZIKV. Our preliminary qRT-PCR data suggests that macrophages can be infected by ZIKV however there is a significant difference between the sexes in terms of infectivity. Males are infected four fold compared to females 24hpi. Our data also suggests that ZIKV causes significant cell death in both male and female macrophages after 24h infection. We also observed a significant increase in mitochondrial activity of ZIKV infected cells over mock, for both sexes. Male and female macrophages have different capability of phagocytosis that can be altered by viral infection. Here we report on the pattern of phagocytosis after ZIKV infection. we will further evaluate the pathways leading to autophagy and apoptosis in ZIKV infected macrophages responsible for sex differences in regulating immune response.

There are Bacteriophages in Your Sponge. Linesha Davis, Lovejit Kaur, Brianna Weiss and Bryan Gibb. New York Institute of Technology, Old Westbury, NY.

Bacteriophages or "phages" are viruses that infect bacteria. It is estimated that bacteriophages outnumber bacteria 10:1 and are found anywhere inhabited by bacteria. In addition to serving as the largest source of genetic diversity on the planet, phages are the subject of renewed interest as alternative treatments for bacterial infections. Kitchen sponges are often touted as one of the most heavily contaminated places in the home, so we hypothesized that that the diverse microbial ecosystem would harbor novel bacteriophages. Seven students isolated bacteria from dirty kitchen sponges brought in from their home, which were then used to search for bacteriophages within the sponge. Two students were successful in isolating bacteriophages that targeted the host bacteria from their sponges. Using 16S sequencing, the hosts were identified as members of Enterobacteriaceae. The phages, named LKsleep and Shaolin, produce hazy plaques and have a high tendency to form lysogens. We have shown that the two bacteriophages can cross-infect the other host suggesting that the hosts are closely related. Based on TEM imaging, Shaolin is a member of the Siphoviridae family. The two isolated bacteriophages and the hosts are especially interesting given that they were isolated from separate sponges taken from different homes, yet they appear closely related. Ongoing efforts to further characterize these bacteriophages will continue to explore the relatedness of the phages and their hosts. Although kitchen sponges harbor bacteriophages, isolating them proved more challenging than anticipated.

Cell Penetrable Inhibitory Probe of Human Cathepsin L. Anna Alicent Dickson[1], Ashif I Bhuiyan[1], Jeremy Garcia[1], Faiza Rafi[2], Uwa Ogbeta[2], Jasmine Kaur[2], Nisar Afzal[1], Laura Joo[1], Suneeta Paroly[2], Karl R Fath[2] and Sanjai Kumar[1,3], [1]Queens College - CUNY, Queens, NY; [2]Bard High School Early College Queens, Long Island City, NY; [3]The Graduate Center of CUNY, New York, NY.

Human cysteine cathepsins are enzymes that play critically essential roles in various cellular processes. Their aberrant function has been implicated in a wide variety of human diseases, including highly invasive forms of cancer. Among these, Cathepsin L is particularly important; it has been found to be anomalously expressed in highly malignant tumors in distinct parts of the body such as breasts, skin, pancreatic, brain, head and neck. The abrogation of cathepsins L activity decreases tumor invasion, thereby making it a potentially a high-value drug discovery target. Nevertheless, the specific biological functions of cathepsin L in specific cell types are yet to be fully understood. In this project, a chemical biology approach is undertaken to understand the functional biology of cathepsin L. Toward this goal, the development of a new class of cell-penetrable, activity-based nonpeptidyl inhibitory chemical probe is reported. This clickable probe exhibits a high potency and selectivity toward cathepsin L, and possess a small clickable acetylene tag for easy detection. Currently, experiments are underway to label active human cathepsin L in cells from diverse origin. This proteome-wide activity profile analysis is anticipated to expedite the functional understanding of cathepsin L biology in both normal and diseased cells.

Poor Girls and Rich Boys? Testing the Trivers-Willard Hypothesis. Kaylin Dominquez, Isabel Soriano, Jonathan Torres, Genesis Torres, Amir Niknejad and Ioanna Visviki, College of Mount Saint Vincent, Bronx, NY.

In most mammalian species females devote more energy to parental investment than males. Males show greater variability in reproductive success than females and experience strong intrasexual selection. Successful males attract a lot of mates and have a lot of offspring, while males in poor condition leave few or no offspring. The Trivers-Willard hypothesis proposes that females can increase their reproductive success by biasing the sex ratio of their offspring depending on the availability of resources and their own physiological condition. Females are expected to produce more sons when conditions are favorable, and more daughters when conditions are unfavorable. We tested this hypothesis using a 19th century human population that we have studied extensively. Initial data were obtained from the Archives of the Sisters of Charity of New York and genealogical trees of their families were constructed using federal and state census data available at www.ancestry.com. With this information we determined the total number of children per family and the number of surviving children. The families were divided into three socioeconomic groups based on the father's profession. The sex ratio of offspring per family was determined by dividing the number of male children with the total number of children born. Contrary to the predictions of the Trivers-Willard hypothesis, women in the highest socioeconomic group did not have more sons and all three socioeconomic groups showed female bias. Our results indicate that there are multiple factors that shape parental reproductive strategies.

Retinoic Acid Induces a Potential Compensatory Mechanism in Response to Downregulated Sonic Hedgehog. Caroline Doran and Renee Haskew-Layton, Mercy College, Dobbs Ferry, NY.

Irregular or non-division of the cerebral hemispheres causes malformation of the central face, Holoprosencephaly (HPE). During embryogenesis, interacting and cross-linking pathways including Sonic Hedgehog (SHH) and retinoid signaling coordinate the development of brain and face. SHH and retinoic acid (RA) signaling are expressed in a reiterated fashion during embryonic development. Hong et al. (2017) assert that ethanol itself is a teratogen, independent of oxidative metabolism, contributing to many HPE phenotypes. Hong et al. (2017) show that chick embryos display craniofacial anomalies distinct from HPE when treated with retinoid receptor antagonists; however, the current study neglected to analyze the effect of RA. Competitive inhibition by ethanol-derived acetaldehyde results in insufficient production of RA required for normal development. Previously, we speculated that ethanol oxidative metabolism causes insufficient RA production leading to HPE phenotypes. We injected a bolus of exogenous RA after ethanol induction in the yolk of E2 chick embryos and dissected at E9. The 5% ethanol plus 0.03 mg/mL RA rescue group showed recovery of midline craniofacial structures and brain hemisphere symmetry when compared to the 5% ethanol group. I aim to reproduce the results to understand the molecular repair mechanisms in the chick neural tube and changes in neural crest cell migration. Ahlgren et al. (2002) investigated the mRNA expression levels of SHH genes after ethanol treatment and showed that transcripts are downregulated in the developing head. Despite the interactions between SHH and RA, researchers neglected to test mRNA levels of RA synthesizing enzymes in the presence of ethanol; therefore, I propose to perform RT-PCR to examine expression levels in both RA synthesizing and SHH gene transcripts post ethanol treatment. Based on Ahlgren et al. (2002), I speculate that modulation of the RA pathway may potentially act as a compensatory pathway when excess amounts of ethanol severely downregulate SHH transcripts.

IFN-γ Regulation of Canonical TLR Pathways. Gabriele D'Orsi, Emily Calderon and Jodi Evans, Molloy College, Centre, NY.

The overuse of antibiotic drugs has led to the development of antibiotic-resistant bacteria that significantly increase patient morbidity in healthcare settings. In order to address this problem, we sought to identify ways to enhance the innate immune response to a bacterial stimulus. Previous research has revealed that the inflammatory mediator interferon-γ (IFN-γ) can amplify the macrophage inflammatory response to lipopolysaccharide in the context of absent or deficient toll-like receptor-4 (TLR-4) signaling. We hypothesize that IFN-γ can regulate components of canonical TLR signaling pathways as a way to mediate its effects. Two murine macrophage cells lines deficient in TLR-4 signaling were treated with IFN-γ and then using gene array analysis, we examined expression changes in canonical TLR signaling pathway components. In both cell lines several genes were regulated by IFN-γ including CXCl10, IL6, Myd88, Nfkbib, Irak2, and TLR3. These results demonstrate that there are pathways other than direct activation of TLR-4 through which macrophage cells can initiate an inflammatory response to gram(-) bacteria. This basic scientific research can lead to future therapeutics designed to strengthen the innate immunity and reduce our reliance on antibiotics.

Evaluating the Function of Genes Implicating Glioblastoma Multiforme (GBM) Formation using *Caenorhabditis elegans*. Agata A. Durda and Matthew R. Marcello, Pace University, New York, NY.

Glioblastoma multiforme (GBM) is an aggressive brain tumor that is difficult to treat and often curable. Recent advances in genomics have led to the identification of many genes that are thought to drive GBM formation. The purpose of the use of nematode *Caenorhabditis elegans* (*C.elegans*) is to determine how these genes control cell division and how their misregulation could lead to cancer. *C. elegans* is a useful organism for studying genes and proteins that are present in humans because of similarity in cellular function between the two organisms. We have identified genes implicated in GBM development that have orthologs in *C.elegans* and obtained *C. elegans* strains with mutations in those genes. One *C. elegans* gene of particular interest is lev-9. The human ortholog of lev-9 is CR1. We first analyzed if the lev-9 mutants had defects in embryo development. In order for proper embryo development, the cell must maintain the proper regulation of the cell cycle and improper embryo development exhibits similar errors that are seen in many cancers. We determine that the lev-9 mutants do show issues with embryo development. Currently, we are analyzing the glial function of these mutants using a touch sensitivity assay. This project will help elucidate how the cellular role for the genes thought to drive GBM formation.

Effect of Single Walled Carbon Nanotubes on Breast Cancer Cell Migration. Tobore Edema and Regina Sullivan, Queensborough Community College Bayside NY.

Biomedical applications of single walled carbon nanotubes (SWCNT) have the potential to expand treatment options for cancer patients. Carbon nanotubes have a high surface area to volume ratio which allows for surface functionalization. The size of these nanotubes facilitates use as a drug delivery system as well. Recent studies have shown that unfunctionalized nanotubes enter cells via endocytosis. In addition the nanotubes may enter cells through cellular gap junctions and ion channels. In previous studies we have shown that nanotubes are not cytotoxic in low concentrations. Currently we are testing the hypothesis that unfunctionalized single walled carbon nanotubes incorporate into the actin cytoskeleton and decrease migration of triple negative breast cancer cells. However our studies have been limited by aggregation of the nanotubes in aqueous solutions which decreases cellular uptake and increases cytotoxicity in in vitro studies. Coating single walled carbon nanotubes with collagen has been shown to facilitate cellular uptake thus allowing for intracellular associations to be investigated. This method has limitations due to the acidic pH of the collagen solution. In this study, we compared the effect of collagen coated single walled carbon nanotubes with debundled single walled carbon nanotubes on breast cancer cell migration. Migration assays were performed and revealed that breast cancer cells treated with collagen coated SWCNT as well as the debundled SWCNT has a reduced rate of migration. These results suggest that the SWCNT may be incorporating into the actin cytoskeletal disrupting rearrangements that are required for the metastatic process. In future studies we plan to measure Young's modulus which is an indicator of the degree of flexibility which in turn can be correlated with changes in the actin cytoskeleton. The study will be expanded to include other types of cancer cells as well noncancerous cells and may reveal potentially novel cancer treatments.

Characterization of DNA Cleaving DNA Enzyme Using KINE. Artiom Efimenko, Kush Patel, Davis Jose and Jonathan Ouellet, Monmouth University, West Long Branch, NJ.

Enzymes are classified as substances that act as a catalyst in a certain chemical reactions, thereby increasing the overall rate of the reaction. Most naturally-occurring enzymes are composed primarily of proteins and are associated with a specific catalytic activity that aid in a variety of biochemical processes. Although most of the proteins discovered have been proteogenic in nature, some enzymes have been produced synthetically from ribonucleic acids (RNA) and deoxyribonucleic acids (DNA). One example of a synthetically generated DNA enzyme is the IR3 DNA cleaving DNA enzyme. The IR3 DNA enzyme functions as an enzyme by catalyzing the reaction of its selfcleavage. But, in order for the IR3 DNA enzyme to be

functionally active, a Zn^{2+} cation must be present in solution. Our research focuses on utilizing a DNA cleaving DNA enzyme to test its function and kinetic properties. The type of DNA enzyme we are concerned with is similar in effect to the IR3 DNA enzyme mentioned previously. The DNA cleaving DNA enzyme is generated from two single-stranded DNA strands, an enzyme and substrate strand. Both strands have been carefully selected through a process known as SELEX, or the systematic evolution of ligand by exponential enrichment. The base pairing of the substrate and the enzyme strand produces the complete enzyme-substrate complex, which is only deemed functionally active when found in the presence of Zn^{2+} ion. Our current hypothesis behind the mechanism is that the zinc cation aid in the cleavage of the DNA backbone by stabilizing the negative charges on the phosphate groups. However, most DNA enzymes have been discovered to cleave in the presence of Mg^{2+}, so DNA that cleaves in the presence of Zn^{2+} is fairly novel and uncommon. Once the kinetic measured by gel, the DNA substrate strand will harbor a fluorescent probe (2-aminopurine) within the cleavage site. Self-cleavage of DNA will then be monitored through fluorescence spectroscopy to generate the rate of cleavage per unit of time.

Immunohistofluorescence Study of the Actions of Manganese on the ß-Arrestin and Gßγ Mechanisms of Dopamine D2 Signal Transduction Pathway in *Crassostrea virginica.* Mohamed Eid[1], Rafael Santos[2], Margaret A. Carroll[1] and Edward J. Catapane[1], [1]Medgar Evers College and [2]Kingsbrough Community College, Brooklyn, NY.

Abstract: Manganese disrupts dopamine neurotransmission causing manganism, a Parkinson's-like disease in people. The mechanism is not completely understood. Gill lateral cell (GLC) cilia of *Crassostrea virginica* are controlled by serotonin-dopamine innervations. Dopamine slows, serotonin increases, cilia beating. GLC post-synaptic dopamine receptors are D2-type (D2R). Manganese disrupts dopamine induced cilio-inhibition. D2R are G protein-coupled receptors. D2R activation splits Gi/o protein into Gßγ and Gai/o. Gai/o inhibits adenylyl cyclase. Gßγ activates phospholipase C, opens GIRK channels and closes L-type Ca^{2+} channels. Continued activation of G protein-coupled receptors causes ß-Arrestin binding, which desensitize them and targets them for internalization. ß-arrestin and Gßγ haven't been well studied in bivalves, nor the effects of manganese on them. We hypothesize ß-arrestin and Gßγ can be visualized in GLC by immunohistofluorescence, and we will determine if manganese or dopamine effects their visualization. Gills were cryostat sectioned, incubated with ß-Arrestin or Gßγ 1° antibodies, FITC labelled 2° antibodies, then photographed with the same camera setting. Fluorescence intensity (FI) was quantified using ImageJ from NIH. GLC had bright green fluorescence indicating ß-arrestin and Gß?. Gills treated 1 or 24 hours with manganese had 10% decreased FI for ß-arrestin and Gßγ for the 1 hour and 15% for the 24 hour treatment. Zinc, used as a comparison, caused either no, or slight decrease in FI for ß-arrestin and Gßγ. One hour dopamine treatment had no effect on FI of ß -arrestin, but increased Gßγ FI, even with manganese present. The study shows ß-Arrestin and Gß? present in GLC and manganese reduced their FI. Dopamine increased Gßγ FI, but not ß-arrestin, providing new knowledge of the actions of manganese on the D2R pathway in bivalve gill. Future experiments will test if manganese effects physiological actions of ß-arrestin and Gßγ on GLC cilia activity. This work was supported by NIGMS-2R25GM06003, NIH-K12GM093854-07A1 and PSC-CUNY.

Sunscreen Properties of Organic Compounds. Lokenauth Elizabeth, Hurtado Juan, Alvarado Victoria and Surendran Geetha, Mercy College, Dobbs Ferry, NY.

Organic compounds with different functional groups-ketones(oxybenzone), esters (homosalate and methyl cinnamate) and a carboxylic acid (cinnamic acid) were studied for their sunscreen properties. The uv absorbance was measured using a UV-Vis spectrophotometer. From the absorbance values, the Sun Protecting Factor (SPF) was calculated, by using Mansur equation. % Transmission erythema (%TE) and % Transmission Pigmentation (% Tp) were also calculated from the uv absorbance spectra. Oxybenzone and homosalate had a higher SPF value and a low % TE and %TP as compared to cinnamic acid and methyl cinnamate. Oxybenzone was found to have superior sunscreen properties as compared to other compounds that were tested.

Evaluation of Enterococcus Levels in the East River and Coney Island Creek During Recreational Boating Season. Jenna Ellington, Marie Boutin, Amber Tucker, Luis Ramirez, Melissa Tiphaine, Robert Buchanan, Kathy Nolan and Victoria E. Ruiz, St. Francis College, Brooklyn, NY and NYC Water Trail Association, New York, NY.

The rivers and estuaries of New York Harbor is a widely used resource for recreational activities. Compounding human use and illegal spilling of industrial and human waste may have detrimental effects on aquatic organisms and impact overall human health. Enterococci enumeration is frequently used as an indicator of fecal contamination and water quality. In collaboration with the Citizens Water Quality Testing Program, we assess levels of the bacterial genus Enterococci over a 20 week period, from the East River at Brooklyn Bridge Park and Coney Island Creek, at Calvert Vaux Park. We hypothesize greater Enterococci levels at Brooklyn Bridge Park (Pier 2, Pier 4, and Dumbo Pier) compared to Coney Island Creek (Calvert Vaux Park) due to increased human and animal activity at Brooklyn Bridge Park. To test this hypothesis, water samples were collected from the East River (Pier 2, Pier 4, and DUMBO Pier) and Coney Island Creek (Calvert Vaux Park). Enterococci levels were measured using the Enteroalert

IDEXX kit. All samples were placed in IDEXX quanti-trays for subsequent enumeration and incubated at 41? for 24 hours. Calvert Vaux Park exhibited higher levels of Enterococcus compared to the sites located at Brooklyn Bridge Park, which had moderate to high levels of Enterococcus. The average Enterococci levels at Calvert Vaux Park were 554 colony forming units (cfu) per 100mls of water, over 15 times the level deemed safe for recreational activities. Increased Enterococcus levels at Calvert Vaux Park was potentially influenced by large amounts of debris, while Pier 4 also displayed high levels of Enterococcus due human activity and the presence of geese and dogs. The sustained high levels of Enterococci may have potential public health implications with respect to antibiotic-resistant organisms and immunocompromised hosts and should be further evaluated throughout the year.

Unknown Bacteria from Ecuador with Strong Antibiofilm Activity. Charlie Encalada, Daniel Antunes, Hagar Mustafa, Sommer Gomez and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

Microorganisms can develop biofilms after attaching to surfaces. These biofilm forming cells generate an extracellular polymeric matrix. Once the biofilm has been established, it provides an environment for microorganisms to exchange genetic material between cells and become resistant to our immune system and antibiotic treatment. Most infectious diseases in hospitals and device related infections, such as catheters 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 unknown bacteria isolated from a volcanic spring from Banos in Ecuador, were tested against known pathogenic biofilm forming bacteria such as *Staphylococcus aureus*, *S. epidermis*, *Escherichia coli*, and *Enterococcus faecalis*. Some unknown bacteria that were tested show strong antibiofilm properties against biofilm forming pathogenic bacteria including *S. aureus* and *S. epidermidis*. Further characterization will be conducted to identify the unknown bacteria as well as the active antibiofilm compound produced.

Quantification and Characterization of Microbial Communities Obtained from The Rocket® Composter System to Tackle a Food Waste Problem at a Community College Campus. Mallory Errichetti, Xaymaraliz Dumeng, Jacqueline Gonzalez, Yulkania Lopez, Adrianna Pinto, Kadiatou Fadiga, Hyunbin Kang, Stephania Vazquez, Lindsey Njanj, Luis Jimenez, and Linda Araya, Bergen Community College, Paramus, NJ.

According to the United States Environmental Protection Agency (USEPA), food waste makes up around 21% of solid landfill waste. Students at Bergen Community College, in collaboration with campus dining services, are working to address this worldwide issue at the grassroots level to serve as the first step in a multi-step process to turn used cooking oil into energy that can be used to power the composter. The Rocket® composter system was used as a tool to take food waste and convert it to usable soil. In order to ensure proper implementation, data on food waste quantities and compost output quality was recorded and analyzed for microbial quantification and characterization. We hypothesize the presence of gram positive bacteria will be found in great quantities, which would confirm the presence of microbial communities necessary for breaking down food waste. PCR was used to test for the presence of important enzymes including nitrogenase (fixes nitrogen to ammonia) and glucosidase (breaks down cellulose to glucose) present within the bacterial colonies. Gram-staining technique was used in conjunction with microscopy to check for the presence of rod-shaped or coccus shaped microbial colonies. DNA was extracted from these microbes and tested for the presence of the enzymes nitrogenase and glucosidase. The presence of gram positive rod bacteria were confirmed as well as the presence of nitrogenase and glucosidase.

Quantifying bioaccumulation of low-level copper exposure in the embryonic zebrafish. Najae Escoffery, Robin Helburn and Alison L. Dell, St. Francis College, Brooklyn, NY.

We observe cardiac and behavioral deficits in zebrafish embryos exposed to low levels of copper. However, environmental dosage is not necessarily an accurate indicator of an organism's uptake of a given environmental pollutant. Here we report the development of spectroscopy based assays to directly measure the levels of metal accumulation in copper exposed embryos. We used a novel nitric acid based method to prepare experimental (copper- exposed) and control (unexposed) samples for atomic emission spectroscopic analysis. The results of these experiments indicate a dose dependent correlation of copper-exposure with increased bioaccumulation of this metal; confirming our hypothesis and validating our experimental model for further studies.

TFIIIB Alterations in Gliomas. Paul Espiritu, Keyla Payano and Laura Schramm, St. John's University, Queens NY.

RNA polymerase (pol) III transcription is specifically deregulated in human cancers. RNA pol III, like all other eukaryotic polymerases, cannot recognize its target promoters directly, and requires a multi-subunit complex termed TFIIIB. RNA pol III initiates transcription from both gene internal (tRNA and VAI) and external (U6) promoters. To initiate transcription from gene internal promoters, RNA pol III requires a form of TFIIIB containing TBP, BRF1, and BDP1. To transcribe gene external promoters, RNA pol III requires a form of TFIIIB comprised of TBP, BRF2, and BDP1. There are very few published

data on TFIIIB expression patterns in the brain and in brain tumors. Herein, we demonstrate differential expression of the TFIIIB subunits BRF1, BRF2, and BRF2 in the brain. As such, we hypothesized if TFIIIB is altered in the most common type of human brain tumors in the United States, gliomas. Using bioinformatics approaches, we report TFIIIB is altered in 17% of sequenced samples from patients with low grade gliomas. Alterations in BRF1/ BRF2, and BRF2/BDP1 tend to be mutually exclusive, but alterations in BRF1/BDP1 tend to co-occur and are statistically significant ($p<0.01$). Employing a Kaplan-Meier analysis estimates the median survival of patients without TFIIIB alterations in low grade gliomas is 108 months and the median survival for patients with TFIIIB alterations in gliomas is 58 months. We also report gender specific TFIIIB alterations in gliomas. Namely, The TFIIIB submit BDP1 is exclusively mutated in low grade gliomas. TFIIIB is altered in 6% of sequenced samples/patients with astrocytomas and 40% of sequenced samples/patients with glioblastomas. Together, these data suggest TFIIIB may be a suitable biomarker for patients with low grade gliomas.

spa Typing Method to Determine the Genetic Diversity of Staphylococcus aureus Isolated in Nasal Samples from a Suburban New Jersey Population. Kadiatou Fadiga, Arianna Pinto, Vanessa Molina, Adelajda Turku and Luis Jimenez, Bergen Community College, Paramus, NJ.

Protein A is a 42 kilodalton surface protein originally found in the cell wall of the bacteria *Staphylococcus aureus*. Protein A is able to bind antibodies disrupting phagocytosis and opsonization. It is encoded by the spa gene. The spa typing technique uses the sequence of a polymorphic X region of the *S. aureus*-specific staphylococcal protein A (spa). The X region is constituted of a variable number of 24-bp repeats flanked by well-conserved regions. Each new base composition of the polymorphic repeat found in a strain is assigned a unique repeat code. The repeat succession for a given strain determines its spa type. DNA was extracted from 77 nasal isolates identified as *S. aureus* by phenotypic tests and 16S rRNA analysis. PCR reactions amplified the spa gene from all isolates. DNA electrophoresis showed the spa DNA fragments ranged from 200 to 500 base pairs. Gene sequencing of the amplified PCR fragments separated the isolates into 3 clusters. Cluster 1 showed the highest genetic diversity and cluster 3 the lowest. Using the Bionumerics software analysis, the 77 nasal isolates were classified into 41 different genotypes. The most common types were t008, t363, and t012. The rapid and accurate typing of isolates provided important information to understand the genetic diversity of *S. aureus* present in nasal carriers.

Using HEK Cells as a Model System to Study Autophagy and it's Regulations. Mohammad Fauzan, Chelsea Anyaegbu, Azka Asim and Reed Carroll, New Jersey City University, Jersey City, NJ.

The body has multiple mechanisms to detoxify and regulate itself to maintain homeostasis. Autophagy functions as a self-recycling mechanism involving protein degradation in autophagosomes. Autophagy is particularly important in neuronal function, and its disruption has been linked to diseases like Parkinson's and Alzheimer's. This study investigates using HEK (human embryonic kidney) cells as a model system to study autophagy and its regulation. LC3 labeling was used as a marker to show the formation of autophagosomes. Serum starvation of HEK cells induced autophagosome formation as shown by a 35% increase in LC3 cluster labeling. Wortmannin, a PI3 kinase inhibitor, inhibited starvation-induced autophagy by 31% when added to the starvation media. Chloroquine treatment induced increased expression of LC3 levels consistent with its blocking lysosome function. Initial investigations have examined the role of CaMKII, a regulator of vesicle fusion, in modulating autophagy. Subsequent studies will investigate the role of autophagy in regulating the surface expression of neurotransmitter receptors. The work was supported by U.S. Education Department Hispanic Serving Institutions- Science, Technology, Engineering, & Math (HSI-STEM) program grant.

Predation Interactions Between Oysters (*Crassostrea virginica*), Mud Crabs (Panopeidae) and Blue Crabs (*Callinectes sapidus*). Jessica Fernandez and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

The purpose of this study was to examine and compare the predation among three trophic levels involving the mud crab (Panopeidae), blue crab *(Callinectes sapidus*) and oysters (*Crassostrea virginica*). To achieve this we performed two experiments, first with live oysters and afterwards with shucked oysters. Our results show that blue crabs prefer consuming the shucked oysters, while the mud crabs did not show much interest in the oysters at all. Examining the feeding of these crab predators provide useful information that can help the management and conservation of oysters.

Osteoclastic Signal Transduction and Activator of Transcription-3 Enhances the Migration of Osteoblastic Cell Line MC3T3. Miguel Fernandez, Stephanie Lochan and Andrew V. Nguyen, Queensborough Community College, Bayside NY.

Osteoblasts are known to regulate osteoclasts but how osteoclasts regulate osteoblasts is not clearly defined. 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 in a number of cytokines and growth factors and was shown to be important in osteoclast maturation. Osteoclast differentiation requires 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. It has been shown that osteoblasts can regulate osteoclast differentiation by secreting RANKL. Recent evidence suggests that osteoclasts can regulate osteoblast recruitment by secretion of sphingosine-1 phosphate. The goal of our project was to analyze the role of STAT3 in osteoclasts regulation of osteoblast chemotaxis and to characterize the association between STAT3 and S1P pathway. We examined the progressive movement of osteoblast cell line, MC3T3, treated with osteoclast conditioned media and STAT3 overexpression and STAT3 knock down. Scratches from the cells treated with the osteoclast conditioned media showed a faster overall healing. The data suggest that conditioned media from osteoclast culture increases MC3T3 migration.

Target Practice for Stem Cells: Modulation of Chemoresistance in Ovarian Cancer. Julia Fiederlein, Brianna McNulty, Samantha Lines, Sandra Riad and Noelle Cutter, Molloy College, Rockville Centre, NY.

The leading cause of death from gynecologic malignancies is epithelial ovarian cancer. These tumors are comprised of a highly heterogeneous population of cells, of which only a small subset of stem-like cells possess the ability to regenerate tumors in vivo. These cancer stem cells (CSCs) represent a significant clinical challenge as they are resistant to conventional cancer therapies and play essential roles in metastasis and tumor relapse. While chemotherapy is the preferred treatment modality, chemoresistance severely limits treatment success. It has been hypothesized that cancer stem cells are at the root of this problem. Their ability to self-renew and proliferate is what causes a large number of ovarian cancers to recur and not respond to normal chemotherapeutic treatments. Recent evidence suggests that deregulation of stem cell pathways is a key factor in the onset and maintenance of chemoresistance. Several key markers such as BMI1, FZD1, NANOG, TWIST1, and OCT4 are hypothesized to play a central role in the development and differentiation of multiple cell lineages. Recent studies have demonstrated that these markers is required for the carcinogenesis in several cancer types. The aim of this study was to investigate the significance of CSC expression in chemoresistant and sensitive ovarian cancer cancer cell lines. CSC mRNA expression was detected by real-time quantitative PCR in sensitive and resistant ovarian cell lines. The objective of such an improved delineation is to develop targeted therapy for selective elimination of cancer stem cells with minimal toxicity to normal stem cells. Our research indicates that there were novel changes in gene expression in the CSCs and decreased rates of apoptosis, as reduced activity of caspase 3 was observed in the chemoresistant cell lines. Further research is needed to gain better understanding of the role that these genes specifically play in cancer survival, metastasis, and chemoresistance.

Secondary Structure Analysis by SHAPE-MaP of the EGFR and VEGFR2 pre-mRNA Transcripts: Uncovering Novel Regions for RNA Anti-sense Targeted Therapy. Ryan Fink, Sawyer Hicks and Martin Hicks, Monmouth University, West Long Branch, NJ.

A common aberration in Glioblastoma Multiforme is the overexpression and constitutive activation of epidermal growth factor receptor, observed in 57% of all GBM. Our lab developed a novel therapeutic approach which delivers a gene directly to the CNS using an adeno-associated virus gene transfer vector to encode either RNA or protein therapeutics. Our current approach is to deliver an RNA molecule with complementarity to critical splicing elements of the EGFR pre-mRNA transcript. Thus, inducing a soluble decoy and driving a reduction in mRNA. Alternative splicing is regulated by secondary structure of the pre-mRNA nascent transcript. To improve our therapeutic strategy, we have begun experiments to analyze the EGFR secondary structure using selective 2' hydroxyl acylation and primer extension followed by mutational profiling (SHAPE-MaP). The SHAPE reagent (1 -methyl-7-nitroisatoic-anhydride) reacts with the 2' hydroxyl of RNA molecules when the RNA molecule is in a conformationally flexible position creating a 2' O-adduct. The modified RNA is reverse transcribed, incorporating mismatches at the acylated positions; a comparison of unmodified to modified RNA will allow us to determine RNA nucleotides that are involved in secondary structure, part of RNA-binding-protein complexes, or single stranded. Single stranded RNAs and RNAs with minimal structure are a preferential target of our therapy. SKMG-3 cells were subjected to 1M7 or DMSO in cellular and cell-free conditions. RNA was isolated using Trizol and phenol:chloroform:isoamyl alcohol respectively. RNA was reverse transcribed with Superscript IV reverse transcriptase. A gene specific cocktail primer was compared to a random nonamer; our data shows that the gene specific cocktail is more efficient at transcribing nascent RNA of interest. Reverse transcription was optimized using Manganese as the divalent ion needed for DNA polymerase to transcribe through acylated nucleotides. Our results show that we are able to isolate and transcribe nascent modified RNA of interest.

Study of Penicillin Tolerance in Group B Streptococcus. B. Fittipaldi, H. Amin, J. Flores, C. Wang and P. Basu, Touro College of Pharmacy and New York Institute of Technology.

Group B Streptococcus (GBS) remains a leading cause of neonatal infection despite careful screening and antibiotic treatment guidelines. All pregnant women undergo screening for GBS at 35-37 weeks of gestation, for which the most common treatment is penicillin where resistance has not been reported. GBS infections may be due to penicillin tolerance (PT) in which a treated organism is growth-inhibited but remains viable for an extended period of time. However, very little is known about this phenotype behavior in GBS, and its underlying mechanisms. Using a variety of assays, our Group B Streptococcus strains will be characterized as susceptible or tolerant to Penicillin, respectively. The Response of the GBS strains to Penicillin is characterized by measuring their survival on exposure to increasing concentrations of the antibiotic determined separately by the cell density and viability counts. Our data indicate that the survival of both strains decreases with increasing concentrations of Penicillin both in terms of cell density and viability counts. The minimum survival of the 090R strain was at 70%-73%; as for the A909 strain it was at 60-63% at the maximum concentration which in this case was 1024x. This shows that even the highest concentration of Pen G is significantly becoming less active on GBS (A909 & O90R). As a result, 090R was determined to have higher survival on exposure to penicillin than A909 for all concentrations; indicating that A909 is susceptible to Penicillin while 090R is tolerant.

Barcoding of Invasive Plants. Johnny Garcia-Sanchez, Erica R. Pate and Margaret Eiden, Mercy College, Dobbs Ferry, NY.

Invasive plants become invasive by rapidly overgrowing an area that is ideally disturbed, taking over and changing that ecosystem, DNA barcoding was used to better identify several randomly selected invasive plants. We were able to observe the presence of invasive plants in Dobbs Ferry in disturbed ecosystems by using standard field survey techniques. Research was done on the trail way on the Old Croton Aqueduct (OCA) during June of 2018. In the meadow on the OCA, an extensive amount of invasive plants can be seen on the trail sides to the back area with a few native plants hidden within. Through a random selection, some of the plants in that area underwent DNA Barcoding to further confirm these observations. DNA Barcoding uses the DNA sequence found within a living organism to identify it. With this information, a total of 10 plants were identified. Out of the 10 plants, 7 were invasive plants (white clove, lesser burdock, amur peppervine, nippleworts, Orientals ladys-thumb smartweed and Asian plantain) and 3 were identified as native plants (tulip tree, Indian hemp and a sugar maple plant). The amount of invasive plants supports the observation that disturbed ecosystems have more invasive plants, we would like to continue analyzing the native plants within the bunch. There can be a possibility that these identified native plants contain genes that can withstand the disturbance. For future testing, DNA Barcoding can be used to make a comparison with these native plants to similar ones in other regions for ecological restoration purposes. This research is supported by the U.S. Department of Education under Title III HSI-STEM Grant P031C160054.

Role of Phospholipase C in the Dopamine D2 Signaling Pathway in the Control of Lateral Cilia in Gill of *Crassostrea virginica*. Edna Georges[1], Krystle Ernest[2], Edward J. Catapane[2] and Margaret A. Carroll[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 post-synaptic dopamine receptors are D2-type (D2R), G protein-coupled metabotropic receptors. Ligand binding splits its Gi/o protein into Gßγ and Gai/o. Gai/o inhibits adenylyl cyclase. Gßγ opens GIRK channels, closes L-type Ca^{2+} channels and activates phospholipase C (PLC). Adenylyl cyclase inhibition and lowering of cAMP slows GLC cilia. The role of PLC in the signaling pathway has not been well studied with respect to GLC cilia. We hypothesized PLC plays a role in cilio-inhibition. We utilized PLC activators and inhibitors on excised gill to determine their effects on GLC cilia. Applying dopamine (10^{-6} - 10^{-}3M) is cilio-inhibitory, decreasing beating rates to 0. Applying m-3M3FBS (10^{-5} - 10^{-4}M), a PLC activator, decreased cilia beating rates. U73122 (10^{-4}M), a phosphatidylinositol 4,5-bisphosphate specific PLC inhibitor, did not alter cilia beating rates by itself, but did effect the dose response to dopamine (10^{-5} - 10^{-3}M). In the presence of U73122, 10^{-5}M dose of dopamine decreased cilia beating rates, but higher dopamine doses did not reduce beating rates further. D609, a PLC inhibitor but specific for phosphatidylcholine, had no effects on cilia beating or the actions of dopamine. The results supports our hypothesis the PLC component of the D2R signal transduction pathway plays a role in inhibition of GLC cilia. Results show both components of the D2R pathway, the adenylyl cyclase component and PLC component, are involved in controlling GLC cilia beating. In humans, D2R signal transduction pathway is involved in actions of antidepressants, neuroleptics, drugs of abuse and implicated in neuropsychiatric and neurodegenerative disorders. This physiology study is helpful in furthering understanding of the pathway and should help to generate further investigations. This work was supported by grant NIGMS-2R25GM06003, NIH-K12GM093854-07A1 and PSC-CUNY-604060048.

Use of Minnow Traps to Analyze Fish and Macroinvertebrate Usage on a Restored Oyster Reef. Christian Giraldo and Allison Fitzgerald, New Jersey University, Jersey City, NJ.

Oyster reefs provide an ideal environment for many aquatic species to feed, develop and reproduce. For many years the oyster reef at Soundview Park has been under restoration by various organizations. This study focuses on abundance of invertebrate and fish species commonly found on oyster reefs as well as transient fish species, and whether the presence of oysters have influenced species habitat preference. Monthly, a total of twelve fish traps were deployed for 48 hours, six containing oyster and six empty. Three with and without oysters were set out on the reef and the other six were set off the reef. The results show that a greater diversity of organisms was found in areas and traps that contained oysters. Sorenson's Coefficient was calculated to acquire community similarity and this supported the idea that organisms were actively searching out habitats with oyster shells. Though not many transient organisms were found, they are present in the surrounding area. An oyster condition index was also taken over a 3-month period. This showed that the oysters were healthy and reproducing. Despite low catch numbers, probably attributed to trap size, the results of this research show that oysters do influence species habitat preference.

Poly(A) Tail Length of p21 Increases Upon UV-induced DNA Damage. Jessica Gonzalez and Emral Devany, Kingsborough Community College, Brooklyn NY.

Regulation of gene expression after UV irradiation is crucial for cells' correct response to UV-induced DNA damage. Gene expression can be regulated at different steps. In eukaryotes almost all mRNAs undergo an extensive processing after transcription, which includes splicing of introns, addition of 5'cap and 3' poly(A) tail. Further translation of mRNAs can be regulated upon stress by shortening or extending the poly(A) tail. Poly(A) tail is important for mRNA stability, export from nucleus and translation. Here, we focus on the effects and impact of UV induced damage in regulation of two mRNAs that are important for cell faith: p53 and p21. To investigate the effects of UV on the poly(A) tail length of these mRNAs, we performed poly(A) tail test using cDNAs from HeLa cells that are either treated with UV or left untreated. Our results indicate that polyA tail length of p21 increase rapidly (within 15 min) upon UV exposure. These results suggest that p21 protein which is responsible for cell cycle arrest is in part regulated by mRNA 3' processing. Further studies will include detection of effects of different doses of UV-irradiation as well as long-term effects of this irradiation on mRNA expression. This work was supported by grants 2R25GM062003 of the Bridge Program of NIGMS and 0537-18-1091 of the CSTEP Program of NYSED.

Feeding Guilds and Oyster Predation on a Restored Oyster Reef. Laura Gonzalez and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

Our goal for this project was to attempt to map out the species of macrobenthic invertebrates that reside in the Soundview Park Oyster Reef Estuary, and identify their predation habits upon oysters. This was to understand the diets of these creatures, and ultimately understand the population risk of the oysters in the reef. We approached this research with the hypothesis that the most common type of invertebrate we would find would be the type that consumed oysters, leading to a threat to the reef's oyster population outside of common human intervention issues. We collected samples from randomly placed baskets on the reef, taking them back to the lab to identify them using morphological structures. We then used literature to confirm whether or not they predated on oysters. Our results showed no significant difference between the abundance of consumers and non-consumers of oysters, leading to the conclusion that the oyster population is currently in balance. The largest taxon identified on the reef was shrimps, which are surface deposit feeders. Their presence, along with the presence of amphipods, assists with reef construction to compensate for the consumption of oysters by the crabs and clam worms present on the reef.

Selection of an Aptamer to Bind 2-Hydroxygluterate Through SELEX. Danielle Guillen, Artiom Efimenko, Krima Patel, Jennifer Lee and Jonathan Ouellet, Monmouth University, West Long Branch, NJ.

Glioma and Acute Myeloid Leukemia are both cancers that have been linked to the formation of 2-HydroxyGluterate (2-HG) during the third step in the Krebs Cycle. A point mutation on Arginine 132 of IDH1 enzyme causes a gain of function that converts α-Ketoglutarate (α-KG), the correct metabolite, into 2-HG, an inhibitor. The carbonyl group in the molecule is converted into a hydroxyl during the gain of function the enzyme preforms. Up to 86% percent of patients with excess levels of 2-HG have been found to have tumors relating to the above cancers. The goal of the research is to isolate an aptamer, or a single strand of RNA, that can bind to 2-HG with high specificity and accuracy, and then act as a biosensor. Once an aptamer is found, it can then be cloned by use of a plasmid and incorporated into a riboswitch, which acts as a mechanism to turn on and off translation of a desired gene that is placed in the plasmid. In the case of this project, snake venom is a likely candidate to be activated by the binding of the 2-HG metabolite. This will effectively kill any cell that can potentially cause cancer. Through cycles of SELEX, Systematic Evolution of Ligands by Exponential Enrichment, a large pool of randomized RNA sequences is narrowed down, close to Avogadro's number, until eventually the addition of 2-HG to the NA pool shows a high percentage of cleavage, while also showing little to no cleavage with the addition of random molecules, like magnesium is added to the pool.We would like to thank Monmouth University's School of Science and Bristol-Myers Squibb for providing the facilities and funding for this research project.

Testing Exogenous Rescue of Adventurous Motility in Slime Secretion Mutants of *Myxococcus xanthus.* Susan Gutekunst, Asia Alexander and David Zuckerman, 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 in the environment. The GspD protein is 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. We found that GspD mutant cells required vanillic acid for motility, consistent with the interpretation that slime contributes to motility. 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. We will repeat this assay using gspD mutants grown in the absence of vanillic acid to test the requirement for slime secretion on the motility of individual cells.

Detection of Microcystins in the Tissues of Freshwater Shrimp Bought From a Fish Market Near Lake Tai. Ronojoy P. Hem[1], Kristen N. Slodysko[2] and Gregory L. Boyer[2], [1]St. Joseph's College - New York and [2]State University of New York College of Environmental Science And Forestry.

Microcystis is a genus of cyanobacteria found in lakes worldwide. Toxic strains of these cyanobacteria produce toxins called microcystins (MCs), which can disrupt the food web, degrade habitats, and cause human and animal illness which may lead to death. There are proposed guidelines for intake of MCs through the consumption of drinking water, but few studies have actually investigated the dangers of MC uptake from consumption of fish and other aquatic organisms. Here, we have quantified the concentration levels of various MC congeners and their metabolites in the tissues of freshwater shrimp bought from a fish market near Lake Tai (China), a lake that experiences prolonged toxic algal blooms. We also compared the recovery of three methods which have been previously used to quantitate MCs in fish tissue. MC concentrations in these shrimp were highly variable (2 out of 22 samples were above detection limit for MCs) and not high enough to exceed guideline values from a single exposure. However, they do have potential to cause harm from frequent and long-term consumption. This work was supported by SUNY-ESF and SUNY Upstate Medical University's SURF program.

Isolation of EGFR RNA Transcripts to Detect Low Abundant Transcripts. Sawyer M. Hicks and Martin J. Hicks, Monmouth University, West Long Branch, NJ.

Glioblastoma multiforme (GBM) is the most common primary intracranial brain tumor in adults with a mean survival of 14-15 months. 60% of GBM tumors are characterized by the upregulation of epidermal growth factor receptor (EGFR), a transmembrane protein involved in signaling for cell proliferation. Alternative isoforms of EGFR transcripts that may serve as natural soluble decoys are candidate targets for gene therapy. To identify isoforms of EGFR RNA, total RNA from GBM cell-culture lines were isolated using TRIzol™ Reagent RNA extraction protocol. Biotinylated probe for EGFR exon junction sites 1,2 and 2,3 was used to isolate EGFR transcripts from total RNA. EGFR transcripts were then reverse transcribed and prepared for cDNA-PCR sequencing. Initial experiments demonstrate that TRIzol™ RNA extraction along with biotinylated probing of EGFR transcripts and reverse transcription with EGFR gene-specific and poly(A) primers is an efficient methodology to generate EGFR cDNA. Data demonstrates successful isolation of high quality and high quantity EGFR RNA transcript. Moving forward, EGFR RNA transcripts will be isolated from multiple cell lines to both generate adequate sample mass for MinION nanopore sequencing and to detect lower abundant EGFR isoforms found in disease and health.

Inhibitor of CBP Histone Acetyltransferase Downregulates p53 Activation-Potential to Prevent Toxicity from Chemotherapy. Loveth Igbineweka[1], Vimal Arora[1], Mihaly Mezei[2], Michael Ohlmeyer[2] and Shiraz Mujtaba[1], [1]Medgar Evers College, Brooklyn, NY and [2]Mount Sinai School of Medicine, New York, NY.

Tumor suppressor p53-directed apoptosis triggers loss of normal cells, which contributes to the side-effects from anticancer therapies. Thus, small chemical molecules with potential to downregulate the activation of p53 could minimize the pathology emerging from anticancer therapies. Acetylation of p53 by the histone acetyltransferase (HAT) domain is the hallmark of coactivator CREB-binding protein (CBP) epigenetic function. During genotoxic stress, CBP HAT-mediated acetylation is essential for the activation of p53 to transcriptionally govern target genes, which control cellular responses. Previously in this project, luciferase-based assay was used to identify the most potent compound.

Later, the biological activity of the most potent compound was tested by Caspase 3 and BrDU proliferation assays. Here, we present the biological activity of a small molecule, NiCur, that was previously identified by luciferase-based cellular assay. Results showed that NiCur treatment attenuates p53-directed apoptosis by inhibiting the Caspase-3 activity and also rescues the cellular proliferation as determined by BrDu proliferation assay. Collectively, NiCur demonstrates the potential to modulate biological outcomes of CBP-mediated acetylation under normal and disease conditions.

Scavenger and C-Type Lectin Receptors Mediate Phagocytosis of Zymosan in LPS and HMGB1 Stimulated Microglia. Gian Izquierdo, Maria Entezari and A. Lucia Fuentes, LaGuardia Community College, Long Island City, NY.

Neuro-inflammation and accumulation of Amyloid ßeta (Aß) protein are critical components of the pathogenesis of Alzheimer's disease (AD). AD is characterized by impairment of Aß clearance as well as secretion of neuroinflammatory cytokines, including high-mobility group box 1 (HMGB-1). Phagocytosis is a highly regulated process in microglia that involves a variety of receptors. Both HMGB-1 and LPS are recognized by common Pattern Recognition Receptors (PRRs), including TLR-4, C-type lectins and scavenger receptors (SR). However, little is known about the role of these receptors in the regulation of microglial phagocytic capabilities. In this study, we conducted in vitro experiments using BV2 mouse-derived microglia, to investigate the involvement of SR and C-type lectin receptors in the cells phagocytic response to pro-inflammatory molecules. BV2 cells were treated with HMGB-1 and/or Lipopolysaccharide (LPS) for 24 hours, then cells were incubated with zymosan and phagocytosis was quantified microscopically. BV2 cells responded differently to HMGB-1 and LPS. HMGB1 significantly downregulated, while LPS upregulated, phagocytosis of zymosan compared to untreated cells. We found that fucoidan, an SR-A antagonist, abrogated, to some extent, the effect of LPS and further downregulated phagocytosis when added to HMGB-1 treated cells. Addition of Laminarin -a soluble beta-glucan known to bind Dectin-1, a C-type lectin receptor-, significantly downregulated phagocytosis in both control and LPS pre-treated cells. These data point to the importance of SR-A and Dectin-1 receptors in the modulation of phagocytosis observed when cells are exposed to both HMGB-1 and LPS. These findings open the possibility of elucidating the pathways involved in phagocytic stimulation in microglia, which may provide a therapeutic target for enhancing microglial phagocytic activity in AD.

Sex Dimorphism of Engulfment of Microspheres by Primary Murine Macrophages Infected by Influenza Virus. Sidra Jabeen[1], Sonia Nagvenkar[1], Bartosz Czuj[1], Joselyn Landazuri[1], Mohammad Javdan[2], Maria Entezari[3], Richard Lockshin[1] and Zahra Zakeri[1], [1]Queens College and Graduate Center, CUNY, Flushing, NY; Queensborough Community College, CUNY, Bayside, NY and [3]LaGuardia Community College, CUNY, Long Island City, NY.

In this study we wanted to determine sex dimorphism in the phagocytotic ability of murine macrophages. Macrophages typically phagocytose pathogens and limit the spread of infection by undergoing apoptosis. Previously we found that 24 hours post infection (hpi) with influenza virus (IAV), male macrophages died more compared to female macrophages. Here we analyzed whether this sensitivity is derived from differences in the ability of male and female macrophages to phagocytose particles. We found that a higher percent of macrophages from female mice, infected in vitro, actively ingest fluorescent microspheres, and they ingest significantly greater number of beads per cell than male macrophages. We hypothesized that this sex dimorphic behavior is derived from different expression of Toll-like receptors (TLRs). TLRs can detect a broad range of human pathogens to induce antigen presentation, inflammation, direct antimicrobial responses and cell survival. TLR2 and TLR4 especially promote phagocytotic clearance during infection. Based on preliminary data, uninfected male cells express 7 fold more TLR2 than female macrophages. When the cells are infected with IAV at 12 hpi the expression of TLR2 is downregulated in both male and female cells. In case of infected male cells TLR2 is reduced to less than 10% of the mock. The expression of TLR4 increases in infected male macrophages almost twofold, but in females the expression decreases during infection to 30% of the mock. In sum, we have identified a sex dimorphism in the ability of IAV infected murine macrophages to ingest microspheres. We have identified a difference in the behavior of TLR2 and TLR4 receptors but we have not yet established a causal sequence or a sequence that links the difference in phagocytosis to the greater lethality of IAV in primary mice macrophages. These questions will be the basis of further studies.

Taurine Protects Against the Neurotoxic Effects of Manganese on the Dopaminergic Control of Lateral Cell Membrane Potential and Ciliary Response in Gill of *Crassostrea virginica*. Alexcia Johnson[1], Aliyah Howard[2], Margaret A. Carroll[1] and Edward J. Catapane[1], [1]Medgar Evers College and [2]Kingsborough Community College, Brooklyn, NY.

Manganese, a neurotoxin causing manganism, a Parkinson's-like disease, disrupts dopaminergic neurotransmission. The mechanism is not fully resolved. Unlike Parkinson's, reports postulate manganese neurotoxicity is more related to downstream neuronal pathways rather than deficits in nigrostriatal function. Lack of effective treatment for manganism has been a major

obstacle in its clinical management. Gill lateral cell (GCL) cilia of *Crassostrea virginica* are controlled by serotonergic -dopaminergic innervations. Dopamine hyperpolarizes GLC and causes cilio-inhibition, while serotonin depolarizes and causes cilio-excitation. Previous work of our lab showed acute and short-term manganese treatments blocked the cilio-inhibitory effect of dopamine, which could be prevented by p-aminosalicylic acid or by taurine, an amino acid with efficacy in other neurodegenerative disorders. In this study we hypothesize taurine would prevent the toxic actions of manganese on dopaminergic membrane hyperpolarization and GLC cilia inhibition. We conducted acute experiments on dopamine dose responses (10^{-6} - 10^{-3} M) of manganese treated excised gill in the presence or absence of taurine. GLC ciliary activity was measured by stroboscopic microscopy and expressed as beats/min ± sem. Cell membrane potentials were simultaneously measured using the fluorescent dye $DiBAC_4(3)$. In control gill, GLC responded normally to dopamine dose responses showing decrease in cilia beating and membrane hyperpolarization. Gills treated with manganese (2×10^{-4}M) had a disrupted dopamine response, cilio-inhibition was impaired and the membrane did not hyperpolarize. Taurine (2×10^{-4}M) prevented these neurotoxic effects in manganese treated gill. This physiological study in *C. virginica* shows manganese disrupts the dopaminergic post-synaptic response of GLC preventing membrane hyperpolarization as well disrupting cilio-inhibition, and taurine blocked these neurotoxic actions. These findings are helpful in furthering the understanding of the mechanism of manganese neurotoxicity and provides evidence suggesting taurine be further investigated as a potential therapeutic agent for manganism. This work was supported grants NIGMS-2R25GM06003, NIH-K12GM093854-07A1 and PSC-CUNY-604060048.

Real Time PCR for Quantification of *Escherichia coli* in Soil and Compost Samples. Hyunbin Kang, Arianna Pinto, Vanesa Molina, Stephania Vazquez and Luis Jimenez, Bergen Community College, Paramus, NJ.

Escherichia coli is a member of the fecal coliform group and is a more specific indicator of fecal pollution than other fecal coliforms. A quantitative real time PCR assay (QPCR) was developed to detect *E. coli* in soil and compost samples. Bacterial DNA was extracted from soil and compost samples. The QPCR assay using the Roche LightCycler 96® system detected the 147 bp beta-glucuronidase (uidA) fragment with SYBR green I, a common double-stranded binding dye. The cycle at which fluorescence from amplification exceeds the background fluorescence was referred as quantification cycle (Cq). Serial dilutions of *E. coli* DNA were analyzed to determine the sensitivity of the assay. The standard curve was able to reliably quantified *E. coli* DNA down to 0.06 ng/ml (R2=1.00). *E. coli* was detected in 6 samples of soil and compost.

Atlantic Oyster Drills (*Urosalpinx cinerea*) from the Hawk's Nest Site in Delaware Bay Do Not Contain DNA from the Dermo parasite (*Perkinsus marinus*). Fatima Kataria, Lilja Nielsen and Craig S. Hinkley, Kingsbororugh Community College, Brooklyn, NY.

Eastern oysters (*Crassostrea virginica*) are both environmentally and commercially beneficial. Oyster reefs serve as habitats for many marine organisms and these organisms form an important part of the marine food web. However, there has been a decline in eastern oyster populations since the early 1900's for several reasons, including diseases such as Dermo. Dermo is a disease caused by an alveolate protozoan, *Perkinsus marinus*, and can be transmitted directly from oyster to oyster. However, there could be a vector besides oysters for the transmission of Dermo. One possible vector is the Atlantic oyster drill, *Urosalpinx cinerea*, a marine snail that is a predator of oysters. Our main question is whether oyster drills serve as a vector for Dermo. However, in order to be a vector, the oyster drill must be capable of harboring Dermo. We hypothesize that oyster drills can harbor the Dermo parasite. To test this hypothesis, we first isolated DNA from twelve oyster drills collected in Delaware Bay. We then used PCR to amplify a region of the *P. marinus* 5S-ribosomal RNA gene from the oyster drill DNA and a positive control. Agarose gel electrophoresis was used to verify the size of the amplified DNA. Dermo DNA was not amplified from any of the oyster drill samples; however, there was a PCR product of the correct size from the positive control DNA. To confirm that we can amplify DNA from the oyster drill, we performed a PCR reaction using a primer set specific for the cytochrome-c-oxidase gene. DNA of the correct size was amplified from of the twelve oyster drills. Taken together, these results suggest that Dermo is not present in the oyster drills we tested. Therefore, our hypothesis is not supported by our results. This work was supported by grant 0537-18-1091 of the CSTEP Program of NYSED.

Identification of Telomere Length Regulating Genes in Bobbi Kennedy, Priscilla Martinez, Tatiana Chauca, Juan Hurtado, Philip Mangerino, Steena Samuel and Chun Zhou, Mercy College, Dobbs Ferry, NY.

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

retrotransposition in Drosophila. There are over 400 genes localized between the sr and e gene markers on the chromosome 3R. We investigated the sequences of these genes and domains of their encoded proteins. The functions of these proteins were obtained from FlyBase, an online bioinformatics database, or revealed by their homologous proteins of known function; the latter was achieved by using the Basic Local Alignment Search Tool (BLAST). We then classified these genes into four categories: Directly Likely (related to chromosomal stability), Potentially Likely (related to the retrotransposition process: transcription, translation, mRNA transportation and targeting to telomeres, reverse transcription, and DNA second strand synthesis), Less Likely (involved in other cellular pathways), and Unknown (protein function unclear). Currently, we are conducting the molecular genetic study, such as real-time PCR, to probe whether the genes in the Directly Likely category can function in regulating telomere length.

Identifying How Signal Peptide Peptidase Functions Together with Linker Histone H1 in Blood Tumor Regulation Caused by Hyperactive JAK/STAT Signaling. Si Man Ao Leong and Na Xu, LaGuardia Community College, Long Island City, 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. We further discovered that the interaction of H1 and STAT plays an important regulatory role in JAK-STAT-induced blood tumor formation in flies. 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 SPP, encoding Signal Peptide Peptidase. Signal Peptide Peptidase cleaves parts of proteins. The SPP knockdown affects EGFRvIII secretion profiles, which associated with JAK/STAT signaling. EGFR is not only involved in regulation of proliferation, but also mediate STAT activation directly. Our data suggested that Signal Peptide Peptidase and/or EGFR signaling may function together with H1 in regulating blood tumor formation caused by hyperactive JAK/STAT Signaling.

Isolation Characterization of Mycobacteriophages at SUNY Old Westbury and Annotation of Rahel, a C1 Cluster Genome. Adwoa Lewis and Karthik Madhira, SUNY Old Westbury, Old Westbury, NY.

SUNY Old Westbury joined the 10th Cohort of HHMI SEA-PHAGES last fall 2017 semester. The phage discovery component was integrated into the general biology I laboratory (BS2401) and the bioinformatics component into the general biology II laboratory (BS2411). Herein we report the results of the Phage Discovery component. The course enrolled 24 students. Twenty three viruses were isolated. Only two of them were isolated using direct isolation. All of them were isolated from soils in Nassau or Suffolk counties. The phages were isolated and purified at SUNY OW. The furthest distance of the collection sites is 29 miles. The viruses use as a host the *Mycobacterium smegmatis*. Using TEM we identified two different morphotypes, 11 are siphoviridae and 12 myoviridae. One of them Rahel, isolated by Jane Thomas from a flower bed in Hicksville, NY. It forms plaques of approximately 1 mm in diameter and its titer is 3.07 x 1012 PFU/ml. It was usesent to the University of Pittsburgh for sequencing using Illumina sequencing with a shotgun coverage of 471. Rahel has a Myoviridae morphotype. It has 155,955 base pairs and 64.7% GC content. It belongs to the C1 cluster of *M. smegmatis* mc2155 phages. As reported by DNA master Rahel has 266 genes of which 32 are tRNAs. Of the 229 protein coding genes 252 are coded in the forward strand and only nine on the reverse strand. Its closest C1 cluster relative ArcherS7 has 268 genes 43 for which the function is known. Using comparative genomics we manually validated the start-up codons, out of the 266 we change the starting codon for 30 genes. Gene density in Rahel is 1.7 genes/kb indicating high gene density. ArcherS7 has 4 more genes and is around 1kb longer than Rahel indicating that genome expansion is due to gene content.

Antibacterial Effects of Yerba Mate. Sabrina Lopez, Yan Wang, Alexandra Greco and Tinchun Chu, Seton Hall University, South Orange, NJ.

Yerba Mate (YM) grows in various areas in South America, Southern Brazil, and in Northeastern Argentina. In addition to being a widely consumed beverage, several studies have suggested that Yerba Mate has antimicrobial activity. The aim of this study is to evaluate the antibacterial activity on Gram-positive bacteria, including S. *epidermidis*, and *S. mutans*; and Gram-negative bacteria, including *E. aerogenes*, *E. coli*, and *P. aeruginosa*. Microplate-based assay and the colony-forming unit (CFU) assays were used to determine half maximal inhibitory concentration (IC50) and minimum inhibitory concentration (MIC). Congo Red Assay was used to test the inhibitory effects of Yerba Mate on biofilm formation. Germination and Sporulation assays were used to test the inhibition of endospore growth on *B. cereus* and *B. subtilis*. The results from the microplate-based assay showed that 4% YM is the MIC for all selected bacteria, while the IC50 concentration ranged from 1.5 - 2.0 % of

YM. Percentage inhibition of bacterial growth was calculated based on the results obtained from the CFU assay. The results from Congo red assay indicated 4% YM was able to inhibit biofilm formation. Preliminary results showed ~6% YM could inhibit both germination and sporulation on *B. cereus* and *B. subtilis*.

Synthesis and Biological Activity of Substituted Pyrroles. Shuai Ma, Sasan Karimi, Gopal Subramaniam, Sounak Ghosh Roy, Panayiotis Koumas and Zahra Zakeri, Queens College of CUNY, Queens, NY and Queensborough Community College of CUNY, Bayside, NY.

Pyrrole skeleton is found in some colored natural products such as chlorophyll, hemoglobin, and indigo. Some of its substituted derivatives have biological activities and its trisubstituted derivative is a biosynthetic precursor to many natural products such as heme. Functionalized pyrroles are used for anti-tumor, anti-inflammatory, anti-bacterial, anti-oxidant, and anti-fungal agents. We recently reported syntheses of several substituted pyrroles based on Cadogan-Sundberg synthesis of indole and carbazole. The approach involves treatment of an aromatic aldehyde with a nitroalkane in the presence of NH4OAc to produce a nitrodiene. Subsequent treatment of nitrodiene with a Mo catalyst and triphenyl phosphine produce substituted pyrroles in one step. This simple procedure developed in our lab allows formation of a variety of substituted pyrroles that can be tested for biological activities. Using MDCK cell lines and caspase-3 (Asp 175) and Sequestosome 1 (p62) assays, we tested cell proliferation, viability and cytotoxicity. We have already examined the effect of two compounds, 2-ethyl-5-(4-methoxyphenyl)-1H-pyrrole (A) and 5-ethyl-3-methyl-2-phenyl-1H-pyrrole (B) in MDCK cell. The results showed the compound B is more toxic than compound A. We then tried a different cell line, Vero cells (African green monkey kidney epithelial cells), and exposed them to these two compounds. The results were completely reversed by MDCK cell lines. In the future, we will examine the effect of these compounds on different cancer cells to investigate cell proliferation, viability and cytotoxicity. This work Supported by Grant from NIH # 2T34GM070387 to Zahra Zakeri.

Comparison of the Response of Microglia and Primary Murine Macrophages Upon Exposure to Pesticides. Amirabbas Maghsoudi, Mohammad Javdan and Zahra Zakeri Queensborough Community College, Bayside, NY and Queens College, Flushing, NY.

The etiology of most neurodegenerative disorders, such as Alzheimer (AD) and Parkinson (PD) diseases attributes to genetic predispositions and exposure to harmful environmental factors. Limited studies have been documenting the long-term/low dose exposure to pesticides as one of the risk factors in developing of AD and PD. Microglia within the central nervous system playing a central role in response to chronic injury or inflammation. In response to chronic injury or inflammation microglia become activated contributing to a cycle of toxicity. In these cases, infiltrating macrophages assist microglia to attenuate inflammation in the CNS. Both microglia and macrophages participate in these responses, but the different function of these two populations under inflammatory stimuli remain to be elucidated. Since most brain macrophages are monoecious, we hypothesized that microglia and infiltrating macrophages have similar responses to inflammatory stimuli. The aim of this study was to compare the cell viability and functional properties of macrophages and microglia in response to challenge with pesticide. Our study was performed using two cell lines, BV2 microglia, and peritoneal macrophages. The cells were treated with 1 and 5μg/ml of Permethrin for 24 hours. Cell viability was assessed by MTT assay and phagocytic function was determined following treatment with Permethrin by counting the number of phagocytic cells as well as the number of particles per cell after incubation with latex beads. Our results showed Permethrin significantly reduced cell viability and the phagocytic ability of microglia at both 1 and 5μg/ml compared to untreated control cells. Both concentrations of Permethrin did not affect on viability and the phagocytic ability of peritoneal macrophages compared to untreated control cells. Our results show the importance of further investigating the behavior of different populations of macrophages to understand the particular mechanisms involved in inflammatory processes in the brain in response to pesticides.

American Horseshoe Crabs (*Limulus polyphemus*) Juvenile Population Growth on Plumb Beach, Jamaica Bay, NY. Kera Mansfield and Christina Colon Kingsborough Community College.

In 2012 just before superstorm Sandy The US Army Corps of Engineers renourished the western side of Plumb Beach (Jamaica Bay, Brooklyn, NY). This was done to protect the Belt Parkways from superstorm Sandy and to stabilize the sandy shoreline. The American Horseshoe Crab (*Limulus polyphemus*) come ashore to spawn, showing a distinct preference for the undisturbed segment. This gave researchers the opportunity to study the horseshoe crab's response to the renourished beach. Shed carapace of juvenile horseshoe crabs reveals information about the population size, distribution, and age. While few carapaces are normally observed only in late summer, in 2018 carapaces were seen all along the east beach starting in June. For this reason, it was hypothesized there will be more carapaces on the Eastern side of Plumb Beach than the Western side, there will be more in 2018 than in past years, and the carapaces will provide an index of growth throughout the season. After collecting and measuring all carapaces found from June to September a total of 606 carapaces were found on the eastern beach and only 9 on the western. In total this season a total of 615 carapaces were collected. As the season went on, the average size of carapaces collected

was bigger, but there were also some smaller ones found. These indicated that juveniles that hatched earlier in the season were present and growing in size. These data served to indicate that the population of horseshoe crabs are doing better than they were in past years and that they are also growing in numbers. This work was supported by grant 2R25GM062003 of the Bridge Program of NIGMS and grant 0537-18-1091 of the CSTEP Program of NYS Department of Education.

Role of Formins in Morphogenesis and Development of the *C. elegans* Pharynx. Jeff Martinez[1], Angelica Barreto-Galvez[2], Sofya Borinskaya[2] and Martha Soto[2], New Jersey City University, Jersey City, NJ and [2] Rutgers University, Piscataway, NJ.

In multicellular organisms actin plays major roles in the developmental processes of cytokinesis, cell polarity establishment, cell migration, and morphogenesis. Actin monomers polymerize into linear or branched actin. Disruptions of these structures are often found in metastasizing cancers having implications for human disease. In the *C. elegans* model organism branched actin was shown to play roles in ventral enclosure and nuclear migration during morphogenesis. I asked if linear actin is important for morphogenesis too. There are 7 formins in *C. elegans* that can regulate linear actin: FOZI-1, INFT-1, DAAM-1, FRL-1, INFT-2, FHOD-1, and CYK-1. I have shown by DIC imaging that inhibiting formins using RNAi causes morphogenetic defects including defects in the pharynx. The lumens of the pharynx and the intestine were wider in CYK-1-depleted embryos. Therefore, I tested two hypotheses about the role of formins in pharyngeal development: formins regulate (1) the fate of pharyngeal cells and (2) the polarity of the pharynx during morphogenesis. Using a genetic cross, I generated a strain with epithelial marker DLG-1 and pharyngeal fate marker PHA-4. To assess protein levels, I acquired confocal images of embryos and measured fluorescence intensity. I found that in DLG-1::RFP; PHA-4::TY1::GFP embryos depleted of CYK-1 and INFT-1, expression of PHA-4::GFP was significantly decreased. At the same time pharyngeal epithelium did develop indicated by the marker DLG-1. These contradictory results call for more investigation of CYK-1 and INFT-1 on pharyngeal fate. I found that cell polarity could be affected because CYK-1 depletion caused a drop in ERM-1::GFP (apical surface marker) and NMY-2::GFP (non-muscle myosin) levels in the apical pharynx. In summary, all seven formins cause morphogenesis defects. It is not clear if CYK-1 and INFT-1 affect pharyngeal fate. However, they affect pharyngeal cell polarity. This work was supported by NIH-funded INSPIRE IRACDA Fellowship (GM093854) and (GM081670) to M.S.

Therapy RNA Interactions With HNRNPS to Induce Alternative Splicing in GBM, Michael R. Mazzucco, Flobater I. Gawargi, Koushik Muralidharan, Ryan N. Fink, Sawyer M. Hicks, Kevin Gallagher, Sarah Falotico and Martin J. Hicks, Monmouth University, Long Branch, NJ.

Glioblastoma multiforme (GBM), a grade IV tumor of the central nervous system, is the most common malignant primary brain tumor, having a median survival of only 14 months. GBM tumors are characterized by angiogenesis, which is essential for tumor growth and survival. To develop a new treatment, our lab has designed an RNA therapeutic vector against the pre-mRNA of the pro-angiogenic transcripts, EGFR and VEGFR2. This therapy induces alternative splicing leading to shortened mRNA transcript isoforms, which translate into soluble decoy proteins as opposed to the canonically spliced full-length transmembrane receptor. These soluble decoys competitively bind the EGF or VEGF growth factors, without activation of the intracellular tyrosine-kinase phosphorylation signaling pathway. Targeting of key splicing elements by RNA antisense therapeutics is complemented by the molecular cloning of a heterogenous ribonucleoprotein hnRNP binding domain into the RNA therapeutic vector, effectively silencing the site by intronic redefinition. Currently, we are developing methods to test hnRNP binding to RNA therapy. I have cultured, isolated and purified recombinant poly-histidine/ FLAG tagged hnRNP vectors. After induction and isolation with IPTG, multiple SDS-PAGE and Western Blots have been performed testing refolding and elution from Ni-NTA column by imidazole or pH gradient demonstrating multiple proteins in final elution. The negative control cell lysate did not show significant difference from the induced to confirm expression. To demonstrate effective induction and expression for isolation of purified hnRNPs, I am cloning a negative control pET expression vector. The pET vector DNA has been restriction enzyme digested, to remove the protein coding region, and Klenow fragment to blunt end overhangs for subsequent ligation and transformation. This would create an empty expression control for definitive negative control in observation of IPTG expression of recombinant hnRNPs efficacy.

Juvenile Hormone Mimics Induce Lamellocytes Through the JAK/STAT Pathway in *Drosophila melanogaster.* Carolyn McGrail, Raquel Calero, Givwnchy Ayisi-Boahene and Rebecca Spokony, Baruch Collegen New York, NY.

The JAK/STAT pathway is conserved across Metazoans, with roles in blood development in both human and Drosophila. Methoprene and pyriproxyfen are juvenile hormone (JH) mimics used as insecticides that prevent metamorphosis. Lamellocytes are hemocytes that are induced upon large parasitic infection. Constitutively active JAK leads to lamellocyte formation in the absence of parasitoid eggs. Typically, the JAK/STAT pathway is activated when a ligand binds to the DOME receptor, leading to phosphorylation of the receptor associated JAK tyrosine kinase HOP and then STAT92e. This allows

STAT92e to enter the nucleus and initiate gene expression. After treating JAK/STAT Green Fluorescent Protein (GFP) reporter lines with methoprene, expression in the muscles for a 10XSTAT92e-GFP construct and in the fat body for DOME-MESO-GFP was greater than in control larvae. A lamellocyte tagged fluorescent line, msn-mCherry, was treated with methoprene and pyriproxyfen which induced a large quantity of lamellocytes while no lamellocytes were produced in the control larvae. Based on these results, we predict that JH mimics induce an immune response in the JAK/STAT pathway through lamellocyte formation. Knockout DOME and STAT92e constructs were crossed with tissue specific drivers to determine the location and genes necessary for JH mimic induced lamellocyte formation. Our preliminary data indicates that there are fewer lamellocytes when DOME and STAT92e are knocked down in prohemocytes. Knocking down STAT92e in muscles and DOME in fat body also produces less lamellocytes and is in accord with our earlier findings of JAK/STAT activation in specific tissues. The quantity of lamellocytes will be compared across the crosses to determine the significance of knocking out genes in specific tissues. Determining the location and genes involved in lamellocyte formation will demonstrate an additional role of methoprene and its effect on immunity in Drosophila and could be relevant for research on environmental triggering of JAK/STAT in humans.

Expression and Purification of the *Streptomyces colicolor* SCO3855. Juan J Mesa[1], Yafit Muladjanov[2], Naydu Carmona[1] and Monica Trujillo[1], [1]Queensborough Community College and [2]Queens College, Bayside, NY.

Rhomboids are intramembrane proteases present in all kingdoms of life with functions loosely associated with cell signaling. Streptomyces are soil bacteria with a complex life style highly regulated through cellular and environmental interactions. Our goal is to identify the role of a rhomboid protease from *Streptomyces coelicolor*, SCO3855, in the regulation network. This study specific aims are: 1) optimize parameters for maximum expression of the SCO3855 rhomboid in E. coli; 2) purify the S. coelicolor rhomboid. Two strains were tested as hosts: BL21(DE3), a widely used T7 expression *E. coli* strain, and pLemo, a rhamnose dependent tunable T7 expression. For each strain we tested different induction temperatures; inducer and/or inhibitor concentrations; and induction times. Our group cloned an *E.coli* codon optimized version of the SCO3855 gene into the pET-28 plasmid. Afterwards, the stop codon of the SCO3855 gene was removed by site directed mutagenesis obtaining an in frame protein fusion with the 6X His coding sequence from the pET-28 vector, SCO3855_6X His (plasmid pET_28b_SCO3855**). Competent cells of the two host strains were transformed with the pET_28_ SCO3855** plasmid using standard procedures. We tested 20°C, 28°C and 37°C as induction temperatures; rhamnose concentrations 250, 500, 750 and 1000 mM and induction times of 3, 5 and 20 hours. Aliquots of the corresponding pellets were loaded on polyacrylamide gels and separated by electrophoresis. Using an anti-his monoclonal mouse antibody the SCO3855_6X His fusion protein was detected by Western blot. The best level of expression was obtained when pLemo pET_28_SCO3855** cells were induced with 400 ?M IPTG and 750 mM rhamnose, and grown at 28°C, 200 rpm, for eight hours. Preliminary results for purification using Ni columns are shown. Pure preparations of the SCO3855 rhomboid will be used for crystallization trials.

LRRC8a mRNA Expression in Chick Astrocytes. Joseph Minkler, Alison Quijano, Antonio Ray and Renee Haskew-Layton, Mercy College, Dobbs Ferry, NY.

Volume Regulated Anion Channels (VRACs) are plasma membrane proteins that defend against cellular lysis. They provide a new avenue towards future drug development to lessen the amount of osmolytes, like glutamate, that are essential in small amounts and toxic in high amounts when released excessively through VRAC activation. VRACs are primarily composed of the leucine-rich repeat-containing protein 8A (LRRC8a) protein. Prior research has determined this protein to be omnipresent in mammalian cells. This study serves to widen the umbrella of VRAC expression to other organisms, and to establish a greater understanding of the regulation of channel expression. Currently, our study has confirmed the presence of LRRC8a mRNA in chicken neurons and astrocytes via real time polymerase chain reaction (rtPCR). The current phase of this study examines the mRNA expression of LRRC8a in chicken neurons in response to cell swelling induced by hypotonic media exposure. We hypothesize that cell swelling will increase LRRC8a mRNA expression as a protective feedback mechanism because of VRACs function in preventing cells from lysing. Methods used to test our hypothesis include obtaining a neuron rich primary culture from chick embryos, isolating RNA, and performing rtPCRs. The neurons were cultured at embryonic day six from the optic tectum of chick embryos. Their RNA was then isolated using an RNA binding column and rtPCR was carried out using primers for both LRRC8a and GAPDH (as a positive control).

DNA Replication Genes Implicated in Heterochromatin Modulation. Tasmiya Moghul[1], Pragati Sharma[2,3], Eve Reilly[2] and Miguel A. Zaratiegui[2], [1]Medgar Evers College, Brooklyn, NY, [2]Rutgers University, Piscataway, NJ and [3]Rutgers-Robert Wood Johnson Medical School, Piscataway, NJ.

DNA is stored in the nucleus in complex with protein factors. The condensed structure, chromatin, is categorized as euchromatin, a loose form and heterochromatin, a denser form. Heterochromatin functions include: suppression of recombination of transposable elements, segregation of chromosomes and

regulation of gene expression. Heterochromatin is vital for maintaining genomic stability. Heterochromatin is classified as facultative (assembles and dissembles for gene expression regulation) and constitutive (condensed throughout the cell cycle). Condensed heterochromatin is unraveled during DNA replication. How cells know when to change heterochromatin for replication or to return to its previous compact state is a question. The goal of this project is to understand molecular factors helping modulate heterochromatin to allow replication through silenced regions. Using fission yeast, we conducted a forward genetic screen with Hermes transposon as a random mutagen to obtain Position Effect Variegation mutants of heterochromatic ade6 reporter gene. We identified mutants showing loss of silencing at the reporter gene; a number of which were found to be in essential genes. Selection for loss of silencing at the pericentromeric ade6 reporter corresponded with enrichment in mutants of DNA replication and repair genes. We hypothesize these mutants can be recreated with CRISPR-Cas9. The aim was to generate mutant alleles of essential genes involved in DNA replication and repair and validate their heterochromatin mutant phenotype. Using CRISPR-Cas9 genome editing, we targeted five genes in fission yeast: Vid21, Orc4, Cut1, Cut9, Drc1, and Dcr1 as a control. We generated viable mutant alleles that otherwise are difficult to generate using conventional genetic manipulations. This study of the characterization of mutant alleles will enable us to understand their role(s) in the coordination of heterochromatin states and DNA replication and/or repair. This work was supported by RiSE at Rutgers, NIH grants K12GM093854-07A1, NIH T32GM8339 and RO1 GM105831.

Microbiology: The Human Microbiome. Vanessa Molina, Kadiatou Fadiga, Arianna Pinto, Adelajda Turku and Luis E. Jimenez, Bergen Community College. Paramus, NJ.

Bacterial samples were analyzed from different parts of the human body to conduct phenotypic and genotypic tests to identify the microbiome of a student population and relatives. All bacterial colonies were analyzed by Gram stain followed by DNA extraction, DNA quantification, Polymerase Chain Reaction (PCR), and nucleotide BLAST analyses. PCR analysis of 16S rRNA and spa genes identified and separated bacteria into different types. Antibiotics and natural oils testing determined the sensitivity of bacteria to the tested compounds. Most bacteria were found to belong to the genera Staphylococcus and Streptococcus. They showed different levels of sensitivity to antibiotics and natural oils. Nostrils samples showed that some people were colonized by *Staphylococcus aureus*. *S. aureus* was found to belong to different genotypes based upon spa gene sequences.

An Investigation in the Immunity Repressor of Gordonia Terrae Phage ShayRa (A15). Mariana P Moraes and Jacqueline Washington, Nyack College, Nyack, NY.

Bacteriophages are one of the most genetically diverse entities on earth. Phages have the ability to infect bacteria and lyse them, and research on bacteriophages has been instrumental in the understanding of phage biology and evolution. Some phages are lytic where they infect and kill their host, while some phages are lysogenic and have the ability to maintain their DNA in the host's genome. Consequently, the investigation of the lysogenic cycle is critical to the understanding of phage-host interactions, which could lead to possible manipulation of pathogenic bacteria for beneficial purposes. In 2016, a Nyack College student isolated bacteriophage ShayRa using Gordonia terrae 3612 as a host. ShayRa is a member of the (sub)cluster A15. Genome sequencing notes revealed that the phage has a deletion in the region where the immunity repressor is typically found. This gene represses the lytic genes which is important for the phage to enter a lysogenic cycle. However, in 2017, a lysogen was unexpectedly recovered from phage ShayRa despite the noted absence of the repressor gene. Primers were designed to investigate the region where the repressor is typically found in A15 phages. PCR was performed using the original ShayRa phage as a control in addition to the ShayRa lysogen. Results showed that the original sequenced phage had the expected 815 bp PCR product but the lysogen produced a much larger PCR product of approximately 3kb. This larger size indicates that there is additional DNA present in the lysogen, not present in the sequenced phage. This indicates that the phage which was sequenced was missing the region including the repressor and that there was a very low level of intact phage in the lysate used to make the lysogen. Consequently, these phages were able to be maintained in the host genome to form lysogens.

Are Music Genres That Are Broadly Accepted As Stress-Reducing As Effective At Reducing Physiologic Stress Parameters As One's Own Choice of Music? Priyanka Moses, Angelica Salgado and Jodi F. Evans, Molloy College, Rockville Centre, NY.

Listening to music brings physiological parameters back to homeostasis after an acute stress and is a well-studied stress-reducing tool. In many studies the music used was chosen by researchers and was generally a type of music broadly viewed as stress-reducing. Our aim was to determine if independent choice reduces physiologic stress parameters to a greater extent than a commonly used music choice or listening to no music. We hypothesized that an independent choice of music by the participant would have a greater impact on physiological recovery after an acute stress. We randomly assigned 30 college students into one of three groups; music provided (OC), individual music choice (TC), and no music (NM). The participants heart rate, blood pressure, and saliva sample were taken before the stressor, after the stressor,

and after the music condition. Saliva samples were used to measure cortisol. Participants also completed the STAI after the music condition. In response to the mild stressor, heart rate and blood pressure increased in 63.3% and 50% of all participants, respectively. On the other hand cortisol levels were increased in only 30% of participants. After the music condition, BP was reduced in a greater percent of students in the OC group compared to the NM and TC groups and cortisol was reduced in a greater percent of students in the NM and TC groups compared to the OC group. When only students who responded to the stressor were considered, BP was reduced in all students in the OC group, HR was reduced in all students in the TC group; and cortisol was reduced in all students in the NM group. Overall our findings indicate that the accepted music piece produced the most disparate physiologic responses when compared to listening to one's own music choice or no music at all.

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

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

Synthesis of Exosome-Associated AAVs to Deliver RNA Therapeutic Strategies to Block VEGFR2 and Angiogenesis in Human Glioblastoma. Koushik Muralidharan, Flobater I. Gawargi, Kerianne Fuoco, 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. GBM tumors are characterized by angiogenesis, which is essential for tumor growth and survival. Endothelial cells form the walls of new blood vessels, connecting the growing tumor mass to the established vasculature of the circulatory system. The membrane receptor that activates tumors to recruit endothelial cells to promote angiogenesis is vascular endothelial growth factor receptor 2 (VEGFR2). In our lab, we are developing therapies to alter the expression of VEGFR2 to block its activation, inhibiting vascularization. We have designed nine antisense sequences that target and block critical elements of the VEGFR2 pre-mRNA transcript. These therapies were cloned into therapeutic vectors that direct the antisense RNA therapeutic to the spliceosome machinery. All clones generated were confirmed using PCR and verified by Sanger sequencing. U87 GBM cells were cultured and transfected with therapy vector KM9, and the total protein was collected and analyzed. Analysis of the collected protein revealed a significant two-fold reduction of VEGFR2 in tissue culture. Currently, we are testing additional clones and analyzing alterations in splicing at the RNA level. Future directions include delivery using an adeno-associated virus (AAV) in a mouse model.

The Effect of Rising Sea Level on Coastal Vegetation in South Carolina. Rahema Nasary, Abiesha Smith, Khadija Yousuff, Jasmine Burkett, Teryn Mingo, Liya Thomas, Enxhi Seitllari, Kimarie Yap, Meryem Toppa and Richard Stalter, St. John's University, Queens NY.

In the present study, we examine the effect of rising sea level, a product of global warming, on the distribution of coastal vegetation at five sites in South Carolina. Rising sea level with a concomitant increase in water salinity and duration of submergence is changing plant diversity in coastal salt marsh and brackish marsh communities. We present data at three brackish marsh abandoned rice fields and a salt marsh at the Baruch Institute, Georgetown County, SC and a fifth site, a skeleton live oak stand in southern Beaufort County, South Carolina. Rising sea level has impacted vegetation at our three abandoned rice fields reducing vascular plant diversity at the two least saline sites, Air Port marsh and

Alderly. *Sporobolous alterniflorus* a salt marsh associate is not present at Alderly, the least saline, abandoned rice field, testimony to rising sea level and increase water salinity. The more flood tolerant *Borrichia frutescens* is replacing *Sporobolus pumilus* at the salt marsh at Clam Bank. A stand of live oak, Quercus virginiana, has been replaced by salt marsh taxa, *Salicornia virginica* and *S. alterniforus* at Beaufort County site. Sea level has been rising at a rate of 3mm/yr since 1930 and may rise at a greater rate in the future, impacting the vegetation of the aforementioned communities and additional coastal marsh and upland communities along the east coast of the United States.

Beta-barrel Assembly Pathway and Quality Control in Gram-negative Bacteria. Lindsey Njanja, Matthew Doyle and Harris Bernstein, Bergen Community College and National Institute of Health, Rockville Pike, Bethesda, MD.

Gram-negative bacteria have 2 membranes: the outer membrane and the inner membrane. They heavily rely on Outer Membrane Proteins (OMPs) for survival and virulence properties. These OMPs are integrated and assembled into the outer membrane by a protein complex, called the Beta-barrel Assembly Machinery Complex (BAM complex). The BAM complex has long been studied for a long time, but one of the challenges in its study is that the integration takes place in a very fast pace. To slow down the process, we created a fusion protein that is attached to a polypeptide chain to 'jam up the system.' We called the protein fusion an OMP-knot. When the bacteria are exposed to an OMP-knot, they die because their OMP supply is cut short. After a series of experiments. it was observed that longer and shorter linkers between the OMP barrel and the protein fusion have a difference in the expression of phentoypes. The cells with the longer linker survive, while those with a shorter linker die. We hypothesized that DegP, a protease in the periplasm could be responsible for clipping out the protein fussion. To test the hypothesis, 2 strains of Escherichia coli (DegP +/-) were used. Out of the two strains, four growth assays were tested. A longer linker with and without a knot (protein fussion), and a shorter linker, with and without a knot. We concluded from our observations that DegP is not the only protease responsible for clipping out the knot. This is because the strains used for this experiment has OmpT, a protease in the outer membrane omitted. This experiment led to a new hypothesis that the observed difference in lethal phenotypes due to OMP-knot (protein fussion) linkers may be multifactorial and probably attributed to OmpT. Supported by the Office of Intramural Training & Education.

***Cryptosporidium parvum* Was Not Found in Eastern Oysters from Delaware Bay. Sandra Perea, Lilja Nielsen and Craig Hinkley. Kingsborough Community College, Brooklyn NY.**

Cryptosporidium parvum causes cryptosporidiosis, a parasitic disease that causes intestinal infections, which may be fatal in individuals with compromised immune systems. The parasite is transmitted through the ingestion of water or food that is contaminated with *C. parvum* oocysts. Oocysts recovered from eastern oysters and other shellfish have been shown to be infective to mice for one to two weeks after they are removed from the shellfish. Millions of people visit Delaware Bay every year and they could become infected with *C. parvum* by accidently ingesting contaminated water or by eating raw oysters from the bay that contain *C. parvum* oocysts. Therefore, we were interested in determining if we could detect C*. parvum* in eastern oysters from Delaware Bay. We hypothesized that Delaware Bay oysters would test positive for *C. parvum*. To test this hypothesis, we used DNA from gill and mantle tissue of twelve eastern oysters collected in Delaware Bay to PCR-amplify a region of the *C. parvum* COWP gene. The amplified DNA was run on a 2% agarose gel to verify that it was the correct size but we did not obtain a PCR product from any of the oyster samples, suggesting that *C. parvum* was not present. To verify that DNA was present in our oyster samples, we PCR-amplified a region of the oyster cytochrome-c-oxidase-I gene, and then ran the PCR product on a 2% agarose gel. An approximately 700 bp PCR product was obtained from each of the oyster DNA samples, verifying that DNA was present in the samples and it was amplifiable. Taken together, these results do not support our hypothesis that Delaware Bay oysters would test positive for *C. parvum*. This work was supported by grant 0537-18-1091 of the CSTEP Program of NYSED.

Bioinformatic Analysis of Heavy Metal Stress Response in Cyanobacteria. Jose L. Perez and Tinchun Chu, Seton Hall University, South Orange, NJ. Cyanobacterial Harmful Algal Blooms (CHABs) are aquatic biomasses of mostly oxygenic, photosynthetic bacteria that have increased in occurrence through the proliferation of heavy-metal polluted, anthropogenic eutrophic, and increasing climate-change conditions. Harmful cyanotoxins within certain CHABs are consequently of growing concern to human health and aquatic ecosystem at large. *Microcystis aeruginosa* is one of the most commonly found toxin-producing cyanobacteria worldwide. Bioinformatic analysis was carried out using Pathosystems Resource Integration Center (PATRIC) analysis and Search Tool, for the Retrieval of Interacting Genes/Proteins (STRING to evaluate genes involved with cyanobacterial heavy metal stress. A Cation putative ATPase gene, ABC-transporter membrane fusion protein, Metallothionein were chosen as target genes for analysis. PATRIC Comprehensive Genome Analysis results suggested that genes

associated with stress response, virulence factors, and membrane transport are upregulated up to 4 folds under heavy metal stress. STRING database demonstrated ~55% sequence conservation between a non-cyanotoxin producing cyanobacteria *Synechococcus elongatus* 7942 and a toxin-producing cyanobacteria *M. aeruginosa* NIES-843 for a heavy metal stress response protein, FtsX-like ABC-transporter Permease Protein. Transcriptome analysis was also conducted to establish the differential gene expression profiles under heavy metal stress. The results from this study could help further understand the metal stress response mechanism in cyanobacteria. The potential impact of metal stress on toxin release may provide insight on the interactions between heavy metals and CHABs.

Direct PCR Detection, Cloning, and Characterization of 16S rRNA from Archaea Species in New Jersey Soils. Stephanie Perez, Arianna Pinto, Sibora Peca, and Luis Jimenez, Bergen Community College, Paramus, NJ.

The Domain Archaea wasn't recognized as a major domain of life until quite recently. The structure and diversity of Archaea in soils is poorly understood. DNA was extracted from Bergen Community College soils using the Zymo Microbe DNA MiniPrep protocol. Archaea gene sequences were amplified by PCR using degenerate primers A21F and A958R. DNA fragments of approximately 950 base pair were detected in all positive soil samples. Clone libraries were constructed with the amplified DNA fragments by ligating the detected fragments with vector pCR®4-TOPO. Transformations were performed using competent Mix and Go Escherichia coli cells. Plasmids were isolated from each clone using the Zyppy Plasmid Miniprep and inserts were screened by PCR using M13 DNA primers. More than 50 clones were screened for the presence of Archaea genes with 39 clones showing a positive reaction. DNA sequencing and BLAST analysis determined the identity of the cloned fragments. DNA sequencing of clone libraries showed that 72% of sequences were unknown Archaea sequences, 15% Thaumarchaeota, and 13% Crenarchaeota. Phylogenetic analyses of clones showed some similaritites with the genera Nitrocosmicus and Nitrosophaera that are associated with oxidation of ammonia in soils.

Pharmacological Inhibition of STAT6 Suppresses Viability and Induces Cell Death of Hodgkin's Lymphoma, *In Vitro*. Jessica Perng[1], Bo Zhang[2], Stephen Redenti[2] and [1]Rajendra Gharbaran, [1]Bronx Community College/CUNY and [2]Lehman College/ CUNY, Bronx, NY.

Studies showed that Signal Transducer and Activator of Transcription 6 (STAT6), a member of the JAK/STAT signaling pathway, play essential roles in the development of several diseases include inflammation, autoimmune diseases, and cancer pathogenesis. A pubmed search revealed several cancers that are affected by the unregulated STAT6 expression. AS1517499 (AS), potent inhibitor of STAT6, is used in the treatment of asthma. Given the role of STAT6 in the development and progression of cancers, we are testing that hypothesis that AS treatment can stop the growth of Hodgkin's lymphoma, in vitro. Research showed that STAT6 is overexpressed in Hodgkin's lymphoma. Water soluble tetrazolium 1 (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-positive HL cell lines, HDLM2 and L428. Live/dead assay of AS-treated L428 cells co-stained with acridine orange (AO) and ethidium bromide (EtBr) showed dose-dependent cell death. In this assay, live cells stain green with AO and EtBr stains the nuclei of only dead cells. Western blot, a technique used to detect the levels of specific proteins expressed by cells or tissue, showed dose-dependent decrease of phosphorylated STAT6 (pSTAT6) in AS-treated L428 cells. These results suggest AS suppressed viability and reduces growth of Hodgkin's lymphoma by inducing cell death.

The Role Of Hexim1 in Stress Induced Apoptosis In Mouse Embryonic Fibroblast Cell Lines. Kristelle Pierre and Sarah A. Sadik, SUNY Old Westbury, Old Westbury, NY.

Tumor growth is regulated by a cancer cells' ability to evade apoptosis. Previous work has demonstrated that in prostate cancer mouse models, whereby levels of hexamethylene bisacetamide-inducible protein 1 (HEXIM1) are low, an aggressive phenotype is exhibited. Mouse Embryonic Fibroblast (MEF) cells?derived from wild type (WT), Hexim1 heterozygous and Hexim1null mice were used as a model to study the role of this protein in cell survival?and apoptosis evasion. MEF cells were exposed to several stressors to induce oxidative and hypoxic conditions. Oxidative stress was induced through exposure to hydrogen peroxide. Hypoxia was induced by exposure to Cobalt chloride ($CoCl_2$). This stimulated a hypoxic microenvironment *in vivo* by inducing Hypoxia Inducible Factor 1 alpha (HIF-1α), a key modulator of hypoxia response *in vivo*. The effect on response to glucose deprivation was also tested. Dose response and time course analysis of cytotoxicity in the different cell types treated with the three stressors were measured using MTT assay, DAPI staining and cell counting methods. Results indicate that loss of Hexim1 confers resistance to apoptosis under the stress conditions. These studies will help understand the role of Hexim1 in activating or inhibiting mechanisms that promote cell survival and tumorigenesis *in vitro* and *in vivo*.

Frequency and Characterization of Pathogenicity Genes in *Staphylococcus aureus* Isolated from a Suburban Human Population. Lisa Pincus, Sibora Peca, Rozan Ramadan, Joy Bochis, Jenifer Vasquez, Stephanie Zapata, Matthew Gardner, Mahtab Tazehabadi, Juan Marte, Stephanie Perez, Arianna Pinto, Vanessa Molina, Adelajda Turku, Kadiatou Fadiga and Luis Jimenez, Bergen Community College, Paramus, NJ.

The nostrils of 709 human subjects were sampled to determine the number of human carriers for *Staphylococcus aureus* in a suburban population. All colonies that were gram positive cocci, fermented mannitol, and had a coagulase positive reaction were identified by 16 rRNA analysis to be *S. aureus*. Results showed that 11% of the people were nasal carriers of *S. aureus*. DNA was extracted from 77 isolates of *S. aureus*. Samples were analyzed by PCR analysis to determine the presence of pathogenic genes encoding for methicillin resistant (mecA), Panton Valentine Leukocidin (PVL), arginine catabolic element (ACME) arcA, enterotoxin A (SEA), and toxic shock syndrome (TSST-1). Positive reactions were confirmed by DNA sequencing of the different DNA fragments. The ACME gene showed the highest gene frequency with 62%. The SEA gene showed the second highest frequency with 38%. The mecA gene was found in 23% of isolates. However, percentages for TSST-1 and PVL genes were 27% and 22%, respectively. However, 17% of the isolates did not show a positive reaction with any of the genes. Healthy individuals in suburbia carried *S. aureus* with mecA, PVL, ACME, SEA, and TSST-1 genes in the nasal cavities representing an unrecognized and understudy human reservoir for pathogenic genes.

Real Time PCR for Quantification of *Staphylococcus aureus* in Pharmaceutical Products Contaminated with Mixed Bacteria. Arianna Pinto, Stephanie Perez, Sibora Peca, Lisa Pincus and Luis Jimenez, Bergen Community College. Paramus, NJ.

A quantitative real time PCR assay (QPCR) was developed to detect *Staphylococcus aureus* in pharmaceutical products contaminated with different types of bacteria. Bacterial DNA was extracted from product suspensions using a Tris-EDTA, proteinase K, Tween 20 buffer protocol. The QPCR assay using the Roche LightCycler 96®system detected the 273 bp 16S rRNA fragment with SYBR green I, a common double-stranded binding dye. The cycle at which fluorescence from amplification exceeds the background fluorescence was referred as quantification cycle (Cq). Serial dilutions of S. aureus DNA were analyzed to determine the sensitivity of the assay. The standard curve was able to reliably quantified *S. aureus* DNA down to 0.01148 ng/ml (R2=0.98). *S. aureus* was detected in all contaminated pharmaceutical products. Rapid detection of bacterial contamination provides faster quality control analysis resulting in expeditious implementation of corrective actions to avoid morbidity and mortality by the use of contaminated drugs.

Expanding Our Knowledge of *Rhodococcus erythropolis* Phages by Determining Cluster Classification. Sucely Ponce and Jacqueline Washington, Nyack College, Nyack, NY.

Bacteriophages have been of great interest to scientists because of their role in our understanding of how life works at the most basic level. During 2017, Nyack College Phage Hunters isolated five phages using Rhodococcus erythropolis NRRL B-1574 as a host. Of these only one was sequenced, Shuman. It is categorized as a Cluster CA phage, which is temperate and thus can form lysogens. As recently demonstrated in mycobacteriophages, some temperate phages show a heterotypic defense mechanism in which they can defend against infection by unrelated phages. It is unknown whether prophages in Rhodococcus have this type of defense mechanism. To determine if Shuman and the other unsequenced phages which include Mogli, Milena, Helix and Cart2 exhibit heterotypic defense mechanisms, lysogens were isolated from the bacteriophages and immunity assays were performed. Mogli is a lytic phage and we were unable to isolate any lysogens. In addition, it was able to infect all lysogens tested. Milena and Shuman behave similarly in all experiments. They are able to infect a Cart2 lysogen but unable to infect each other's lysogens. Consequently, Milena and Cart2 are related to each other. A Cart2 lysogen was unable to be superinfected by Cart2 phage as expected, due to homotypic defense mechanisms but this lysogen was unable to be infected by Helix phage. This suggests that Cart2 has a heterotypic defense mechanism. Also, Helix phage was unable to infect the other lysogens tested. In addition, as we have several unsequenced Rhodococcus phages, not much is known about them. To determine cluster categorization, partial digests will be cloned into plasmids followed by sequencing. The sequenced inserts will be blasted to determine similarity to other Rhodococcus phages and thus determine possible cluster identification of our unsequenced phages.

Identifying Cyanobacterial Communities in Barnegat Bay. Roksana Rahman, Christian J. Rios-Ruiz, Yan Wang, Paul (Jyung) Yoon and Tinchun Chu, Seton Hall University, South Orange, NJ.

Barnegat Bay is a 600 square miles estuary containing rich biological resources and is an ideal environment for a wide range of microbial communities. Cyanobacterial harmful algal blooms (HAB) in Barnegat Bay has been a more frequent occurrence in recent years. In order to detect possible HAB causing cyanobacteria, water samples were collected from 12 sites across Barnegat Bay. Each water sample was filtered through a 30- and a 0.4-micron polycarbonate filter sequentially. Flow cytometry was carried out for the filtrate between 0.4 and 30 micron. Chelex DNA extraction, polymerase chain reaction (PCR), and gel electrophoresis were then performed for all sites with the four primer sets 27FB/785r, PSf/Ur, CYA359f/CYA781r, and MSf/MSr. Viral plaque assays were also conducted on the < 0.1 micron filtrate to

detect the presence of cyanophages. Flow cytometric results indicated the water samples contained a wide range of cyanobacteria, including Anabaena spp., Oscillatoria spp., *Microcystis aeruginosa*, Spirogyra spp., and Synechococcus sp. IU 625. PCR-based assays suggested that phytospecific species and general cyanobacteria were present for all sites. No toxin-producing *M. aeruginosa* were detected. Cyanophages were detected in 3 out of 12 sites from the plaque assays.

Mechanisms of Genome Expansions in C-cluster of Bacteriophages. Iman Raja, Fernado Nieto and Christos Noutsos, SUNY Old Westbury, Old Westbury, NY.

Microorganism expansion is tightly linked with gene numbers. In this project, using Bacteriophages as model organisms we study the mechanisms of genome expansion. Thirty-six Phages from the C-cluster was obtained and used. Phages were blasted resulting to 18 pairs of closely related phages. Upon alignment, three modes of expansion were noted: Expansion of existing genes by inteins, insertion of completely new genes, and presence of de novo genes. For the first mode, certain Phams were repeatedly expanding among pairs. These Phams were unique in C-cluster. Fasta files of the genes within the pairs belonging to such phams were obtained and tested for Synonymous/Non-synonymous substitutions. Out of seven such phams, six showed neutral/negative selection, whereas Pham 6159 showed neutral/positive selection. For the second mode, insertions, it was indicated that the new genes were part of the ancestral genes and may have been passed down through negative selection. This was seen particularly in the first (Bxz1 and Pio) and ninth pairs (LRRHood and Lukilu). Regarding the first pair, the ancestor was a non-C-Cluster phage called Pier. However, for the ninth pair, the ancestor was already a part of the C-Cluster, Drazdys. For the presence of de novo genes, a mechanism was described using pair 15 (Audrick and Ghost Genomes) as an example. A deletion within Audrick resulted in the presence of multiple de novo genes. When that deletion was filled in to match the nucleotide sequence of Ghost, those genes disappeared. In other less similar pairs, the presence of these de novo genes were not caused by a deletion. However, there were indications in several pairs that the de novo genes may have been caused by a currently unknown combination of transitions and transversions. Overall, several factors causing genomic expansion among Bacteriophages were uncovered during the procedure of this research.

Effects of Tetrodotoxin Concentration on Action Potentials: a Computational Study. Shaina Raklyar and Chiaki Yanagisawa, CUNY City Tech, Brooklyn, NY and Borough of Manhattan Community College, New York, NY.

Japanese Fugu (Puffer fish) is a member of the Tetraodontidae and like majority of members of this family is poisonous due to the presence of tetrodotoxin (TTX). Every year a number of people become affected due to consumption of not properly prepared raw Fugu or Fugu soup. The death rate is below 10%. TTX blocks Na channels in cell membrane, which leads to changes in action potential behavior. We hypotheses that there should be some critical concentration of TTX which will block generation and signal propagation of action potential in nervous system. To investigate behavior of action potential in neuron under the TTX influence we performed computational simulations. We wrote Python scripts using modified time-honored Hodgkin-Huxley model. Instead of directly working on TTX concentration, we introduced to the model, a parameter f which accounts for the fraction of Na channels blocked by TTX. We investigated in detail behavior of action potential due to change in parameter f which correlates with concentration of the toxin in addition to change in input stimulus current such as its amplitude and duration. Longer stimulus produces a train of action potentials and we investigated whether TTX would affect its generation. We found that, as the stimulus becomes weaker, the critical value of the parameter f, above which axon fails to generate action potential, decreases. Also, as expected, another critical value of f exists, above which generated action potential fails to propagate along the axon. We also found that the effect of TTX depends on temperature.

An Increase in Three Species of Marine Mammals: "Repercussions" of the Marine Mammal Protection Act? Luis Ramirez, Kathleen A. Nolan and Kristy Biolsi, St. Francis College, Brooklyn, NY.

The numbers of wild California sea lions on the west coast have increased dramatically, especially since 2013. In observations of sea lions made while recording vocalizations at both the Queens Zoo and Bronx Zoo, we noted branding marks on some of these animals. Upon further investigation we learned that these animals were branded as "trouble-makers" because they were eating too many endangered salmon at the Bonneville Dam in Oregon and/or other places. Some of these animals were "rescued" and sent to zoos and aquaria, while the government euthanized others. Since marine mammals are normally protected under the Marine Mammal Protection Act of 1972, this was a variance that was applied for and granted. A second animal that is "in trouble" since it has increased in numbers is the seal, notably the gray and the harbor seal on the east coast. An increase in number of seals has been associated with an increase in the number of great white sharks. The death of the first swimmer in over 80 years in Cape Cod by a shark

occurred in September 2018, and has touched a raw nerve in many. Through personal observation we have noted a cooling of sentiment toward seals on Cape Cod, and have decided to investigate and report on attitudes toward seals there and off Long Island and the greater New York metropolitan area. We will also show the trends in population growth of these three species that are sparking this controversy.

Diversity and Abundance of Plankton in the Hackensack River. Margaret Ramirez and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

Hackensack River is a river that extends 45 miles from New York to Newark Bay. Its salinity ranges from 0 to 16. Many species from plankton to birds use the river as a habitat. The river's habitat range from freshwater to brackish wetlands. For our survey, we focused on the microscopic plankton throughout different gradients. Three sites were surveyed, and sample was sieved and collected at each site. Species identification was obtained at the lab with a microscope. A diversity and abundance record was created to compare sites. Our results demonstrated that species diversity and abundance did in fact change with the gradient. Species diversity and abundance was higher in lower salinity levels. Nutrients were obtained from each site, and results showed that along with an increase in diversity, there was also a higher level of nutrient count due to CSO runoff.

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

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

Invasive Species: Do We Stand a Chance Against Them? Jordon Reid, Jasmine Pasan and Margaret Eiden, Westchester Community College, Westchester, NY.

Invasive organisms can alter an ecosystem. They are the leading cause of decline in native plant and animal numbers. The Tree of Heaven is an invasive plant which is the main host plant for the spotted lantern fly. The Spotted Lantern Fly insect is currently threatening fruit and timber crop production in Pennsylvania and it is moving rapidly to neighboring states including New York. The goal of this project was to determine where the tree of heaven is present in Dobbs Ferry, NY. The hypothesis is that if the Tree of Heaven is present in the area the destructive Spotted Lantern Fly may also invade the area. Many regions are concerned about the wildlife that also lives in this area and are questioning if the presence of these invasive organisms will alter an ecosystem. Invasive species data was collected in June of 2018 using standard field survey protocols which include identification based upon morphology, GPS location, abundance and setting of the invasive plant. GPS localization of plants was gathered using Avenza and apple map navigation. Additional information on plant localization was gathered using apps like iNaturalist, and Imapinvasives. Tree of Heaven was found extensively throughout the survey area. This local data add to the maps of the Tree of Heaven in the New York region, this will contribute to the hypothesis by showing that if the host plant is present, there is a threat of the Spotted Lantern Fly moving in and the area should remain under surveillance for presence of the Spotted Lantern Fly. This research is supported by the U.S. Department of Education under Title III HSI-STEM Grant P031C160054.

Can Ras-GTP Be Regulated in Cancer by NMDA Receptor Antagonists? Johanna Riera, Chevere Samuel, David Donatacci, Alix Duarte, Jan Osea and Natalia Coleman, New Jersey City University Jersey City, NJ.

Over 1.5 million individuals in the United States and more than 14 million individuals worldwide were expected to be diagnosed with cancer in 2015. The estimated cost of cancer treatment and care is predicted to be $15 billion by 2020. The search for effective cancer therapies continues to be an essential focus and high priority of health and medical research. There is growing evidence of the importance of glutamate signal transduction in cancer. N-methyl-D-aspartic (NMDA) receptors are one of the three glutamate receptors found in the mammalian central nervous system. While it is common knowledge that NMDA receptors are essential for spatial learning and memory, little is known about its function relative to cancer. We, and other investigators, previously showed that human prostate, breast and lung cancer cells express NMDA receptors and increase Ras activity. We hypothesize that by antagonizing NMDA receptors, we will be able to decrease Ras activity and that this strategy might be used in anti-cancer therapy. To analyze the effect

of the NMDA receptor antagonists, MK-801 and Memantine, on human cancers cells viability we used the MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay. The cells were treated with antagonists at a concentration of 75, 100, or 500 uM for 24, 48, and 72 hours. The level of Ras-GTP was later measured via western blot analysis. Our preliminary results suggest that Memantine at concentration 500 uM reduces the level of Ras-GTP in human breast, lung, and prostate cancers. Presented work has significant potential to enhance our understanding of cancer biology and to lead to a novel direction in cancer treatment.

Native Plants Grow in Natural Areas; Invasive Plants Grow After a Disturbance to the Ecosystem. Stephanie Saintil, Catherine Jordan, Taesook Jun and Margaret Eiden, Westchester Community College and Mercy College, Valhalla, NY.

Past studies have shown that the Old Croton Aqueduct had an abundance of invasive plants. Our hypothesis is that in disturbed areas of the ecosystem we would find more invasive plants than in undisturbed areas of an ecosystem. Field surveys of the Old Croton Aqueduct and Juhring Estate Park, both in Dobbs Ferry , NY were conducted in June of 2018 to determine the frequency and abundance of invasive plants in both disturbed and non-disturbed areas. Observations of the ecosystem were recorded every fifty feet. The abundance of invasive plants, GPS location, habitat and notes on the sites were recorded. All the data collected shows that land disturbance leads to invasive plant growth. Reporting of the abundance and precise GPS location of invasive plants to conservagtion agencies in New York State assists with tracking the spread of invasive plants and can help with plans for ecological restoration. This research is supported by the U.S. Department of Education under Title III HSI-STEM Grant PO31C160054.

The Impact of Urbanization on Soil Bacterial Diversity and Community Composition in Long Island, New York. Kaung Myat San[1], John J Dennehy[1], Nidhi Gadura[2], [1]CUNY Queens College, Flushing, NY and [2]CUNY Queensborough Community College, Bayside, NY.

Soil microorganisms play essential role in terrestrial ecosystem services such as provision of nutrients to plants and other macro-organisms through driving carbon and nitrogen cycles, amending the soil structure, maintaining the soil fertility by recycling the organic wastes. However, the environmental drivers that cause variations in soil microbial communities have not been fully explored, especially on how human activities impact soil microbial communities via urbanization. Urbanization gradually increases the number of people living in one area. The impact of this movement is not only evident on plants and animals but also on bacterial communities. Urbanization-driven pollution influences microorganism in the soil through changes in soil properties. In this study, we collected surface soil samples from 30 locations along urbanization gradient that spanned from Flushing, NY to Montauk, NY. We used a 16srRNA metagenomic approach to measure the bacterial diversity. The anthropogenic activities cause changes in soil chemical and physical properties such as soil water content, pH, salinity, nutrient availability and the presence of heavy metals. In order to examine which environmental variables drives the bacterial diversity and their community composition, the physical and chemical properties of soil were characterized. We found out that urbanization has an effect on soil bacterial community based on the observation that there is more bacterial species diversity in urbanized areas than in rural areas. I also found out that urban soil pH was higher than those of the rural soil. As for other characteristics, there was no correlation between the soil bacterial diversity and the soil water content. However, we found out that pH is one of the environmental drivers that controls the bacterial diversity in soil. Among classes of bacteria: Acidobacteria-6, Acidobacteriia, Anaerolineae, Chloracidobacteria, Ellin6529, Solibacteres, Spartobacteria, Verrucomicrobiae respond to changes in pH.

Image Processing and 3D Reconstruction of Hard and Soft Tissues From Contrast-enhanced High-resolution MicroCT Images in an Osteoarthritis Animal Model Based on Destabilization of the Medial Meniscus (DMM). Shadia Sarmin, Assia Bouizy and Louis Cardoso, LaGuardia Community College, Long Island City. NY.

Osteoarthritis (OA) is a slowly progressing disease resulting in vivo articular cartilage fibrillation and loss. This research is to evaluate the destabilization of the medial meniscus (DMM) surgical instability models of osteoarthritis (OA) in the mouse knee joint. The research question is whether there exist differences in both hard and soft tissues due to the onset of osteoarthritis in the DMM animal model. A sample of mice model is used in this experiment and the sample was used in mimics software to create a 3D image. Thresholding is the methods of mimics used to create a first definition of the segmentation object and region growing tool used for the capacity to split the segmentation into separate objects. The method of multiple slide edit used to create a different mask to identify each part of images. Also, the method of Boolean operations applied to add and subtract pixels and pores and morphology operation to perform an action on the mask. And finally, calculate 3D on the mask to create micro-CT 3D images. In mouse models of OA generated by either SHAM or DMM, it showed that phase contrast micro-CT distinguished control and OA cartilage by providing quantitative measures with high reproducibility and minimal variability. Based on the micro-CT DMM images we saw that the meniscus start moving out from the tibia which causes the friction between the tibia and femur but if we look at the meniscus still in their place after

10 weeks. Features of OA at the cellular hard tissue or soft tissue levels also observed in images generated by phase contrast micro-CT. Application of this technology is facilitated the rapid and high throughput assessment of genetic and therapeutic models of OA in mice. This work was supported by 41436-00-16 of the Bridge Program.

A Preliminary Study on the Effects of Luteolin on Hodgkin's Lymphoma, *In Vitro*. Evangelina Sarpong[1], Stephen Redenti[1] and Rajendra Gharbaran[2], [1]Lehman College/CUNY and [2]Bronx Community College/CUNY, Bronx, NY.

Luteolin (LUT), 3',4',5,7-tetrahydroxyflavone, is a common flavonoid that is present in a number of plants including fruits, vegetables, and medicinal herbs. In Chinese traditional medicine, plants rich in luteolin have been used to treat a number of diseases including hypertension, inflammatory disorders, and cancer. Studies showed that LUT exert tumor suppressive activities in several cancer types. However, the effects of LUT on HL, a lymphoma of predominantly B cell origin, remained an unanswered question. Given the anti-tumor activities reported for LUT in different cancer types, we decided to test the hypothesis that LUT will limit growth of HL, in vitro, by suppressing cell viability, inducing cell death, and decrease cell proliferation. Water soluble tetrazolium 1 (WST-1) cell viability assay showed that LUT suppressed the viability of HL cell lines L428 in a dose-dependent manner, 48 hours after treatment. These results are supported by bright field images of live LUT-treated L428 cells. In addition, live imaging of LUT-treated L428 cells co-stained with acridine orange (AO) and ethidium bromide (EtBr) showed dose-dependent cell death. In this assay, AO stains live cells green and EtBr stains the nuclei of only dead cells orange to red. EtBr staining of DNA extracted from LUT-treated L428 and resolved on 1.2 % agarose gel electrophoresis showed fragmentation of DNA of cells treated with 20 and 40 uM LUT. These preliminary results suggest that LUT may be useful in HL therapy. However, future studies are needed to study the mechanisms of the anti-proliferative and apoptotic activities of LUT in HL.

Salinity Tolerance of Bacteria Isolated from the Turtle Pond in Central Park. Marie Sayas, Fadel Yerima and Christine Priano, Borough of Manhattan Community College, New York, NY.

Since 1988, the Turtle Pond in Central Park, New York has been home to over 500 turtles of more than five different species, including painted turtles, musk turtles, yellow bellied sliders, red eared sliders, and snapping turtles. The pond is also subject to possible pollution due to runoff water from the nearby Great Lawn. A sample of the pond water was collected aseptically. Using a refractometer, the salinity of the water was measured and it was determined that there was no salt, indicating a completely freshwater environment. Microscopic examination of the water sample revealed bacteria and ciliated protists. Standard microbiological and biochemical tests were used to isolate and characterize bacteria that were filtered from the water. Isolated bacteria were grown on selective media, including mTEC and McConkey agars. These preliminary tests indicated that the bacteria were likely *Escherichia coli*. Because New York City is a coastal region, it was hypothesized that these freshwater bacteria could survive saltwater conditions. Experiments were performed in which Turtle Pond bacteria were grown in varying salt concentrations relative to ocean water salinity and bacterial growth rates were measured by spectrophotometry. Results indicated that these pond bacteria could tolerate salinity up to 60% that of seawater. Slower growth rates were observed at higher salinities. One clone was tested further and was shown to tolerate salinity levels higher than that of natural seawater. This result is significant in that it suggests that these bacteria can transfer between local freshwater and coastal ecosystems. Future experiments will include identification of all isolated organisms by DNA analysis. In addition, isolated bacteria and protists will be cultured together to determine conditions of coexistence and possible symbiotic relationships in this local aquatic ecosystem. This research was funded through a U.S. Department of Education MSEIP-RISE Program and a N.Y.S. CSTEP Program.

The Theophylline Riboswitch; Its Design and Implementation. Mika Schievelbein, Lauren Lucia, Sonia Dadlani, Toni Zangrilli, James Tilton and Jonathan Ouellet, Monmouth University, West Long Branch, NJ.

Fluorescence Activated Cell Sorting, or FACS, is a method that was used to convert the Theophylline aptamer into a riboswitch. This method could theoretically be used to convert other discovered aptamers into riboswitches, however it is a costly method and is only available to those with the high-tech, expensive FACS machines. The Theophylline riboswitch was previously discovered by implementing the Theophylline aptamer with random sequences into a specifically-designed plasmid and using a FACS machine to sort the cells. We can structure a new system that would select only the sequence containing the Theophylline riboswitch without the use of a FACS machine. To do so, we place the aptamer with random sequences into a plasmid and transform the plasmid into bacteria cells. Then, the use of replica plating along with screening selects the cells that only contain the correct riboswitch sequence. By doing so, we confirm that this system is efficient in converting aptamers into riboswitches without the need for a FACS machine. After an aptamer has been successfully converted into its riboswitch, the system of ratiometric fluorescence will allow for testing of the riboswitch's function. This is done by designing a plasmid that contains genes for two fluorescence proteins on either side of the inserted riboswitch. The two florescent proteins will provide the ability to measure the riboswitch's function through fluorescence readings. Both of these systems are

the key to innovating the next step in creating synthetic riboswitches. We would like to thank Monmouth University School of Science for providing the facilities and funding needed for this research project.

Microbes on the Rise in Hudson Raritan Estuary Sites Causing Detrimental Impacts to Water Quality. Rameen Shah, Daniel Antunes, Charlie Encalada, Allison Fitzgerald and Meriem Bendaoud, New Jersey City University, Jersey City, NJ.

Excess wastewater after rainfall leads to combined sewer overflows (CSOs) that contain untreated or partially treated waste with high toxicity and increased pathogenic bacterial concentration. CSOs have a high impact on water quality leading to compromised drinking water supplies and endangered human health. Our project focuses on studying the concentrations of pathogenic bacteria at selected Hudson Raritan Estuary (HRE) sites in correlation with nearby CSOs and rainfall events. Weekly testing and monitoring of water were conducted in designated sites for a period of 15 weeks. Modern bacterial identification techniques were used in the laboratory to determine the concentration of fecal coliform bacteria and Enterococcus bacteria. High concentrations were recorded at designated sites and days, showing poor water quality and the presence of potential pathogenic bacteria. The results of this study will not only inform management practices but will also become an important resource for decision-makers to advance environmental protection.

Functional Characterization of the Microbacterium Phage Paschalisputative ADP Ribosyl Tranferase. Camillah Shoo and Jacqueline Washington, Nyack College, Nyack, NY.

The SEA-PHAGES program has facilitated the advancement of our knowledge of genetic diversity in Mycobacteriophages and other bacteriophages as well as involving students in authentic scientific enquiry. Bacteriophages are viruses that infect bacteria and can exhibit either lytic or lysogenic life cycles. The reported increase of antibiotic resistance has led to renewed interests in the research community on the possibility of employing bacteriophages to treat common bacterial infections. Tuberculosis is an infectious disease caused by *Mycobacterium tuberculosis* which is responsible for millions of deaths worldwide, especially in the developing world. Multidrug resistance to common TB treatment drugs has been reported and these include the antibiotic rifampin. The majority of the rifampin-resistant *M. tuberculosis* isolates have been linked to mutations in rpoB, which encodes a subunit of RNA polymerase. Other actinobacteria, such as *Mycobacterium smegmatis* are rifampin-resistant due to mutations in another gene arr, which encodes ADP ribosyltransferase. We recently isolated the lytic phage Paschalis through direct plating on the bacterial host *Microbacterium foliorum* which is related to mycobacteria. Following DNA isolation, sequencing, and bioinformatics analysis it was interesting to find that gene product 52 potentially codes for ADP ribosyltransferase. As the phage was isolated on M. foliorum, we tested investigated its resistance to rifampin. Results show that the host bacteria is sensitive to rifampin even though the phage carries the ADP ribosyltransferase gene. As phages often acquire genes via horizontal gene transfer, these results suggest that the phage may have acquired the gene from another host. Other actinobacteria were also tested for sensitivity to rifampin and ability to be infected by Paschalis. As expected *M. smegmatis* and *Gordonia terrae* are resistant to rifampin but *Rhodococcus erythropolis* is more sensitive to the antibiotic. Paschalis was unable to infect any of these bacterial hosts.

Development of a Selection System to Identify Chloroplast Regulatory Genes in *Brassica napus.* Liya Simon[1], Lisa LaManna[2], Pal Maliga[2] and Kerry Lutz[1], [1]Farmingdale State College, Farmingdale, NY and [2]Rutgers University, Piscataway, NJ.

The plastid genome of higher plants is 120-160 kb and encodes for ~110 genes. To understand the role of nuclear and chloroplast encoded genes in plant processes, such as photosynthesis, chloroplast transformation can be used. Chloroplast transformation utilizes homologous recombination to incorporate transgenes into a specific region of the chloroplast genome. Transformants are identified by the ability to regenerate in the presence of the antibiotic spectinomycin. Therefore, for successful chloroplast transformation, it is critical to have a strong tissue culture plant regeneration system and spectinomycin sensitivity in the target leaf tissue. *Brassica napus* (rapeseed) is an economically important agricultural crop. Current tissue culture regeneration protocols used for chloroplast transformation of Brassica napus are inefficient. My project was to determine the best tissue culture regeneration protocol for *B. napus* using different plant hormone combinations identified from the literature. Leaf tissue was cut into small squares and placed onto different media types to identify the hormone combination that provided the best regeneration capacity. Results suggest that media containing 6-Benzylaminopurine (BA) and zeatin yielded the highest amount of regeneration. Therefore, we will perform chloroplast transformation experiments using this hormone combination to enable efficient regeneration of rare transplastomic plants. Chloroplast transformation experiments will be performed using plastid transformation vectors containing a reporter gene (yfp) flanked by the regulatory sequences of psbA or rbcL, two essential genes that control the expression of chloroplast proteins. Upon acquiring fertile transplastomic plants from tissue culture, we will mutagenize the transplastomic seeds with ethyl methanesulfonate and screen the mutant progeny. Once germinated, mutants that do not express the yfp reporter gene will be further analyzed. This selection system will facilitate the identification of candidate nuclear genes that regulate psbA or rbcL chloroplast gene expression.

Developmental Lead Exposure Causes Imbalances in Neurochemical Signaling, Decreased Encephalization Quotients, Increased Cortical Thinning and Altered SP1 Gene Expression Resulting in Frontoexecutive Dysfunction in the Rat. Jourvonn C. Skeen, Jalen R. Bonnitto, Ericka Canabas, Isra Ahmed, Cyrus Jo, Jean -Martin J. Chrisphonte, Kirsten Lynch, Eric Khairi, Arwa Ahmed, Jewel Joseph, Samantha Rubi, Asma Iqbal, Nimra Hameed, Eddy D. Barrerra, 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 and behavior, but also overall global brain excitability. The present study hypothesized that developmental Pb-exposure would decrease brain volume, cause cortical thinning, 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), alter SP1 mRNA expression, and disrupt frontoexecutive behaviors in the Attention Set-Shift Test (ASST). The 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. These data corroborated with decreases in SP1 mRNA expression responsible for offering neuroprotection against metallotoxicity. Lastly, the rats showed a persistent intellectual deficit that remained well-after development Pb-exposure that reduced their ASST test performance. The data suggest an emerging neurotransmitter profile in specific brain regions may be more vulnerable to volume reduction and thinning, increased excitability, inability to compensate through SP1 neuroprotection, and manifest in a lifelong intellectual impairments of frontoexecutive functions. These findings are important since little is known regarding the effects of lead on frontoexecutive function and animal models simulating these human conditions are scarce. Thus, this study paves the way for screening assessments in a concerted effort to find an appropriate and specific psychopharmacotherapy for addressing developmental disabilities caused by longstanding environmental toxins.

Imidazole as a Novel and Robust Gold Binding Group at STM-BJ Method. Shanelle Smith, Xiaofang Megan Yu, Tianren Fu, Jiayi Xue, Latha Venkataraman and Sujun Wei, Queensborough Community College, Columbia University, Bayside NY and New York, NY.

Recent technological advances allow for the fabrication of single molecule electronic circuits. In particular, the Scanning Tunneling Microscopy based Breaking Junction method (STM-BJ) developed in 2003 provides reliable, reproducible generation and measurement of electronic properties of molecular circuits. In order to complete the circuit with gold electrodes, special gold atom binding groups are installed at the both terminals of organic compound of interest. Typical gold binding groups include amino, thiol, methyl sulfide, thiochroman and pyridine. To expand this toolbox, we plan to investigate the imidazole as a potential candidate for the first time. We have quickly synthesized a series of di (imidazolyl) alkanes (Im-n-Im, n=4, 5 & 6) by one-step SN2 reaction. Their conductance results by STM-BJ shows exponential decay as the molecules expands longer. These initial promising results confirms our original hypothesis – imidazole can be utilized as gold atom binding group in STM-BJ. Further explorations into the detail of binding-releasing mechanism as well as synthetic application of imidazole in conjugated systems are under way.

Optimization of a Method to Enrich Chick Astrocytic Primary Cultures. Michele Stafford, Yuribel Rosario and Renee Haskew-Layton, Mercy College, Dobbs Ferry, NY.

The volume regulated anion channel (VRAC) is important in cell volume control. The exact mechanism responsible for VRAC activation is unknown. The channel is found throughout the body, including the central nervous system (CNS). Cells of the CNS, particularly astrocytes, undergo swelling due to acute or chronic pathological conditions, the channel opens and releases organic osmolytes including the amino acid glutamate. High levels of glutamate lead to cell death and ultimately damage the brain. The VRAC channel protects the cells from severe swelling, but simultaneously harms the cells due to the high concentration of glutamate released from astrocytic astrocytes. Primary chick astrocyte cultures provide an ideal model for studying VRACs. Our goal is to optimize culture conditions to preferentially grow astrocytes with minimal microglia or neuronal contamination. To culture astrocytes, the optic tectum was dissected from the chicken embryo on days 7-8, an optimal developmental time point for the growth of astrocytes. Several methods have been used in rodent cultures to enhance the purity of astrocyte cultures including: low plating densities, treatment with the mitotic inhibitor Ara-C, or shaking the culture plate to dislodge contaminating cells. We hypothesize that these same methods will increase astrocyte purity in chick cultures. Our preliminary results show that Ara-C treatment enriches the purity of the

astrocyte cultures. Future goals include utilizing the pure astrocyte culture to monitor VRAC activity using high performance liquid chromatography to measure glutamate release from swollen cells exposed to hypoosmotic medium. These conditions mimic the cell swelling-induced glutamate release that occurs during stroke and brain trauma.

Optimizing Electrolytes for Dye-sensitized Solar Cells Using Ionic Liquid and Single-walled Carbon Nanotube Mixtures. Rawlric A. Sumner[1], Katelyn Urena[2], Tirandai Hemraj-Benny[2], Sharon I. Lall-Ramnarine[2] and James F. Wishart[3], [1]Queens College, Flushing, NY, [2]Queensborough Community College, Bayside, NY and [3]Brookhaven National Laboratory, Upton, NY.

The use of dye-sensitized solar cells (DSSCs) to replace silicon-based solar cells is attracting increased attention. However, it is necessary for more efficient electrolytes to be developed to facilitate their increased commercialization. It has been reported that ionic liquids (ILs) with high intrinsic conductivities are ideal media for dispersing single-walled carbon nanotubes (SWCNTs) improving their ion diffusion properties. In this study, the transport properties of mixtures containing SWCNTs in imidazolium ionic liquids (ILs) bearing cations with side chains of different functionality coupled with bis (trifluoromethylsulfonyl)amide -NTf2- or bis(fluorosulfonyl) amide -FSA- anions were determined to assess their potential as electrolytes in DSSCs. H-1 and C-13 Nuclear Magnetic Resonance (NMR) spectroscopy were used to confirm the structures of the ILs. SWCNT-IL mixtures were prepared using an ultrasonication method and were analyzed by UV-Visible and Mid-IR spectroscopy. It was observed that the ILs facilitated some degree of de-bundling of the SWCNTs. UV-Visible data indicated that the electronic properties of a specific diameter semiconducting SWCNT (1.75 nm) were affected upon the incorporation of the ILs. Mid-IR data indicated that all characteristic vibration of the ILs were maintained in the mixtures with the SWCNTs, suggesting that the ILs' structural properties were unaffected upon sonication. In addition, the temperature dependent conductivity, viscosity and the thermal profile of the pure ILs and SWCNT-IL mixtures were measured and compared. In general, ILs mixed with SWNTs (0.25 wt.%) exhibit conductivities of about 5.0 mS/cm (an increase by ~ 1.0 mS/cm compared to the pure ILs). This suggests that SWNTs when mixed with imidazolium ILs bearing NTf2- and FSA- anions, are promising electrolytes for the use in dye-sensitized solar cells. This work was supported in part by the U.S. Department of Energy, Office of Basic Energy Sciences, Division of Chemical Sciences, Geosciences and Biosciences under contract DE-SC0012704.

Effect of Single Walled Carbon Nanotubes on Breast Cancer Cell Migration. Yingxian Tan, Tobore Edema, Sunil Dehipawala, Tirandai Hemraj-Benny and Regina Sullivan, Queensborough Community College, Bayside, NY.

Biomedical applications of single walled carbon nanotubes (SWCNT) have the potential to expand treatment options for cancer patients. Carbon nanotubes have a high surface area to volume ratio which allows for surface functionalization. The size of these nanotubes facilitates use as a drug delivery system as well. Recent studies have shown that unfunctionalized nanotubes enter cells via endocytosis. In addition the nanotubes may enter cells through cellular gap junctions and ion channels. In previous studies we have shown that nanotubes are not cytotoxic in low concentrations. Currently we are testing the hypothesis that unfunctionalized single walled carbon nanotubes incorporate into the actin cytoskeleton and decrease migration of triple negative breast cancer cells. However our studies have been limited by aggregation of the nanotubes in aqueous solutions which decreases cellular uptake and increases cytotoxicity in in vitro studies. Coating single walled carbon nanotubes with collagen has been shown to facilitate cellular uptake thus allowing for intracellular associations to be investigated. This method has limitations due to the acidic pH of the collagen solution. In this study, we compared the effect of collagen coated single walled carbon nanotubes with debundled single walled carbon nanotubes on breast cancer cell migration. Migration assays were performed and revealed that breast cancer cells treated with collagen coated SWCNT as well as the debundled SWCNT has a reduced rate of migration. These results suggest that the SWCNT may be incorporating into the actin cytoskeletal disrupting rearrangements that are required for the metastatic process. In future studies we plan to measure Young's modulus which is an indicator of the degree of flexibility which in turn can be correlated with changes in the actin cytoskeleton. The study will be expanded to include other types of cancer cells as well noncancerous cells and may reveal potentially novel cancer treatments.

Functional Validation of Drosophila Blood Cell Development Genes. Brian Tang, Henry Wu, Harmeet Kaur and Rebecca Spokony, Baruch College, CUNY, New York NY.

Drosophila melanogaster blood development, or hematopoiesis, can be used as a model to investigate human immune and blood diseases due to gene conservation. However, fruit fly hematopoiesis is not yet fully understood. The fly innate immune system is simplified to three main cell types: plasmatocytes, lamellocytes, and crystal cells. Crystal cells (CC) are platelet-like cells that participate in wound healing and fighting infection by undergoing melanization. In this study, we misexpressed seven genes identified through a genome-wide association study to be highly linked to increased CC expression, including four human disease

orthologs. Overexpression and RNA interference was performed using the GAL4/UAS system of targeted gene expression with hemocyte drivers He-GAL4, Hml-GAL4, and Srp-GAL4. Srp-GAL4 is expressed in embryonic and larval prohemocytes and fat bodies, Hml-GAL4 in differentiating prohemocytes and mature hemocytes, and He-GAL4 in hemocytes and the lymph gland. Crystal cells in wandering third instar larvae (w3L) were made visible by heating larvae and scored to determine the effects of misexpression. Based on GWAS analysis of CC data from 78 lines of inbred wild-type flies, we chose to test seven genes with p-values <10-5 that are related to mesodermal cell function. We found that misexpression of Hemese, Exex, PPO1, Heartless, Domino, Btk29A, and Dad produced driver-specific CC counts, suggesting different temporal expression patterns in blood cell development. Increased expression of Hemese, PPO1, Domino and Heartless disrupted differentiating prohemocytes, suggesting novel regulatory functions. Exex overexpression increased CC count in all drivers. Knockdown of human disease orthologs Btk29A and Dad by He-GAL4 decreased CC count, highlighting them as candidates for leukemia studies. By using the fly model, we identified seven genes involved in blood pathways, allowing for better understanding of hematopoiesis and innate immunity in flies that can then be applied to humans.

Microplastics in Local Waters and its Accumulation in Bivalves. Johanny Tejada and Allison Fitzgerald, New Jersey City University, Jersey City, NJ.

The presence of microplastic contaminants have been reported in a whole variety of habitats; from water surfaces to coastal sediments and even sea ice. This experiment intends to examine the accumulations of microplastics inside mussels and their relationship with microplastic concentration in the waters. A manta trawl was used for microplastic sampling. Organic matter was removed using Fenton reaction. Pieces of plastics were counted by hand under a dissecting scope and arranged into different categories. It was found that the Hackensack river has the highest abundance of microplastic pollution out of the three sites examined (Passaic River, Newark Bay, Hackensack River). Mussels in the Hackensack River were found to have microfibers in their guts. Soft tissue digestion of mussels and other bivalves from other location is still pending for further investigation.

Understanding the Role of Motivation to Learn Science in Science and Non-Science Majors. Sophia Touri, Rebecca Olcese and Christina Mortellaro, Saint Peter's University, Jersey City, NJ.

A common learning objective of core curricula in higher education and science educational programs specifically is to develop student's critical thinking skills via their development of scientific literacy. However, a consistent challenge in developing science literacy in the classroom is student's motivation to emerge themselves in the learning of "science". A mixed-method analysis of undergraduate students in introductory level biology courses was conducted to understand both STEM and non- STEM major's motivation to learn science. A concurrent triangulation design was utilized, with students completing both the Science Motivation Questionnaire (SMQ-II) and open-ended questions further exploring the topic of motivation to learn. Results from both the survey and open-ended responses identified that motivation to learn science is significantly different between STEM and non- STEM majors. The study findings offer support for the infusion of introductory biology courses designed specifically for STEM majors separate from introductory biology courses designed for non- STEM majors in order to provide each group with active learning experiences that capitalize upon, and promote student's level of motivation to learn science and seek to advance the development of their critical thinking skills.

What lurks in the Laboratory? Environmental Molds! Amber Tucker, Victoria Ruiz and Kathleen A. Nolan, St. Francis College, Brooklyn, NY.

Through contamination of some Luria-Bertani (LB) agar plates that were prepared for a course in Fall 2017, we learned that there was a significant difference in numbers of molds on plates that were enriched with ampicillin (amp) versus those without amp. This summer LB plates with and without amp were exposed to air in a microbiology teaching laboratory under the following conditions: covered or uncovered for three hours at room temperature (21oC), in a refrigerator (10℃) or in a 30℃ incubator (this temperature is commonly used to grow molds). There were significant differences in numbers of growths (molds and/or yeasts) between covered and uncovered, with and without ampicillin, and among temperatures. An interesting black mold was noted on the LB plates plus amp that was not noted on the LB plates alone. Mold growth has been known to be a side effect of media that has ampicillin added to it, and has also been noted as a side effect of ampicillin use in humans. We are attempting to further characterize and DNA bar code these molds. We would also like to repeat the experiment with additional antibiotics such as kanamycin and streptomycin.

Rapid Detection of *Escherichia coli* Contamination in Pharmaceutical Products Using Real Time PCR. Adelajda Turku, Arianna Pinto, Vanesa Molina and Luis Jimenez Department of Biology and Horticulture, Bergen Community College, Paramus, NJ.

Non-sterile pharmaceutical products contain a microbial bioburden that is not detrimental to the formulation and hazardous to consumers. However, they

require the absence of specific bacterial indicators to provide safe and efficacious treatment to common diseases. Microbiological testing requires the absence of four different bacterial indicators such as *Escherichia coli, Staphylococcus aureus, Salmonella typhimurium,* and *Pseudomonas aeruginosa. E. coli* is also a common fecal indicator. A quantitative real time PCR assay (QPCR) detected E. coli in all pharmaceutical products contaminated with different types of bacteria. The QPCR assay targeted the 147 bp beta-glucuronidase (uidA) fragment specific for *E. coli*. The Roche LightCycler 96® system with SYBR green I, a common double-stranded binding dye, detected *E. coli* after a PCR amplification reaction based upon 30 cycles. The cycle at which fluorescence from amplification exceeds the background fluorescence was referred as quantification cycle (Cq). Melting curve analysis confirmed the presence of *E. coli* in the DNA solution extracted from contaminated products. Based upon standard curve analysis of E. coli DNA, the detection limit for the QPCR assay was found to be with a DNA concentration of 0.6 ng/ml (R2=0.91). Total time for assay completion was within 30 hours. The QPCR assay provided a fast and accurate method to assess the quality control of non-sterile pharmaceuticals contaminated by *E. coli*.

Efficacy of Infraslow Fluctuation Training (ISF) in the Attenuation of Anxiety, Utilizing Brainmaster Discovery Quantitative Electroencephalogram (qEEG) and Self-Report. Adelejda Turku, Jacqui Gonzalez, Alexander Thomas, Hynbin Kang, Sadik Erisen and Coleen DiLauro, Bergen Community College, Paramus, NJ.

Neurofeedback is growing and prior research on a specific paradigm, Infraslow Fluctuation Training (ISF), suggests that the training might be an effective stimulus for the alleviation of generalized anxiety. Changes in brain cordance have been shown to be a reliable anxiety measure. Research has shown decreases in frontal beta and theta frequency cordance after administration of anxiolytic stimuli. Through quantitative electroencephalogram (EEG) analysis, the anxiety-reducing effects of ISF will present themselves. This is a training, not a treatment. The designation allows for individuals outside of nursing and medicine to administer the stimulus. The determination of a positive effect would allow for greater relief in the general population from the effects of anxiety. EEG has a broad spectrum of applications. Research shows that EEG has a range from predicting relapse in alcoholics to treating ADHD to determining the potential effectiveness of antidepressant medications. This preliminary research on ISF has shown that there were significant changes in state amongst participants with the application of the ISF stimulus. As EEG become increasingly valid in the literature, the prevalence of this multi-purpose tool will grow. ISF is part of a number of novel trainings and treatments that might be elevated to widespread use with the validation of the stimulus through randomized, blinded, and controlled trials.

The Role of Dectin-1 Receptor in LPS-Induced Phagocytosis Stimulation In Microglial Cells. Darlene Urena, A. Lucia Fuentes and Maria Entezari, LaGuardia Community College, Long Island City, NY.

Neuro-inflammation and accumulation of Amyloid ßeta (Aß) protein are the main neuropathological hallmarks in Alzheimer's disease (AD). AD is characterized by impairment of Aß clearance as well as secretion of neuroinflammatory cytokines. Phagocytosis is a highly regulated process in microglia that involves a variety of receptors, including several known Pattern Recognition Receptors (PRRs). Lipopolysaccharide (LPS) is recognized by common (PRRs), including TLR-4, and C-type lectins, such as Dectin-1. However, little is known about the role of these receptors in the regulation of microglial phagocytic capabilities. In this study, we conducted in vitro experiments using BV2 mouse-derived microglia, to investigate the involvement of Dectin-1 receptors in the cells phagocytic response to pro-inflammatory molecules. BV2 cells were treated with LPS for 24 hours, then cells were incubated with zymosan and phagocytosis was quantified microscopically. We found that LPS upregulated, phagocytosis of zymosan, compared to untreated cells. This effect of LPS was significantly reduced by pre-treating cells with laminarin, a soluble beta-glucan known to bind Dectin-1 right before incubating the cells with zymosan. The data point to the importance of Dectin-1 receptors in the modulation of phagocytosis observed when cells are exposed immune-modulators such as LPS. These findings open the possibility of elucidating the pathways involved in phagocytic stimulation in microglia. This work was supported by 41436-00-16 of the Bridge Program.

Drosophila Genetics: Mapping of mps-1 Transgenes. Angela Valle, Steven Almazan, Kaitlyn Weiler, Kyra Hughes and Elizabeth A. Manheim, Kean University, Union, NJ.

Meiosis and mitosis, essential to the survival of all organisms, rely on the formation of a bipolar spindle to segregate chromosomes and complete cell division successfully. Many of the spindle assembly mutants are lethal, requiring the use of transgenic constructs (both wild type and mutant) to compensate for the lethality and study the protein. monopolar spindle-1 (mps-1) is a spindle checkpoint gene responsible for monitoring kinetochore attachment to the microtubules and ensuring that the spindle is properly built before giving the cell permission to enter Anaphase and progress through the cell cycle (InteractiveFly: Genebrief altereddisjunction 2018). Since mps-1 null alleles are usually embryonic lethal, transgenic flies carrying a mutant (or wild-type) construct must be generated allowing for analysis in an mps-1 null background, with the embryonic lethality bypassed. Due to the nature of Drosophila genetics, one must first map the transgene by determining which chromosome the construct integrated into followed by balancing the transgenic chromosome, resulting in true-breeding stock lines that will not lose the integrated transgene to meiotic recombination. Once the transgenic stocks are

established, phenotypic analysis can begin. This study presents the results of mapping and balancing 500 injected Drosophila embryos (250 per construct). Of the surviving 402 larvae, 30 individual transgenic lines were identified and are currently being balanced. Ultimately, genetic and immunofluorescent analysis of the transgenic flies will help us understand how mps-1 plays such an integral role in Drosophila, allowing us to infer its role in larger eukaryotic organisms such as mouse and human.

Identifying How Thiolase Functions Together with Linker Histone H1 in Blood Tumor Regulation Caused by Hyperactive JAK/STAT Signaling. George Varvatsoulis and Na Zu, LaGuardia Community College, Long Island City, 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. We further discovered that the interaction of H1 and STAT plays an important regulatory role in JAK-STAT-induced blood tumor formation in flies. 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 Thiolase. Thiolase encodes the enzyme, Thiolase, which cleaves ketoacyl-CoA into acyl-CoA as well as acetyl-CoA. Thiolases are dimers that have also been discovered to be important to various pathways which include the likes of lipid metabolism and steroid synthesis. A lack of Thiolase leads to a beta-ketothiolase deficiency which can lead to various symptoms. Our data suggested that Thiolase may function together with H1 in regulating blood tumor formation caused by hyperactive JAK/STAT signaling.

Quantification of Protein Concentrations in *Primula vulgaris*: A Comparison of Soluble Protein Content of a Reproductive Tissue and a Non-Reproductive Tissue. Lisa M. Vetere and Farshad Tamari, Kingsborough Community College, Brooklyn, NY.

Primula is a genus of some 500 angiosperm species. Most members of this genus are herbaceous. *Primula vulgaris* is a member of this genus and is used mainly ornamentally in the United States. *P. vulgaris* exhibits distyly as a breeding system where two distinct morphologies exist within the same species. It is normally insect pollinated and self-incompatible- a mechanism that promotes outcrossing. The genetics of distyly and self-incompatibility in this species is well documented, however, the molecular aspects of this interesting breeding system is not well known. Our research focused on quantification of proteins in the styles of *P. vulgaris*, which can play a role in distyly and self-incompatibility and its comparison to a non-reproductive tissue. To achieve this, tissue from reproductive and non-reproductive organs from flowers of each morph were extracted in PBS. The samples were centrifuged at 14,000 rpm for 10 minute, and 3 µL of each sample was used in a standard Bradford assay. The samples were subjected to spectrophotometry using a microplate reader. Preliminary analysis of the data indicates a difference between the short- and long-styled plants in protein content (shorts: 1.73µg/µL ±0.48, longs: 1.26µg/µL ±0.46) for pistils. A modest difference was also observed for sepals (shorts: 0.45µg/µL ±0.27 longs: 0.38µg/µL ±0.27). Currently, we are comparing the results to determine whether there is a statistical difference. This work was supported by grant 2R25GM062003 of the Bridge Program of NIGMS and grant 0537-18-1091 of the CSTEP Program of NYS Department of Education.

Characterization of Excitoxicity Model in Chick Embryo Neuronal Culture. Fredy Reyes Vigil, Nohely Cabrera, Natalia Elizarraras and Renee Haskew-Layton, Mercy College, Dobbs Ferry, NY.

Cerebral ischemia is the loss of blood flow to the brain due to the obstruction of arterial blood flow. The term stroke refers to the resulting brain damage and dysfunction caused by this loss of blood flow. Excessive glutamate release, resulting from the energetic failure of cells, overstimulates NMDA receptors (NMDA-Rs) and contributes to extensive neuronal damage in stroke. Understanding how to minimize damage caused by glutamate release is of high importance in treating stroke. We aim to understand and characterize sources of glutamate release in the brain, including glutamate release from the volume regulated anion channel (VRAC). To better understand the relationship between glutamate released from VRAC and brain damage, we first sought to verify that our chick neuronal cultures are susceptible to excitotoxic cell death. We therefore exposed primary neurons derived from embryonic day 6 chick embryos to the NMDA-R agonist, N-methyl-D-aspartate and compared this to oxidative stress induced cell death caused by hydrogen peroxide (H_2O_2). Our results show that our neuronal cultures are vulnerable to NMDA-R activation, which lead to increased cell death, as indicated by the membrane-impermeable DNA dye ethidium homodimer-1. Future experiments will determine if glutamate released from neighboring astrocytes induces excitotoxic cell death as seen with the NMDA treated cells.

Measures of Sustained Attention in a Rat Model of Sporadic Alzheimer's Disease. Kaiming Wang, Julio Salas, Adrian Guerrero, Abbas Kouzani and Francisco Villegas, Queensborough Community College and Deakin University, Australia.

Deep brain stimulation (DBS) is currently used as a treatment option for several neurological disorders such as Parkinson's disease, essential tremor, dystonia, movement disorders, major depressive disorder, Tourette's syndrome, chronic pain, and obsessive–compulsive disorder. Sporadic Alzheimer's disease (sAD) is the most common neurodegenerative disorder associated with cognitive deficits and disturbances in behavior. In this study, DBS was delivered in a rat model of sAD through a surgically implanted bipolar electrode which stimulated the medial forebrain bundle (MFB) at the level of the lateral hypothalamus, a region of the brain associated with reward and "pleasurable" sensations. This experiment observed measures of sustained attention based on the time of DBS administration. The naturally occurring alkylating neurotoxin Streptozotocin (STZ) was administered via an intracerebroventricular (ICV) injection to induce the rodent model of sAD. Long-Evans rats were organized into four groups: (1) ICV-aCSF control group, (2) ICV-STZ control group, (3-4) ICV-STZ injection and electrode implantations. The control groups participated in the sustained attentional task without DBS, while the experimental groups received continuous DBS before or after the attentional task. We hypothesized that DBS administered to the animals after the sustained attentional task would lead to an increase in correct responses and decrease in incorrect responses as opposed to animals who received the DBS before the sustained attentional task. In general, the data showed that the animals that received ICV injections of STZ had performed less reliably in all measures tested (percent correct, percent incorrect and percent omissions) than that of the aCSF group when tested in the sustained attentional task. However, contrary to our original hypothesis, our results have shown that rats administered DBS before the sustained attentional task demonstrated an increase in correct responses and decrease in incorrect responses as opposed to the rats that received DBS after the sustained attentional task.

Investigating the Population Density and Developmental Biology of Juvenile American Horseshoe Crabs (*Limulus polyphemus*) at Plumb Beach, Brooklyn, New York. Akankaye Waul and Christina P. Colon, Kingsborough Community College, Brooklyn NY.

The American Horseshoe Crab (*Limulus polyphemus*) is a life-saving, living fossil that faces constant threats from beach erosion and human disturbance. After Super Storm Sandy hit New York in 2012, juvenile crabs at Plumb Beach were at a risk. Since 2011 researchers have investigated the juvenile population to monitor their survival. It was hypothesized that juveniles would continue to increase at the undisturbed Eastern region, and remain higher than at the eroded and restored Western region. Further, the juvenile population at Beach East is hypothesized to remain lower than that of a nearby Tidal Creek. Timed visual surveys on each area, were performed bi-monthly at low tide. Dial calipers were used to measure prosoma width to approximate age. In summer 2018, we discovered 360 juveniles, with most (316) on Beach East. None were found on Beach West, which supports the first hypothesis. Counts are higher than 2017 (222). Peak catch/hr. for 2018 was 192.8 at Beach East, far beyond 2016 at 157.6 crabs/hr. and 2017 at 68 crabs/hr. Average catch/hr at Beach East was higher at 60.4 compared to the Tidal Creek 7.9 crabs/hr. Beach East showed massive improvement, while the West Beach remains at zero, despite the restoration, thus supporting the hypothesis. In the Tidal Creek, average prosoma width in 2018 (56mm) was slightly larger than 2017 (51mm) and 2016 (39mm); this lack of smaller individuals reflects a lack of recruitment. The population increase at Beach East indicates it can once again serve as a nursery. With strong evidence of replacement and survival, the juveniles are showing improved survival. Because Beach East's population has surpassed the Tidal Creek the second hypothesis is not supported. This work was supported by grant 2R25GM062003 of the Bridge Program of NIGMS and grant 0537-18-1091 of the CSTEP Program of NYS Department of Education.

Methylation and Expression Patterns of C3 and C4 Photosynthetic Genes. Brian Weil and Christos Noutsos, SUNY Old Westbury, Old Westbury, NY.

My research entails analyzing the proteomes of *Arabidopsis thaliana*, a C3 photosynthesis plant, and *Zea mays*, a C4 photosynthesis plant, focusing on proteins targeted to chloroplasts. To locate the proteins, I used a program called TargetP, which I ran through a cloud service called Atmosphere offered by Cyverse. I focused on genes whose products were functional to chloroplasts to find differences in gene expressions and to study the mechanisms of gene regulation. I am also studying the effect that DNA methylation has on these *A. thaliana* and *Z. mays* genes, which will give us more insight on the why they are turned off. By doing this we will get an understanding of the evolution of photosynthetic mechanisms with practical applications of engineering efficient C4 photosynthetic cycle genes into C3 plants. Because C4 photosynthesis is more efficient than C3 photosynthesis, finding genes specific to C4 chloroplasts can be placed into a C3 plant. This will make said C3 plant, like rice and potato's, more productive even in less optimal conditions to support a growing global population.

The Anti-biofilm Activity of Black Tea Polyphenol. Ayuni Yussof, Nayab Qamar and Tinchun Chu, Seton Hall University, South Orange, NJ.

The black tea polyphenol theaflavin (TF) extracted from the leaves of Camellia sinensis has shown to have anti-inflammation, anti-cancerous, antioxidant, antibacterial and antiviral effect. The aim of this study is to determine if TF can inhibit the biofilm-forming bacteria and remove the mature biofilm in these microorganisms. The bacteria included in this study were: Gram-positive *Staphylococcus aureus*, *S. epidermidis*, *S. mutans*; and Gram-negative *Enterobacter aerogenes*, *Escherichia coli* and *Pseudomonas aeruginosa*. Previous studies indicated that 0.2% TF80, theaflavin with a purity of 80%, can significantly inhibit the growth of the selected microorganism. Based on this data, Congo Red Assay and Resazurin Assay was carried out to determine the anti-biofilm activity of TF 80. The Congo Red Assay suggested 0.5% TF80 was able to inhibit the biofilm formation in all of the selected microorganism. Resazurin Assay further confirmed the results that 0.5% TF80 was able to inhibit biofilm formation up to 99.47% after 24 hours. Furthermore, Congo Red Assay showed 0.5% TF80 was able to decrease the mature biofilm slightly while the Resazurin Assay indicated 0.5% TF80 was able to reduce the mature biofilm up to 76.48% after 24 hours. In summary, the aflavin could be a promising anti-biofilm agent that is able to inhibit the biofilm formation and to potentially reduce mature biofilm.

Developing an Inexpensive Method, Loop Mediated Isothermal Amplification, for detection of Dengue Virus in Mosquitoes in Sri Lanka.
Dinuka Ariyaratne, Dharshan Aruna DeSilva, Jagathpriya Weerasena, Shiroma and Andrew Van Nguyen, Queensborough Community College, Bayside, NY.

Dengue virus is an RNA virus of the Flaviviridae family which is transmitted mainly by two types of mosquitoes: Aedes aegypti and Aedes albopictus. There are four distinct antigenic serotypes of dengue virus (DENV1-4) which can cause a wide range of symptoms from asymptomatic infection, to a flu-like dengue fever (DF), to life-threatening dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS). In Sri Lanka, the number of new cases has been increased in recent years suggesting that dengue infection continues to pose serious public health risks. There are several tests available for detection of DENV but they are either too expensive or very time consuming. The standard test for clinical samples known as enzyme-linked immunosorbent assay (ELISA) relies on the antibody production in the serum of the patient suspected of having dengue infection. However, ELISA for NS1 antigen can be compromised if the patient serum contains NS1-IgG complex from prior exposure. Furthermore, cross-reactivity with other Flaviviridae viruses have been reported. In collaboration with the scientists at IBMBB, I have developed an assay called reverse transcription loop-mediated isothermal amplification (RT-LAMP), which was based on the principle of strand displacement reaction and the stem-loop structure. In this procedure, the inner primers initiate the amplification of the target DNA and the outer primers are then used to displace the amplified product. The outer primes form loop where by the single stranded template can serve as target for further amplification using two additional primers. The amplified product can be observed in less than an hour and it is highly specific in identifying different serotypes of the DENV. We are in the process of broadening the scope of the research to include detection of DENV in infected mosquitoes at multiple testing centers and clinical samples from several hospitals in Colombo.

Plant Tracer, an App to Quantify Movement in Plants.
Eric D. Brenner, Winnie Zhao, Samantha Ciarfello, Yao Wang, Yixiang Mao, Jiazhen Zhang, *et al*., Pace University, New York, NY.

Even though plants may seem static in stature, in reality, plants are in constant movement including nutations and tropisms. Plant movements have been explored by isolating mutants to identify the molecular players directing positional changes. However, to date most mutants were isolated by screening at static time points, typically from images recorded before and after positional changes. Time-lapse photography analysis promises to detect mutants that are impaired throughout the movement dynamic. Creating time-lapse movies has recently become inexpensive with the ubiquity of smartphones and tablets. Plant Tracer is an NSF funded App designed to quantify movement characteristics that occur during gravitropism (movement towards or away from gravity) and circumnutation (the periodic regular swaying found in plant organs). As part of a crowdsourced method, Plant Tracer is being used by both students and researchers to detect mutant genes in Arabidopsis that are impaired in gravitropic or circumnutation responses. Plant Tracer represents a new approach to draw young scientists into the field of plant biology through research and inquiry with their omnipresent digital device and also will be useful to more established scientist wishing to study these movement characters

Computational Analysis of Electronic Properties of S-Adenosyl Methionine Derivatives.
Daily Despradel and Madhavan Narayanan, Mercy College, Dobbs Ferry NY.

S-Adenosyl Methionine (SAM-e) is a methyl (-CH3 group) donating compound that serves as a cosubstrate in several enzymatic methyl transfers, transsulfuration, and aminopropylation reactions in biology. In humans, SAM-e circulates in the blood and provides maintenance to many metabolic reactions in the body. In plants, SAM-e is important in the production of ethylene which serves as a signaling molecule. Structurally, SAM –e is composed of an adenosyl molecule (adenenine bonded to ribose) attach to the sulfur molecule of a methionine. Our ultimate goal is to develop fluorescent analogs of SAM-e which will help in optically tracking biological reactions. Towards this goals, as a first step, we have analyzed the contributions of various moieties in the SAM-e structure to its absorbance properties. Using ab initio methods and Time-Dependent Density Functional Theory (TD-DFT) we have presented and compared the electronic structure properties of the various moieties. This study will serve as a control in the further design of fluorescent analogs of SAM-e

Workshop: Teaching Biology to Non-STEM Students.
Sara Danzi Engoron,
Queensborough Community College, Bayside, NY.

Scientific literacy has become an important general education objective in higher education. Most students in a Liberal Arts program, in both 2-year and 4-year colleges, must fulfill a minimal science requirement. Scientific literacy includes a basic understanding of scientific concepts and of scientific methodology. These concepts are essential for personal and political decision-making. Many students opt for lecture courses as part of that requirement and some are tentative at best about studying science. There is great interest and need in professional development to enhance teaching biology to these non-science students. In this workshop we will demonstrate creative ways to teach selected topics in biology, including the M&M experiment for using the scientific method, classroom contest for understanding the properties of water, and using creative art as a learning tool. Participants will experience each activity and receive full instructions for using them in the classroom.

Modeling Close Collaboration Among Senior Researchers For Undergraduate Students.
Maria Entezari and A. Lucia Fuentes,
LaGuardia Community College, Long island City, NY.

Providing undergraduate students with the opportunity to conduct research has been shown to increase retention and success in STEM areas, particularly for students from underrepresented minorities. One dimension of research that is rarely mentioned in studies examining students' success is the effect witnessing and partaking in the rich, dynamic interaction which occurs between closely collaborating researchers. For the past five years, we have engaged in a collaborative research project and involved students in all discussions. Here we present an anecdotal account of the response to this experience, from both the students' and the researchers' perspective. We also discuss the importance close collaborations have for students with parenting and family responsibilities as a way of allowing them to get involved in research early in their undergraduate studies.

Poems in a Science Classroom - Collaborative Writing Between English and Biology Classes.
Urszula Golebiewska and Susan Lago,
Queensborough Community College, Bayside, NY.

Biology students often fall into the pitfall of memorizing material. Employing methods that would encourage students to approach the subject from a different perspective, such as poetic expression, might help to deepen their understanding of this difficult material. Poetry is deeply personal and requires a particular use of language skills. Faced with another form of writing, students are forced to find different words and explain concepts often in a metaphorical way, which helps them to make more a personal connection with the subject. Students majoring in scientific disciplines are usually not too excited about reading and writing poetry, but once they are exposed to it in an easy and playful way, they have a tendency to open up. There are multiple ways to include a little bit of poetry into the biology classroom. As a test, students in General Biology 2 were asked to write a poem for an extra credit assignment. The response was generally positive and we decided to include poetry as a regular assignment for an interdisciplinary collaborative writing project. Students were divided into groups of four, two from English class and two from Biology class. The groups first had to choose a topic associated with the book, The Immortal Life of Henrietta Lacks. Next, each student had to write at least one stanza of a poem, and then, in their interdisciplinary groups, had to collaboratively edit the poem. Finally, they created a Power Point presentation based on their poem. Students in both classes were at first apprehensive about the challenging project, but with the help of examples, many of them broke the barriers and pushed their limits.

Gaming in the Classroom: Active Learning, Student Engagement and Formative Assessment.
Mark K. Kenny,
Suffolk County Community College, Selden, NY.

Are you and your students tired of the same old Powerpoint presentations? Spice up your lectures with Kahoot! Kahoot is a web-based gaming platform that quizzes students and allows for formative assessment. Students generally love the competitive nature of the game, which can be played individually or in teams. It is played on cell phones or other mobile devices and does not require clickers. It encourages student participation and information recall. Instructors get immediate feedback on student comprehension and can save the quiz results as well. Kahoot is easy to learn and use. It can even be given as homework. Come find out how to get started. Kahoot makes learning fun!

Effect of Cannabidiol Extract of *Cannabis sativa* on the Viability and Structural Integrity of Human Adenocarcinoma Cells Grown in Monolayer Culture.

Steven M. Lipson[1], R.E. Gordon[2], D. Rodriguez[1], F. S. Ozen[1], K. Casares[1] and L. Karthekayan[3],
[1]St. Francis Col., Brooklyn, NY, [2]Mount. Sinai Medical. Centrr. New York, NY and [3]NYC College of Technology, CUNY, Brooklyn, NY.

The medical and recreational use of marijuana (Cannabis sp). has been decriminalized in 31 and 9 states respectively, reflective of the drug's ameliorative effects on a range of maladies from chronic pain, spasticity in multiple sclerosis, and to nausea/vomiting resulting from chemotherapy. However, the toxicological consequences of marijuana use on the brain, lung, immune system, and other organs, remains the subject of considerable debate. The growing number of "heavy" marijuana users additionally, has resulted in the appearance of cannabinoid hyperemesis syndrome (CHS), characterized by severe intestinal cramps, nausea, and vomiting. A need exists to investigate the mechanism of Cannabis - associated CHS. Human adenocarcinoma of the colon [epithelial] (HT-29] cells grown in monolayer culture were treated with increasing concentrations of cannabidiol and examined for the development of a cytopathic effect (CPE). Cell membrane destruction was determined by the non-destructive cytotoxicity assay ToxilightR). Comparative testing was performed using the health promoting compounds/phytochemicals epigallocatechin gallate (EGCG) of green tea and Procyanidin B1 (PB1), a member of the proanthocyanidin class of flavonoids in grapes, red wine, cranberries, and other plant species. Cannabidiol-treated HT-29 ultrastructural integrity was assessed by transmission electron microscopy. CBD produced a CPE at 13 to 51 μg/ml in HT-29 cells; Neither EGCG, PB1, nor each flavonoid in combination displayed a CPE in HT-29 monolayers at identical concentrations. Cytotoxicity (loss of HT-29 membrane integrity) by CBD concentrations occurred at > 13 μg/ml. Within the confines of the tested concentrations, CDB only at > 6.3 μg/ml showed ultrastructural anomalies especially among mitochondrial particulates. A pre-cytotoxicity and pre-CPE loss of mitochondrial integrity by CBD treatment of epithelial (HT-29) cells in monolayer culture is proposed. Our findings suggest a possible mechanism between CBD/marijuana consumption and the recurrence of severe intestinal cramps, nausea, and vomiting, referred to as cannabinoid hyperemesis syndrome among "heavy" marijuana users.

The Use of Mini Case Studies to Enhance Learning of Microbiological Concepts.

Susan K. McLaughlin and Joan Petersen,
Queensborough Community College, Bayside NY.

Case studies offer an effective means of incorporating active learning into the classroom. However many published case studies require a large amount of class time, and rarely include hands-on materials. We have developed a series of mini case studies that are used as the culminating exercise in our microbiology laboratory. They have been designed to 1. help students synthesize information covered throughout the entire semester, 2. incorporate laboratory materials (growth media, microscope slides, etc...) to enhance hands-on learning, 3. include connections to topics covered in the lecture portion of the course and 4. provide students with clinically relevant applications for the concepts covered in the course. In this presentation we will describe how we developed these mini case studies, how we implemented them in our microbiology lab and how we used one case study to assess student learning. We will also discuss how similar materials can be developed for other courses, and suggest alternative ways to use mini case studies to enhance student learning.

Incorporating Peer Mentors into General Biology Labs: The Impact on Student Retention, Engagement and Grades.

Peter A. Novick[1] and Jennifer Valad[2],
[1]Queensborough Community College, Bayside, NY and [2] Queens College, Queens, NY.

Introductory science courses at Queensborough Community College (QCC) and many senior colleges have high attrition rates. In conjunction with Queens College (QC), QCC received a 5-year grant, titled HSI-STEM: Bridges Across Eastern Queens, designed to increase retention in these important introductory, or "landing"courses and ease the transition from a 2-year school (QCC) to a 4-year school (QC). One of the three major aims of the grant is to incorporate peer mentors into the classroom to facilitate small peer-led learning communities (learning collectives). Peer mentors are students who previously took the introductory course in which they are mentoring. While they can help students review course material, they are not tutors. Instead, mentors are trained in pedagogical methods by science education experts to help students learn how to: read textbooks, take notes, study, and take exams. Experts also train mentors in crucial teaching methods, such as scaffolding, and in techniques to assist students in developing a growth mindset.

Optimization Methods for Cyanobacterial Detection, Identification and Seasonal Monitoring in Recreational Water.

Christian J. Rios-Ruiz and Tinchun Chu,
Seton Hall University, South Orange, NJ.

Increasing occurrence of Cyanobacterial Harmful Algal Blooms (CHABs) has been reported globally over the past decade. Not only has it been recognized that cyanobacterial blooms are a serious threat to aquatic life, but some species, such as Microcystis, Cylindrospermum and Anabaena, have the ability to produce toxins harmful to local wildlife as well as humans. This study focused on method optimization to rapidly detect, identify cyanobacteria and the potential presence of cyanotoxin in various water sources. Freshwater samples were collected weekly 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 documented. Flow cytometry was carried out to detect cyanobacteria and other related species in the water sample with phycoerythrin (PE) and side scatter (SSC) parameters. Microscopic observation and polymerase chain reaction (PCR)-based assays help further confirm the species. In South Orange Duck Pond (SODP), DO ranged from 0.42 to 7.28 mg/L; pH ranged from 6.48 to 9.45 and water temperature ranged from 3.80 to 25 °C. For Branch Brook Lake, DO ranged from 0.20 to 3.10 mg/L; pH ranged from 5.89 to 10.07 and water temperature ranged from 19.7 to 31.4° C. Water chemistry results showed that the dissolved oxygen decreased as the water temperature of the water increased in general. Additionally, higher concentrations of cyanobacteria were detected via flow cytometry during the summer collections compared to fall collections as expected. Flow cytometric results indicated the presence of multiple common cyanobacterial species in both South Orange Duck Pond and Branch Brook Lake. PCR assays confirmed the cyanobacterial presence, with over 75% of the samples processed showing the presence of photosynthetic species. In summary, flow cytometry with confirmation from PCR-based assays allowed for a rapid detection of cyanobacteria in freshwater bodies.

Enyuan Shang[1], Yiru Zhang[2], Chang Shu[2], Chiaki Tsuge Ishida[2], Elena Bianchetti[2], Mike-Andrew Westhoff[3], Georg Karpel-Massler[3] and Markus D. Siegelin[2]
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XPO1 has recently emerged as a viable treatment target for solid malignancies, including glioblastoma (GBM), the most common primary malignant brain tumor in adults. However, given that tumors become commonly resistant to single treatments, the identification of combination therapies is critical. Therefore, we tested the hypothesis that inhibition of anti-apoptotic Bcl-2 family members and XPO1 are synthetically lethal. To this purpose, two clinically validated drug compounds, the BH3-mimetic, ABT263, and the XPO1 inhibitor, Selinexor, were used in preclinical GBM model systems. Our results show that inhibition of XPO1 reduces cellular viability in glioblastoma cell cultures. Moreover, addition of ABT263 significantly enhances the efficacy of XPO1 inhibition on the reduction of cellular viability, which occurs in a synergistic manner. While selinexor inhibits the proliferation of glioblastoma cells, the combination treatment of ABT263 and selinexor results in substantial induction of apoptosis, which is accompanied by activation of effector- initiator caspases and cleavage of PARP and partially blocked by pan-caspase inhibition. Mechanistically we find that XPO1 inhibition results in down-regulation of anti-apoptotic Mcl-1 and attenuates ABT263 driven Mcl-1 up-regulation. Consistently, siRNA mediated silencing of Mcl-1 sensitizes for ABT263 mediated cell death and partially for the combination treatment. By using a human patient-derived xenograft model of glioblastoma in mice, we demonstrate that the combination treatment of ABT263 and Selinexor reduces tumor growth significantly more than each compound alone. Collectively, these results suggest that inhibition of XPO1 and Bcl-2/Bcl-xL might be a potentially strategy for the treatment of malignant glial tumors.

Unlocking Students' Research Potential: Expanding Undergraduate Research Experience in a Biology Classroom with a Curriculum-based Approach.

Anuradha Srivastava[1] and [2]Anupam Pradhan,
[1]Queensborough Community College, Bayside, NY and [2]Kingsborough Community College, Brooklyn, NY.

There is convincing evidence that there are numerous benefits to exposing students to authentic undergraduate research activities. It is one of the approaches to embed experiential learning in their academic experiences. While mentored student research is a popular way to expose students to authentic research experiences, involvement in undergraduate research can be efficiently expanded using a curriculum-based approach. The Research in the Classroom initiative of CUNY represents one such way of bringing research experiences in a classroom setting by embedding it into a regular course. This method utilizes a systematic, collaborative active learning approach and allows the students to connect course content with applied research. The presenters will consist of biology faculty members from Queensborough and Kingsborough Community Colleges who have been awarded the 2018-2019 Research in the Classroom Idea Grant by RF CUNY. The development and implementation of their research projects in two different biology courses -Public Health and Microbiology at their colleges will be discussed. Attendees will learn about the classroom activities, assignments and assessment strategies carefully tailored to connect the research projects to course objectives.

The Effect of Rising Seal Level on Coastal Vegetation in South Carolina.

Richard Stalter, Rahema Nasary, Abiesha Smith, Khadija Yousuff, Jasmine Burkett, Teryn Mingo, Liya Thomas, Enxhi Seitllari, Kimarie Yap and Meryem Toppa,
St. John's University, Jamaica, NY.

In the present study, we examine the effect of rising sea level, a product of global warming, on the distribution of coastal vegetation at five sites in South Carolina. Rising sea level with a concomitant increase in water salinity and duration of submergence is changing plant diversity in coastal salt marsh and brachish marsh communities. We present data at three brackish marsh abandoned rice fields and a salt marsh at the Baruch Institute, Georgetown County, SC and a fifth site, a skeleton live oak stand in southeastern Beaufort County, South Carolina. Rising sea level has impacted vegetation at our 3 abandoned rice fields reducing vascular plant diversity at the two least saline sites. Air Port marsh and Alderly. *Sporobolus alterniflorus* a salt marsh associate is not present at Alderly, the least saline, abandoned rice field, testimony to rising sea level and increase water salinity. The more flood tolerant *Borrichia frutescens* is replacing *Sporobolus pumilus* at the salt marsh at Clam Bank. A stand of live oak, *Quercus virginiana*, has been replaced by salt marsh taxa, *Salicornia virginica* and *S. alterniforus* at Beaufort County site. Sea level has been rising at a rate of 3 mm/ yr since1930 and may rise at a greater rate in the future, impacting the vegetation of the aforementioned communities and additional coastal marsh and upland communities along the east coast of the United States.

Incorporating Undergraduate Research Experiences in Biology Classroom.

Mangala Tawde,
Queensborough Community College, CUNY, Bayside, NY.

Undergraduate Research (UR) experience is one of the most transforming experience students can have in their undergraduate years of education. To make it accessible to all students, incorporating authentic research experiences in the classroom is important and it is a major initiative at Queensborough community college and CUNY; we have institutionalized UR as a High Impact Practice. I have incorporated an authentic research project into the Microbiology course that I teach for allied health majors. The research project is to isolate and identify antibiotic-resistant microbes from diverse environments. Students are aware that antibiotic resistance is a serious concern in today's medicine, so they get interested and enthusiastic about participating in the research project. Students collect soil samples from various environments or locations of their choice and then they isolate and identify bacteria that may exhibit antibiotic resistance. The microbes isolated from diverse environments are identified by sequencing the 16s rRNA gene. The research experience is relevant and aligned to the course curricula, course learning objectives as well as college's General Education objectives. When surveyed, the students taking the research-based course expressed greater inclination towards STEM fields, they exhibited independent thinking, analytical reasoning, enhanced teamwork skills, and better scientific literacy.

A Revision of an Introductory Biology Laboratory.
William Velhagen, Agnes Berki and Darryl Aucoin,
Caldwell University, Caldwell, NJ.

At Caldwell University, the laboratory component of General Biology I had emphasized animal diversity while the lecture centered on molecules, cells, and genetics. We revamped the course curriculum by: (1) coordinating the laboratory coverage with that of the lecture, (2) incorporating data collection technology, and (3) emphasizing research and data analysis skills. We surveyed student opinions before and after the course revision. Students under the new curriculum were more interested in research, and in biochemistry and cell biology, and were more confident about speaking in front of their classmates, but these gains were not statistically significant. These students were also more confident about designing experiments, analyzing data, interpreting tables and graphs, and writing a lab report, and these gains were statistically significant. This project was supported by a grant from the Pfizer Undergraduate Research Endeavors Science Program.

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